Faculty of Resource Science and Technology

Phylogeography of Bornean Shrew (Family Soricidae: *Crocidura foetida*) inferred from Cytochrome *b* Gene and Species Distribution Modeling of Three Shrews from Malaysia Using Maximum Entropy Approach

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DECLARATION

I hereby declared that the thesis is based on my original work except for quotations and citations which have been duly acknowledged. This thesis has not been accepted for any degree and is not concurrently submitted in candidature for any other degree.

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(Julius anak William Dee)

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ABSTRACT

Malaysia is known as one of the biodiversity hotspot for small mammals including shrews given the complex geological and climatic settings. Lack of studies on genus *Crocidura* from Southeast Asia has led to the constraint of its taxonomic assessment. The distribution of three shrew species in Malaysia has been poorly known due to limited data. This thesis aims to determine the relationship between *Crocidura foetida* and other *Crocidura* species in Southeast Asia and also to predict the distribution of species from genus *Crocidur*a using Maximum Entropy (MaxEnt) modelling. The sampling for shrew was conducted in 25 sites across Malaysia using 100 pitfall traps per site between 2014 and 2017. Thirty-two individuals of shrew from genus *Crocidura* were captured from 13 out of 25 sites. *Crocidura foetida* recorded the highest number of species captured with 28 individuals and four other individuals recorded are *C. malayana*. Partial cytochrome *b* gene sequences were analysed and reveal noticeable intra-specific divergences among *C. foetida* (2.2-2.8%), which were collected in Sarawak. Principal component analysis conducted on the cranio-dental measurements of 15 samples revealed no distinct grouping between localities. The phylogeny with estimation time of divergence is produced in which species in genus *Crocidura* are grouped into several clades. The S-Diva analysis highlights six major dispersal events among genus *Crocidura.* We are able to compare the phylogeography relationship of the Bornean shrew, *C. foetida* using mtDNA cytochrome *b*. Three predicted distribution models of three shrew species from Malaysia were presented. *Crocidura foetida* and *C. monticola* prefers climate with low temperature in the dense montane forest while *C. malayana* is distributed abundantly across Peninsular Malaysia.
Keywords: *C. foetida*, phylogeography, mammals, species distribution modelling.

Filogeografi Cencurut Borneo (Keluarga Soricidae:* Crocidura foetida*) disimpulkan dari Genetik Cytochrome* b *dan Pemodelan Tiga Spesies Cencurut di Malaysia Menggunakan Pendekatan Maximum Entropi

ABSTRAK

Malaysia dikenali sebagai salah satu daripada titik panas biodiversiti untuk mamalia kecil termasuk cencurut memandangkan tetapan geologi dan iklim kompleks. Kekurangan kajian terhadap genus Crocidura *dari Asia Tenggara telah menyebabkan kekangan penilaian taksonominya. Pengagihan tiga jenis spesies cencurut di Malaysia kurang dikenali kerana data terhad. Tesis ini bertujuan untuk menentukan hubungan antara* Crocidura foetida *dan spesies lain* Crocidura *di Asia Tenggara dan juga untuk meramalkan pengedaran spesies dari genus* Crocidura *menggunakan pemodelan Maksimum Entropy (MaxEnt). Pensampelan untuk cencurut telah dijalankan di 25 tapak di seluruh Malaysia menggunakan 100 perangkap di antara tahun 2014 dan 2017. Tiga puluh dua individu cencurut daripada genus* Crocidura *ditangkap dari 13 daripada 25 tapak.* Crocidura foetida *merekodkan bilangan spesies tertinggi dengan 28 individu dan empat individu lain yang direkodkan ialah* C. malayana*. Susunan gen 'cytochrome* b*' telah dianalisis dan mendedahkan perbezaan dalam kalangan* C. foetida *(2.2-2.8%), yang dikumpulkan di Sarawak. Analisis komponen utama yang dijalankan ke atas pengukuran kranio-pergigian sebanyak 15 sampel menunjukkan tiada pengelompokan yang berlainan di antara kawasan. Filogeni masa penganggaran divergensi dihasilkan di mana spesies dalam genus* Crocidura *dikelompokkan ke dalam beberapa kumpulan. Analisis S-Diva menonjolkan enam peristiwa penyebaran utama dalam kalangan genus* Crocidura*. Kami dapat membandingkan hubungan filogeografi dari cencurut Borneo,* C. foetida *menggunakan cyt* b*. Tiga model pengedaran tiga spesies cencurut dari Malaysia telah dibentangkan.*

Crocidura foetida *dan* C. monticola *lebih suka iklim dengan suhu rendah di hutan paya padat manakala* C. malayana *diagihkan secara meluas di Semenanjung Malaysia.*

Kata kunci: C. foetida, *filogeografi, mamalia, model penyebaran spesies.*

TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

LIST OF ABBREVIATION

%	Percentage
µL	Micro Liter
ApoB	Apolipretein B
bp	Base pair
Cyt *b*	Cytochrome *b*
ENM	Ecological Niche Modelling
g	Gamma
ha	Hectares
Kya	Thousand years ago
mL	Milliliter
mm	Milli metre
mtDNA	Mitochondrial DNA
Mya	Million years ago
NP	National Park
ºC	Degree Celcius
PCR	Polymerase Chain Reaction
SDM	Species Distribution Model

CHAPTER 1

INTRODUCTION

1.1 Project Overview

Malaysia is known as one of the biodiversity hotspot for small mammals including shrews given the complex geological and climatic settings. Therefore phylogeographic studies of shrews have been the major focus in Southeast Asia over the last ten years to explore the biogeographic dynamics that shaped the diversity. With 335 species described in the world, shrew is composed of an ecologically diversified taxon (Wolsan & Hutterer, 1998). Shrew is classified into order Soricomorpha, family Soricidae. It can be categorised into two subfamilies, namely Soricinae (red-toothed shrews) and Crocidurines (white-toothed shrews) (Repenning, 1967). *Crocidura* is the largest genus, comprising of 170 species distributed in Europe, Asia, and Africa (Dubey et al., 2007). Genus *Crocidura* is of Indo-African origin, specifically Peninsular India and Ethiopian Africa (Aswathanarayana, 2003). It is not related to rodent, but is more closely related to moles. In Malaysia, there are 12 species of shrew, which are *Crocidura foetida, C. baluensis, C. monticola, C. fuliginosa, C. malayana, Suncus hosei, S. ater, S. murinus, S. etruscus, S. malayanus, Chimarrogale phaeura*, and *C. hantu*. They have short legs, small eyes, short fur, very active, nocturnal and a terrestrial insectivore. A sparsely-haired tail is also one of its physical characteristics (Payne et al., 1985). Shrew can be differentiated into its genus by counting the number of teeth. Shrew from the genus *Suncus* has nine teeth on each side of the upper jaw while *Crocidura* shrews only have eight teeth. One species of shrew, namely *Chimarrogale hantu* or Malaysian water shrew is mainly an aquatic animal, but partially terrestrial (Liat et al., 2013). The water shrew has webbed-feet which helps in movement in water and also has short and stiff hair on its feet. Shrews generally can be found widely across montane forest, riverine forest, dipterocarp forest, primary forest and urban area (Payne et al., 1985). Phylogenetic study is a study on the evolutionary relationships between species or individuals and is used to determine the evolutionary relationship between the organisms. Similarities and differences of different taxa are able to provide information and data to derive a hierarchical structure showing which taxa are most similar to others. Phylogeography is a study on the geographic distributions of closely related or within species (Avise, 2000). Study on phylogeography potentially integrates the information on geographical and historical components among and within species (Avise., 2000; Hoffman & Baker., 2003).

Shrews can be found distributed widely across Southeast Asia and probably represent a recent entrance to the region. According to Aswathanarayana (2003), genus *Crocidura* originated from Ethiopian Africa, other studies suggests that the highest species-level diversity is in Africa and the fossil date of shrews in Africa is much older than shrews in Eurasia, with *Crocidura* is believed to enter and colonise east Asia in a much recent time (Butler, 1998; Hutterer, 2005; Dubey et al, 2007). Dubey et al., (2007) estimated the evolution of shrew to take place about 5.4-10.7 mya in the event of divergence of Africa from Eurasia. Differences in genetic and morphology of species may be caused by the distribution of the species in wide ranges of habitat. This proved the density-dependent diversification that highlights the concept of correlation between speciation rates and ecological opportunity (Seehausen, 2007).

The predictive modelling of species distribution is becoming increasingly important in conservation, ecology, evolution and other fields (Corsi et al., 1999; Peterson & Cohoon, 1999; Scott et al., 2002; Peterson & Shaw, 2003). Species distribution modelling is able to provide precise assessments of species ranges. Species distribution models (SDMs), also known as ecological niche modelling (ENM) are numerical tools that can be used to obtain prediction of the distributions of flora and fauna across freshwater, marine and terrestrial realm, where extrapolation in space and time is sometimes being used (Elith & Leathwick., 2009). SDM is used to explore different settings that are useful in the study of biogeography, ecology and conservation (Babar et al., 2012). SDM is define as a model that connects species distribution data in an area with environmental information of the area. By combining data of species abundance and environmental parameters, SDMs can predict the potential area of species occurrence. Variables such as temperature, elevation, soil type, habitat suitability, human population density, precipitation seasonality, land-use classes, and spatial deforestation were used as the environmental parameters. Researchers and conservationists use SDM as they give full understanding of species distribution's prediction across any landscape and provide estimation of the area that is suitable for a species (Elith et al., 2002).

To predict the distribution of a species, several statistical models can be used (Franklin, 2009). Maximum Entropy (MaxEnt) algoritm is one of SDM tool that is commonly used among conservationists in giving prediction of species distribution based on a set of data and environmental predictors (Fourcade et al., 2014). It is one of the most efficient methods in handling the complex relationship of predictor variables and data (Elith et al., 2011). WorldClim database, which provide the environmental layers, provides continuous information on an extensive area (Kozak et al., 2008). The data exists in a presence-only type that can be used in MaxEnt (Fourcade et al., 2014).

In this study, we aim to assess the phylogeographic relationship of *Crocidura foetida* by comparing the specimens obtained from this study with other species in genus *Crocidura* from Southeast Asia based on molecular data and to predict the distribution of three shrew species from Malaysia using Maximum Entropy approach. The alternative hypotheses for the study are there are differences in genetic structures and cranio-dental characters for *C. foetida* with other species in genus *Crocidura* and the three shrew species from Malaysia has more specific distribution across Malaysia.

1.2 Problem Statement and Current Project

To date, most of the studies of shrews had focused on the materials from Peninsular Malaysia while neglecting materials from Borneo Island. However, no work has been done to predict the distribution of forest-dwelling shrew, specifically from the genus *Crocidura* and to explore the genetic variation within currently recognized *Crocidura* species in Malaysia with representative of material around Southeast Asia. Shrews from genus *Crocidura* in Malaysia is poorly studied due to difficulty in catching them (Omar et al., 2013). The process of species identification which is based solely on morphological characteristics may produce confusion on taxonomic status as several species may have overlapping measurements. To explain the phylogenetic relationship of shrew, specifically the genus *Crocidura*, molecular approach using mtDNA is essential in providing information regarding the taxonomic status of species, and also be able to identify cryptic species. Little information is available on the range and distribution of shrew in Malaysia. Previous studies suggest that shrews in Malaysia is a widespread and adaptable species (IUCN, 2016), but there is a need in reassessing the potential current distribution and its conservation status. According to the International Union for Conservation of Nature

(IUCN), the population trend of shrew in Malaysia is unknown as there is not much research on its diversity and distribution were done. Difficulty in catching shrew limits the museum and recent record. Limitation of data may result in low accuracy in most species distribution models. However, Maximum Entropy is suitable for shrew as its configuration appears to be performing well with only a few presence data available (Wilting et al., 2010).

Here, I present Chapter 1 as an introductory chapter to give the overview and objectives of the study. Chapter 2 provide relevant literature from the past research. Chapter 3 discusses the phylogeographic relationship of *Crocidura foetida* using mitochondrial DNA gene, Cytochrome *b*, and also the analysis of morphological measurements. In Chapter 4, the distribution modelling for each of the shrew from genus *Crocidura* in Malaysia were predicted using species distribution modelling. This modelling allows us to study the range of distribution and the potential area of the species occurrence. Finally, Chapter 5 summarizes the overall discussion and conclusion resulting from each chapter.

1.3 Research Objectives

This study aims

i. To determine the relationship between *Crocidura foetida* and other *Crocidura* species in Southeast Asia
ii. To predict the distribution of species from genus *Crocidur*a (*Crocidura foetida*, *C. malayana*, and *C. monticola*) using Maximum Entropy (MaxEnt) modelling.

CHAPTER 2

LITERATURE REVIEW

2.1 Family Soricidae – Genus *Crocidura*

Shrew is classified in order Soricomorpha, family Soricidae, It can be categorised into two subfamilies, namely Soricinae (red-toothed shrews) and Crocidurines (white-toothed shrews) (Repenning, 1967). Genus *Crocidura* or the White-toothed shrews are considered as the most diverse genus among mammals with no less than 164 species distributed widely in the Oriental, Ethiopian and Palearctic regions (Hutterer 1993; Wolsan & Hutterer, 1998; Motokawa et al., 2005). The shrew habitat can range from ground surface to underground burrow, desert to semi-aquatic, tropical rainforest to arctic tundra and highland to lowland (Abe, 1983; Churchfield, 1990; Ohdachi et al., 2006).

In Southeast Asia and East Asia, there are 43 recognised species known from the genus *Crocidura.* However, there are many lineages that are taxonomically confused and also cryptic that yet to be described still present in this region. In 2017, Demos et al distinguished *Crocidura umbra* from West and Central Java, comparing with larger *Crocidura* species known to the area. The newly described species overlap with *C. monticola*, however is larger on average in external measurements. Such finding within a common shrew species that is widely distributed in Southeast Asia, indicates that there are more to explore on the diversity of shrew in Southeast Asia than previously thought to be a similar species. Malaysia is home to 12 species of shrew, namely *Crocidura foetida, C. baluensis, C. monticola, C. fuliginosa, C. malayana, Suncus hosei, S. ater, S. murinus, S.*

etruscus, S. malayanus, Chimarrogale phaeura, and *C. hantu*. Two of the species, *C. foetida* and *C. baluensis,* are endemic to Borneo Island with the latter is constricted to the mountain of Kinabalu.

Shrew has short legs, small eyes and short fur. A sparsely-haired tail is also one of its physical characteristics (Payne et al., 1985). They are nocturnal, active and terrestrial insectivores. Shrew can be differentiated into its genus by counting the number of teeth. Shrew from the genus *Suncus* has nine teeth on each side of the upper jaw while *Crocidura* shrews only have eight teeth. One species of shrew, namely *Chimarrogale hantu* or Malaysian water shrew is mainly an aquatic animal, but partially terrestrial (Liat et al., 2013). In terms of weight, they range from *Suncus etruscus* of 1.3 g to *S. murinus* of 120 g (Churchfield, 1990). They are forest dwellers, preferring forest floors with the abundance of the leaf-litter as they can move around easily under the leaf to avoid predators. Its main diet is the insect's larvae and pupae and also earthworms (Yoshino & Abe, 1984).

In a study by Ford et al. (2005), two forest types were used to differentiate the habitat used by shrew species, namely mesic and xeric type. For mesic type, the forest includes red (*Picea rubens*), yellow birch (*Betula alleghaniensis*), and black cherry (*Prunus serotina*), located at the highest elevation. For xeric type, the forest includes several oak and hickory species, mixed pine located at the lowest elevation or the most exposed area. Riverine communities were dominated by black willow (*Salix nigra*) and alder (*Alnus serrulata*). A study by Rickart and Heaney. (2001), at Mount La Sal managed to trap *Sorex cinereus, S. monticolus,* and *S. nanus* in an area that was dry, and have no permanent surface water with a presence of grove of small aspen (*Populus tremuloides*). *Sorex palustris* was trapped around ponds, near springs, along streams and in wet meadows with 8-10% trap success recorded in its habitat. The information proved that only *S. palustris* has a high affinity towards water source compared to three other shrew species. According to Woodman et al. (2012), shrew species have greater success in trapping when pitfall were set up in the moister area, mossy hillside and an area with a high abundance of decaying tree fall. A heavily wooded montane forest with deep leaf litter also produced high number of capture. In general, shrews can be found across the dense forest with almost no limitation on the elevation. Kinabalu Shrew (*Crocidura baluensis*) was recorded in the montane forest of Mount Kinabalu with the altitude ranging from 1600 until 3700 m a.s.l (Hutterer, 2005).

Genus Crocidura or the White-toothed shrews has being studied poorly yet it is the most diverse group of shrew species (Heaney & Ruedi, 1994). In Borneo, there are three recognised species, namely *Crocidura foetida* (Bornean Shrew), *Crocidura baluensis* (Kinabalu shrew) and *Crocidura monticola* (Sunda shrew) (Ruedi, 1995).

Crocidura foetida (Peters, 1870)

Crocidura foetida is an endemic species to the island of Borneo that can be found distributed throughout the island (Figure 2.1). Ranging from the lowlands to mid-montane elevations, this species can be found in Sarawak and Sabah. The type locality of this species is in at Bengkayang, Indonesia (Ruedi, 1995). Three subspecies of *C. foetida* is recognised based on morphometric data, *C. f. foetida*, *C. f. kelabit* and *C. f. doriae* (Ruedi, 1995). *C. f. foetida* is the smallest and is found in the lowland, while *C. f. doriae* is larger and can be found in the upland of Mount Kinabalu up to 1200 m a.s.l (Cranbrook & Piper, 2007). Long-tailed form of *C. f. kelabit* is unique to the Kelabit highland in Sarawak (Cranbrook & Piper, 2007).

Figure 2.1: Adult *Crocidura foetida* caught in Borneo Highlands

Crocidura fuliginosa (Blyth, 1855)

This species can be found in Peninsular Malaysia and is presumed to have a large population in protected areas (IUCN, 2016). Confusion with *C. fuliginosa dracula* from the Indochina region was clarified with *C. fuliginosa* having a smaller external and skull dimension (Heaney & Timm, 1983). Most of the originally included 31 described taxa of *C. fuliginosa* species complex found in Southeast Asia is reduced to a single polymorphic species named *C. fuliginosa* based on the cranial and external morphology (Jenkins, 1976; Jenkins, 1982; Medway, 1977). This species can be commonly found at Cameron Highlands, Pahang, several individuals were caught in montane forest approximately 1500 m a.s.l (Ruedi et al., 1990). Most likely this species is restricted to highland forest and does not occur in other locality.

Crocidura malayana (Robinson & Kloss, 1911)

Crocidura malayana is the largest wild shrew in Peninsular Malaysia based on the average skull dimension (Ruedi, 1995). Endemic to Peninsular Malaysia and the adjacent islands located at the south of the Isthmus of Kra, it is a widespread species and is most common in Peninsular Malaysia, and recorded from lowland to montane forest up to 1200 m (Ruedi et al., 1990). According to Davidson (1984), this species occur in sympatry with *C. monticola* but seemingly not with *C. fuliginosa*. Robinson and Kloss synonymised the species under *C. fuliginosa* based on the size and colour variation of a single specimen (Medway, 1983; Corbet & Hill, 1992). In 1990, Ruedi et al managed to separate into at least two cryptic species in Peninsular Malaysia, with *C. malayana* having a polymorphic chromosome formula of 2n= 38-40 and *C. fuliginosa* (2n= 40).

Crocidura monticola (Peters, 1870)

This species is widely spread across Malaysia and is restricted in primary lowland and montane forests over an altitudinal range of 100-1144 m a.s.l (Corbet & Hill, 1992; Davidson, 1984) (Figure 2.2). *Crocidura maxi* is considered as subspecies of *C. monticola* (Ruedi, 1995). C*rocidura. neglecta*, a small forms of *Crocidura* from Indonesia is also synonymized with *C. monticola* (Jenkins, 1982; Ruedi, 1995; Hutterer, 2005). Confusion occurs due to inaccurate descriptions of type and lack of comparison with sufficient data from the large distribution range of *C. monticola* thus accurate taxonomic assessment could not been achieved. Therefore, there are still debate on the taxonomic status of *C. monticola* and its geographical distribution (Omar et al., 2013). However, a study by Omar et al in 2013 proved that *C. monticola* and *C. maxi* are two separate species.

Figure 2.2: Adult *Crocidura monticola* caught in Kubah National Park.

Crocidura baluensis (Thomas, 1898)

Crocidura baluensis or Kinabalu shrew can be found on the upper elevation of Mount Kinabalu, between 1600 until 3700 m a.s.l (Hutterer, 2005). This species has also been recorded in Kelabit Highlands above 1000 m a.s.l (Phillips, 2016). The distinction between *C. baluensis* and *C. foetida* can be observed from its size and lack of bristle hair at the base of the tail with long mid-dorsal fur (Thomas, 1898). Other distinct characteristics include bigger feet and footpads, ventral parts have silver colouration, light-tipped dorsal fur and larger skull (Ruedi, 1995).

2.2 Genetic studies on genus *Crocidura*

Within the Palearctic-Oriental region, they are only a few studies conducted on the taxonomy and phylogenetics of *Crocidura* shrews (Motokawa et al., 2005). Based on these studies, few theories about the evolutionary history and phylogenetic relationship has been suggested and tested (Maddalena & Ruedi, 1994; Ruedi et al., 1998; Motokawa et al., 2000; Biltueva et al., 2001; Ohdachi et al., 2004; Motokowa et al., 2005). About 150,000 years ago, the island of Cheju was separated from Kyushu (Western Japan) while its separation from the Korean Peninsula was 12,000 – 16,000 years ago (Ohshima, 1990; Ohdachi et al., 2004). Shrew species were unintentionally introduced onto Cheju Island by ships (Vogel & Sofianidou, 1996). The genetic divergence between populations from Cheju and Kyushu should be higher compared to those from Cheju and Korean Peninsular, if the population was naturally distributed (Ohdachi et al., 2004). According to Motokawa et al (2005), *Crocidura* shrews are a good model for studying animal phylogeny and biogeography due to its high level of molecular diversity, high chromosome variability and species richness. However, this also may lead to taxonomic confusion and complications due to limited sample size for comparisons.

Mitochondrial DNA (mtDNA) was used in this study as it has been widely used to study phylogenetic relationship, gene flow, and biogeography (Avise et al., 1987). The length of the molecular base pair (bp) of mammals typically ranging from 15000 to 17000 bp and differs in order, family and genus (Wallace, 1986). With a fast rate of evolution than the average nuclear gene, mitochondrial DNA (mtDNA) is significantly used in species genetic differentiation and higher order taxonomic study. According to Koscher et al (1989), mtDNA is used by most of the research studying evolutionary history as it effectively resolves species-level discrimination. Mitochondrial cytochrome *b* (cyt *b*) is one of the most sequenced genes across vertebrates (Figure 2.1) (Irwin et al., 1991; Lydeard & Roe, 1997; Moore & De-Filippis, 1997). Compared to another gene, the biochemistry of the protein product and the evolutionary dynamics of cyt *b* much better characterised (Esposti et al., 1993).

To study the genetic relationships of *C. monticola* species complex, Omar et al (2013) used two genes, mitochondrial cytochrome *b* (cyt *b*) and Apoliprotein B nuclear gene (ApoB). Mitochondrial lineages indicated that the phylogeography of *C. monticola* in Sundaland is more complex than as expected. Samples from Borneo and Peninsular Malaysia shows large genetic differences of up to 6.8 % of Kimura-2 parameter genetic distance, which is unexpected for intra-specific comparisons in shrews (Ruedi et al., 1998; Dubey et al., 2006; Bannikova et al., 2011; Omar et al., 2013).

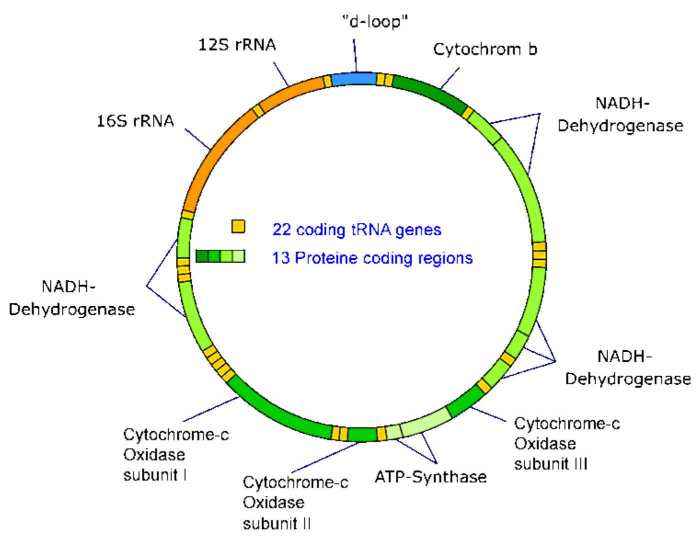

Figure 2.3: The mitochondrial DNA (mtDNA) map. Adapted and modified from Lott et al., 2007

2.3 Biogeography in Southeast Asia

Southeast Asia consists of Malaysia, Brunei, Indonesia, Singapore, Myanmar, Thailand, Laos, the Philippines, the Andaman and Nicobar Island (Woodruff, 2010). In 1876, Wallace categorised the region into Sundaic (Sunda Shelf), Indochinese, and the Philippines zoogeographic sub regions with the fourth sub regions situated to the east and consist of mostly Australian biota, called Wallacea. World Wildlife Fund (WWF) has proposed a more detailed classification of the biota into smaller units called ecoregions; 28 Sundaic, 31 Indochinese and Philippine ecoregions (Wikramanayake et al., 2002; Woodruff, 2010). Countries in the region are one of the richest in terms of plants, mammals, and birds species.

Speciation rates were believed to be adjusted by altering barriers to dispersal potentially by geological and climatic processes (Esselstyn et al., 2009). The repeated fluctuation of sea level during the Pleistocene and the volcanic uplift during the Miocene-Pliocene resulted in the fragmented land connections among islands (Esselstyn et al., 2009). These historical processes encourage evolutionary diversification by allopatric speciation (Heaney, 2000; Steppan et al., 2003; Jansa et al., 2006; Outlaw & Voelker, 2008; Esselstyn et al., 2009). Sunda Shelf consists of Java, Sumatra, Palawan, Borneo and the Malay Peninsular and was revealed as dry land in numerous occasions during Pleistocene glacial maxima (Rohling et al., 1998). Rising sea levels during interglacial has flooded the shelf (Dunn & Dunn, 1977; Heaney, 1978; Heaney, 1984). Sunda Shelf is one of the largest geographic features, however hidden below sea level in present time (Woodruff, 2010). It is an important source for the Philippines and Wallacea as their animal and plant species were originated from Sunda Shelf (Dickerson, 1928; Corbet & Hill, 1992).

Shrew from Southeast Asia is a perfect model to test the impacts of geological climatic history on phylogenetic diversification due to its wide distribution across the region and may represent a recent arrival. The shrews may have originated from Africa or western Eurasia before establishing a population in East Asia (Butler, 1998; Storch et al., 1998; Hutterer, 2005; Dubey et al., 2007, Esselstyn et al., 2009). The divergence between African and Eurasian *Crocidura* is estimated at 5.4-10.7 million years ago, indicating that the evolution of shrew in Southeast Asia may take place approximately 10 million years ago (Hall, 1998; Hall, 2002; Esselstyn et al., 2009).

In the Pleistocene era, the vegetation types and its distribution were widely influenced by the climatic condition as the seasonal forest in Java and Southeastern Borneo extended due to the decreasing moisture content in monsoonal winds (Heaney, 1991). The growth of rainforest and different abiotic conditions results in various natural vegetations that is present today such as tropical seasonal forest, deciduous forest, montane forest, mangrove forest and tropical rainforest (Corlett, 2009).

2.4 Morphological Analysis of *Crocidura feotida*

The dispersal of a species can be perceived more by morphological data analysis. The overall body size, condyloincisor length and body weight are significantly correlated with the distance from mainland or large island (Kitchener et al., 1994). Three subspecies of *C. foetida* has been distinguished based on its morphometric data. *Crocidura foetida foetida* occurred in the lowlands; *C. f. doriae*, a larger subspecies found at the upland of Mount Kinabalu; and *C. f. kelabit*, specifically found at the Kelabit upland (Ruedi, 1995).

According to Ruedi (1995), the skull of *C. f. foetida* is narrower and its cranial dimensions are usually smaller compared to other medium-sized shrews found in Borneo.

Studies have been done previously on the morphological analysis of shrews. Compared with *C. fuliginosa, C. attenuata* has smaller measurements as it commonly smaller in size and shorter tail. It also measures differently compared to *C. horsfieldii* with *C. attenuata* having a larger head (Heaney & Timm, 1983). Demos et al. (2016) described a new species captured in Mount Gede, West Java based on its cranial measurements and genetic data. *Crocidura umbra* is a newly described shrew with a type locality from Mount Gede (1611m and 1950m elevation). The new species is larger than the sympatric population of *C. monticola* based on 11 cranial characters and tail length.

2.5 Species distribution modelling

Species distribution modelling has become a widely used technique to identify suitable habitat and to evaluate the species distribution of diverse taxa (Singh, 2013). Species distribution models (SDMs) is a tool to estimate and evaluate the relationship between the environmental variables of a site and the species distribution record of the site (Franklin, 2009). The utilisation of SDMs include in biogeography, ecology and conservation biology (Elith & Leathwick, 2009). One of the models that has been widely used is Maximum Entropy (MaxEnt), a model that utilise presence-only data (Phillips et al., 2006; Phillips & Dudik, 2008).

Due to its highly competitive predictive performance compare with other high performing methods, MaxEnt has been extensively utilised with various aim and purpose, including to predict the current distribution of species to obtain information on conservation planning and risk assesments (Tinoco et al., 2009; Tittensor et al., 2009); to understand more on genetic diversity, phylogeography, and evolutionary niche dynamics (Lamb et al., 2008; Young et al., 2009); to predict the potential distribution of invasive species (Ward, 2007); to observe distribution for any patterns of endemism or vicariance (Cordelier & Pfenninger., 2009; Carnaval & Moritz., 2008); and to understand more on environmental correlation with species occurences (Wollan et al., 2008; Monterroso et al., 2009).

Rare species that have small or specific geographical distributions due to its unique habitat preferences provides particular challenges in modelling the species (Williams et al., 2009). These species often have small sample sizes, thus may affect model robustness (Stockwell & Peterson, 2002; Pearson et al., 2007; Wisz et al., 2008, Williams et al., 2009). There are also possibilities to wrongly identify the small climatic distribution as a basic niche limitation as it can actually reflect other ecological limitation such as dispersal barrier and biotic interactions (Schwartz et al., 2006; Wisz et al., 2008). Often, these rare species that are habitat specialist have a patchy distribution. These create big challenges for SDM as it is meant to distinguish an overall extent of a species (Pearce et al., 2001; Seoane et al., 2005; McPherson & Jetz, 2007). Species distribution modelling is able to discover new species occurrence where models show high probability and proving that the model able to discriminate between the background matrix and the potential habitat in a fine scales (Williams et al., 2009). With adequate and suitable environmental variables, paired with a high number of presence-only data, better results can be generated (Williams et al., 2009). However, a broader geographical range is recommended to identify a suitable area outside the historic distributions (McLachlan et al., 2007). Modelling rare species can become more accurate with the increase in sample size as more occurrences available, the more complete the niche of the species being described (Stockwell & Peterson, 2002; Hernandez et al., 2006; Breiner et al., 2015).

Mapping the potential suitable habitat and geographical distribution of a species is a technique which is still new in Malaysia. Flagship species such as the Malayan Sun Bear (*Helarctos malayanus*) and the Asian tapir (*Tapirus indicus*) were among few faunal species that has been modelled due to its lack of information in distribution (Nazeri et al., 2012; Clements et al., 2012). In 2012, Nazeri et al conduct a research to predict the distribution of *H. malayanus* in Peninsular Malaysia using MaxEnt modelling. Currently this species is listed as Vulnerable according to the IUCN Red List of Threatened Species; however there is little knowledge on its distribution. Based on the climatic, topographic and biological variables along with the presence record of the species, *H. malayanus* has a strong preference towards dense and primary forest (Nazeri et al., 2012).

The Malayan tapir or *Tapirus indicus* has been threatened by forest fragmentation and habitat loss, alongside hunting by the locals in Peninsular Malaysia (Khan, 1997; Jasmi, 2000; Holden et al., 2003; Corlett, 2007; Clements et al., 2012). MaxEnt is used to predict the range of *T. indicus* distribution in Peninsular Malaysia, in which the data obtained, can be used in updating the IUCN range map for *T. indicus* in Malaysia (Clements et al., 2012). The results suggest that the occurrence of *T. indicus* is decreasing swiftly in areas with high temperature (>26ºC). This species also prefers tropical montane forest as its habitat (Clements et al., 2012).

CHAPTER 3

PHYLOGEOGRAPHY OF THE BORNEAN SHREW (FAMILY SORICIDAE: *CROCIDURA FOETIDA*) INFERRED FROM CYTOCHROME *B* GENE SEQUENCES AND CRANIO-DENTAL DATA

3.1 Introduction

There are more than 210 known species from the genus *Crocidura* that has been diversified in Africa and Eurasia (Hutterer, 1993; Wolsan & Hutterer, 1998; Motokawa et al., 2005; Dubey et al., 2007). Insufficient sampling on the Sunda Shelf (Borneo, Java, Sumatra, the Philippines and many other smaller islands) has inhibited the taxonomic assessments of genus *Crocidura* (Demos et al., 2016). One of the described species is *Crocidura foetida* (Peters, 1870), and its type locality is from West Kalimantan (Ruedi, 1995). This species has three subspecies, namely *C. f. foetida, C. f. doriae,* and *C. f. kelabit* which were described based on morphometric data (Ruedi, 1995). Other white-toothed shrews that can be found in Malaysia are *C. fuliginosa*, *C. monticola*, *C. malayana*, and *C. baluensis*. *Crocidura monticola* can be found across Malaysia while *C. baluensis* has only been recorded at the mountainous area of Kinabalu and Kelabit Highlands.

Quaternary climatic fluctuations have been widely accepted to shape the genetic diversity of terrestrial biota of the Holarctic (Hewitt, 2000). Barriers such as mountain ranges and seas isolate the populations in different glacial refugia and limiting the post-glacial migration routes (Taberlet et al., 1998; Hewitt, 1999; Dubey et al., 2006). There was much cooler temperature during the late Pleistocene climate in Southeast Asia, with 5-6ºC below current values (Cranbrook & Piper, 2008). Theoretically, the temperature near sea-level during the late Pleistocene is similar to the temperature at high altitudes (400-1000m) at present time (Cranbrook & Piper, 2008). Following the last glacial maximum (18 Kya), the increase in temperature may assist in the restoring of the lowland mixed dipterocarp forest.

Ruedi (1995) identified three subspecies of *C. foetida* based on morphometric data. The subspecies, *C. foetida foetida*, *C. foetida doriae*, *C. foetida kelabit* occupy different elevations and area; *C. foetida foetida* in the lowlands, *C. foetida doriae* in the highlands, and *C. foetida kelabit* can only be found in Kelabit Highlands of Sarawak. The study benefited from 25 separate mandibles that were excavated from the Niah Caves complex. Results indicated that zooarchaelogical data support the taxonomic separation between the lowland and highland population.

There are little information known for *C. foetida* and its subspecies. Comparison of this species with other *Crocidur*a from Southeast Asia could provide information on the geographical distributions of genus *Crocidura* in Sundaland. Genetic data obtained in this study may help in discussing the phylogenetic relationship of *C. foetida*.

3.2 Materials and Methods

3.2.1 Study sites

Shrew sampling were conducted between 2014 and 2017 in protected and non-protected areas throughout Malaysia. A total of 25 sites were chosen, with nine in Peninsular Malaysia, two in Sabah and 13 in Sarawak (Figure 3.1) (Table 3.1).

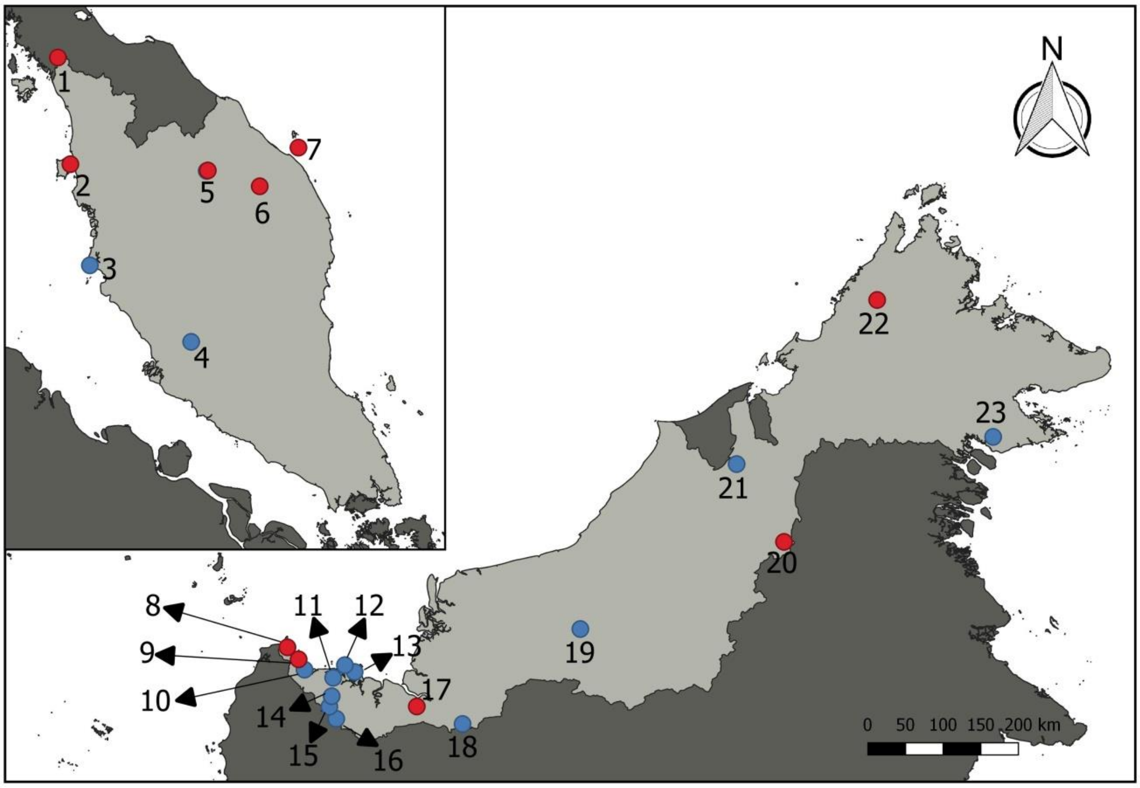

Figure 3.1: The study sites of shrew sampling. (1 = Wang Kelian State Park, 2= Penang Island, 3 = Pulau Pangkor, 4 = Ulu Gombak Forest Reserve/Sungai Dusun, 5 = Gua Ikan/Gunung Stong, 6 = Lawit, 7 = Pulau Bidong, 8 = Samunsam Wildlife Sanctuary, 9 = Sematan, 10 = Gunung Gading National Park, 11 = Dered Krian National Park, 12 = Bako National Park, 13 = Santubong National Park, 14 = Kubah National Park, 15 = Bungoh Range National Park, 16 = Mount Penrissen, 17 = Gunung Lesung National Park, 18 = Kumpang Langgir, 19 = Nanga Benin, 20 = Long Banga, 21 = Mulu National Park, 22 = Kinabalu Park, 23 = Tawau Hills Park.

Table 3.1: The selected study sites with its habitat type and status of the sites. *Long Banga is in the Heart of Borneo

Study sites	Habitat type	Status
Peninsular Malaysia		
Ulu Gombak Forest Reserve, Selangor	Mixed dipterocarp forest, semi-urban area	Protected
Sungai Dusun, Selangor	Riverine forest, mixed dipterocarp forest	Protected
Gua Ikan, Dabong, Kelantan	Limestone forest	Not protected
Gunung Stong, Kelantan	Montane forest, mixed dipterocarp	Protected
Lawit, Tasik Kenyir, Terengganu	Mixed dipterocarp forest	Protected
Pulau Bidong, Terengganu	Beach forest	Protected
Wang Kelian State Park, Perlis	Limestone forest	Protected
Pulau Pangkor, Perak	Secondary forest, semi-urban area	Not protected
Penang Island	Secondary forest, semi-urban area	Not protected
Sarawak		
Kumpang Langgir, Engkelili	Mixed dipterocarp forest	Not protected
Kubah National Park, Matang	Montane forest	Protected
Gunung Gading National Park, Lundu	Montane forest	Protected
Sematan, Lundu	Secondary forest, semi-urban area	Not protected
Mount Penrissen, Padawan	Montane forest	Not protected
Dered Krian National Park, Bau	Limestone forest, mixed dipterocarp forest	Protected
Santubong National Park, Kuching	Montane forest, mixed dipterocarp forest	Protected
Mulu National Park, Miri	Montane forest, limestone forest	Protected
Samunsam Wildlife Sanctuary, Lundu	Mangrove forest, riverine forest, mixed dipterocarp forest	Protected
Bako National Park, Kuching	Mangrove forest, riverine forest, mixed dipterocarp forest, cliff	Protected
Gunung Lesung National Park, Engkelili	Montane forest, secondary forest	Protected
Long Banga, Miri	Montane forest, mixed dipterocarp forest	Not protected*
Bungoh Range NP	Montane forest, mixed dipterocarp forest	Protected
Nanga Benin, Kapit	Montane forest, mixed dipterocarp forest	Not protected
Sabah		
Taman Kinabalu	Montane forest	Protected
Taman Bukit Tawau	Mixed dipterocarp forest	Protected

3.2.2 Sampling methods

Sampling was conducted at an area with high amount of leaf litter, moist and secluded area. Forest-dwelling shrews were captured using pitfall traps (Yu et al., 2001; Rickart & Heaney, 2001; Ford et al., 2005; Nicolas et al., 2009; Krysˇtufek et al., 2011; Woodman et al., 2012). One hundred pitfall traps (height = 248mm, width = 232 mm) were buried every five metres. Root digger was used to dig a hole with the height and diameter equal to the pitfall trap, and the trap was put inside the hole. Pitfall traps were buried in a straight line or in a grid formation and aluminium or canvas fencing was deployed to increase the capture rate. The traps were checked in the morning around 1000 every sampling day. Collected samples were identified based on Payne et al., (1985), Francis (2008), and Phillips and Phillips (2016). The external measurements and weight were taken using callipers and Pesola spring balance. Captured individuals were euthanised using chroloform and the muscle and liver tissue were isolated and stored in 95% ethanol for genetic analysis. The whole body of the samples were preserved in 70% ethanol.

3.2.3 Molecular methods

The DNA extraction was conducted using DNeasy Blood and Tissue Kit by QIAGEN. Approximately 25 mg of muscle or liver tissue were minced finely and placed into a 1.5 mL microcentrifuge tube. 20 µL of Proteinase K is added into the tube and is mixed by vortex. The tube containing minced tissue and Proteinase K is incubated at 56ºC until completely lysed. During the incubation period, the tube is occasionally vortexed. 200 µL of Buffer AL is added and is mixed thoroughly by vortexing. The tube is then being incubated again for 10 min at 56ºC. Then, 200 µL of absolute ethanol is added and the tube is mixed by vortex. The mixture is pipetted into a DNeasy Mini spin column that is placed in a 2 ml collection tube. After that, the tube is centrifuged at 8000 rpm for 1 min. The flow-through and collection tube are discarded. The spin column is placed into a new 2 ml collection tube. Then, 500 µL of Buffer AW2 is added and the collection tube is centrifuged for 3 mins at 14000 rpm. The flow-through and collection tube are discarded. The spin column is then transferred to a new 2 ml centrifuge tube. The DNA is eluted by adding 200 µL Buffer AE to the center of the spin column membrane. The tube is incubated for 1 min at room temperature. After the brief incubation, the tube is centrifuged for 1 min at 8000 rpm.

The Polymerase Chain Reaction (PCR) amplification was conducted by using a single mitochondrial gene, Cytochrome *b* (Primer: LGL 765, LGL 766). This method successfully amplified approximately 1200 base pair (bp) of Cytochrome *b* (Cyt *b*) gene by using Mastercycler Nexus X2 (Eppendorf) thermal cycler. The primer details are listed in Table 3.2 and the master mix for the PCR reaction is shown in Table 3.3. The amplification parameter of the desired gene region was listed in Table 3.4. Gel electrophoresis and visualisation was conducted using 1% agarose gel stained with Ethidium bromide (EtBr) to examine the successful PCR product amplification. Purification and sequencing of the successful PCR product were done by a private laboratory.

Table 3.2: Summary of primers and annealing temperature used

Locus	Primer name	5' 3'	Annealing temperature (°C)	References
CytB	LGL 765	GAAAAACCAYCGTTGTWATTCA ACT	50	Bickham et al., 1995
	LGL 766	GTTTAATTAGAATYTYAGCTTTG GG	50	

Table 3.3: Component of mastermix preparation for each reaction of Cyt b gene using GoTaq® Flexi DNA polymerase PCR kit (Promega Co.)

Component	1X Reaction (25 µl)
5x reaction buffer	5.0
$MgCl_2$, (25 mM)	1.5
dNTP mix (10 mM)	0.5
Forward primer (10 mM)	1.0
Reverse primer (10 mM)	1.0
ddH_20	13.8
Template DNA	2.0
Taq polymerase, (5u/µl)	0.2

Table 3.4: Amplification parameter for Cytochrome *b* gene

Step	Temperature (^oC)	Time	No.cycles
Pre-denaturation	93	5 minutes	1
Denaturation	93	45 seconds	
Annealing	50	45 seconds	30
Extension	72	1 minute	
Final extension	72	1 minutes	1
Soak	4	∞	

3.2.4 Phylogenetic analyses

The results of DNA sequencing were used to construct phylogenetic analysis. Sequencher version 4.1.4 (Gene Codes Corporation, 2002) was used to visualise and to check the quality of the nucleotide bases of DNA sequences. Nucleotides deemed as 'noise' (N) were replaced or cleaned by choosing the sequence peak shown in the chromatogram. The cleaned sequences alongside additional sequences obtained from GenBank were then aligned using ClustalW model. Table 3.5 shows the sequences used in this study. Molecular Evolutionary Genetics Analysis version 7.0 software (MEGA7) was used to convert the aligned "FAST-All" or "FASTA" file into MEGA file.

Using MEGA 7.0 software, a total of 932 base pairs of Cyt *b* partial sequences were used in constructing phylogenetic analysis. According to the best-fit substitution model, the Tamura-Nei (TN93) using discrete Gamma distribution (G) and also assuming that a certain fraction of the sites are evolutionary invariable (+I) is the best to describe the substitution pattern for the analysis as the model has the lowest Bayesian Information Criterion (BIC) score (Akaike Information Criterion). Neighbour-Joining (NP), Maximum Likelihood (ML), and Maximum Parsimony (MP) trees were constructed with 1000 bootstrap replicates.

Bayesian Inference (BI) was conducted using Bayesian Evolutionary Analysis Sampling Trees (BEAST) software version v2.5.0 (Bouckaert et al., 2014), with Tamura-Nei model of substitution. The nexus file of the aligned sequences was loaded into Beauti v2.4.7. The molecular clock was set to Strict Clock along with Calibrated Yule Model priors. Priors were set according to the divergence time following Dubey et al. (2008). Two calibration points were used; the split between Eurasian and African *Crocidura* that occurred around 8.0 Myr (95% CI; 5.4-10.7) and the split between *C. fuliginosa* and *C. paradoxura* and other *Crocidura* in Sunda Shelf (4.39 Mya). Metropolis-Coupled Markov Chain Monte Carlo (MCMCMC) was implemented with 100 million generations with trees sampled every 1000 generations. Its effective sample size (ESS) and posterior values were checked using Tracer software v1.6v (Rambaut & Drummond, 2007). The first ten percent of the 100 million trees were discarded. The remaining trees were annotated to produce one consensus tree using TreeAnnotater software and the consensus tree was viewed using FigTree software.

Table 3.5: The details of samples used for cytochrome *b* mtDNA phylogenetic analyses. Bold indicates specimen obtained from this study.

Species	Location	Genbank accession no/**Specimen no**.
C. batakorum	Palawan Island	FJ813977
C. beccarii	Sumatra	KX469583
C. brunnea	Java	KF283272
C. foetida	Borneo Highland, Sarawak	**BH15-063**
C. foetida	Bako, Sarawak	**BNP16-001**
C. foetida	Dered Krian, Bau, Sarawak	**DKB16-035**
C. foetida	Engkelili, Sarawak	**ENG16-133**
C. foetida	Lundu, Sarawak	**GGNP15-001**
C. foetida	Kubah, Sarawak	**KWT15-007**
C. foetida	Mulu, Sarawak	**MNP17-050**

Table 3.5: continued

C. foetida	Nanga Benin, Kapit, Sarawak	**NB14-002**
C. foetida	Dered Krian, Bau, Sarawak	**DKB16-036**
C. foetida	Santubong, Sarawak	**SNP16-036**
C. foetida	Matang, Sarawak	**VM16-010**
C. foetida doriae	Bintulu, Sarawak	FJ814053
C. foetida doriae	Bintulu, Sarawak	FJ814055
C. fuliginosa	Yunnan, China	GU981271
C. fuliginosa	Vietnam	AB175079
C. fuliginosa	Taiwan	GU358522
C. fuliginosa	Peninsular Malaysia	FJ813925
C. fuliginosa	Peninsular Malaysia	FJ813924
C. grayi	Philippines	FJ813874
C. lepidura	Sumatra	FJ814023
C. lepidura	Sumatra	FJ814022
C. malayana	Ulu Gombak, Peninsular Malaysia	EF524619
C. malayana	Ulu Gombak	DQ630831
C. malayana	Gua Ikan, Peninsular Malaysia	**GI15-047**
C. malayana	Pangkor Island, Peninsular Malaysia	**PPS15-043**
C. malayana	Sungai Dusun, Peninsular Malaysia	**SD15-015**
C. mindorus	Philippines	FJ813843
C. monticola	Java	KF283271
C. neglecta	Sumatra	KX469629

Table 3.5 continued

C. negrina	Philippines	FJ813962
C. nigripes	Sulawesi	FJ813926
C. orientalis	Java	FJ814029
C. palawanensis	Palawan Island	FJ813978
C. panayensis	Philippines	FJ813950
C. paradoxura	Sumatra	KF801079
C. umbra	Java	KF283233
S. murinus	Perak, Peninsular Malaysia	LU14191
Species A	Kinabalu, Sabah	**TK16-001**
Species B	Lundu, Sarawak	**GGNP16-006**
Species C	Kubah, Sarawak	**KWT15-019**

3.2.5 Morphological measurements

Fifteen skulls of *C. foetida* captured across Sarawak were used in the craniodental measurement analysis (Table 3.6). The skull measurements were measured using Mitutoyo digital calliper. The measurements taken were mandible length (MAL), condyle to glenoid length (CTG), lower tooth row length excluding first incisor (IM3I), greatest length of skull (GLS), post palatal length (PPL), post palatal depth (PPD), upper tooth row length (IM3S), length of upper molariform teeth (PM3), rostral length (ROL), rostral breadth (ROB),breadth of braincase (BB), interorbital breadth (IOB), palatal width at second molar (M2B), and palatal width at third molar (M3B) (Heaney and Timm, 1983; Ruedi, 1995).

Table 3.6: Skull specimens used in craniodental measurements

No	Specimen no	Species	Location
1	BRNP17-052	*C. foetida*	Bungo Range NP, Kuching, Sarawak
2	DKB16-035	*C. foetida*	Dered Krian NP, Kuching, Sarawak
3	DKB16-036	*C. foetida*	Dered Krian NP, Bau, Sarawak
4	DKB16-039	*C. foetida*	Dered Krian NP, Bau, Sarawak
5	DKB16-041	*C. foetida*	Dered Krian NP, Bau, Sarawak
6	GGNP15-001	*C. foetida*	Gunung Gading NP, Lundu, Sarawak
7	GGNP15-002	*C. foetida*	Gunung Gading NP, Lundu, Sarawak
8	GGNP15-098	*C. foetida*	Gunung Gading NP, Lundu, Sarawak
9	GGNP16-001	*C. foetida*	Gunung Gading NP, Lundu, Sarawak
10	KWT15-021	*C. foetida*	Kubah NP, Kuching, Sarawak
11	MNP17-050	*C. foetida*	Mulu NP, Miri, Sarawak
12	NB14-002	*C. foetida*	Nanga Benin, Kapit, Sarawak
13	SNP16-036	*C. foetida*	Santubong NP, Kuching, Sarawak
14	SNP16-037	*C. foetida*	Santubong NP, Kuching, Sarawak
15	SNP16-043	*C. foetida*	Santubong NP, Kuching, Sarawak

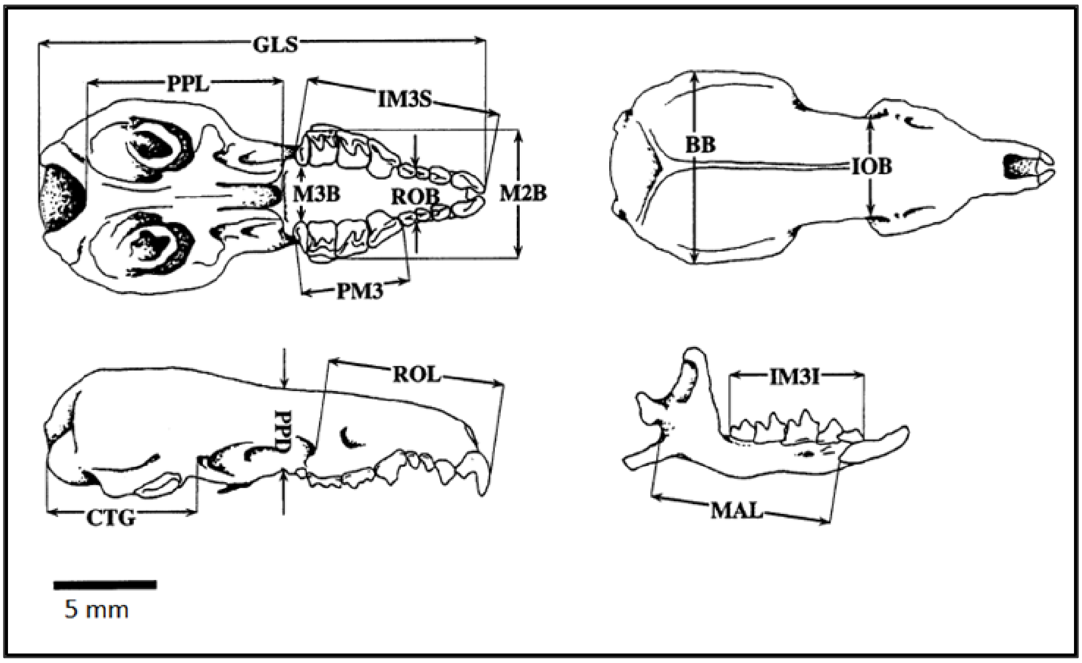

Figure 3.2: Fourteen cranio-dental measurements of shrew (Figure adapted from Omar et al., 2013)

3.2.6 Reconstruct Ancestral State in Phylogenies (RASP)

The possible ancestral ranges for these species were predicted using Reconstruct Ancestral State in Phylogenis (RASP) software (Yu et al., 2015). The collective and consensus trees obtained from BEAST software were loaded into the software and Statistical Dispersal-vicariance Analysis (S-Diva) were performed to describe the evolutionary histories of studied species. The plausible routes of radiation were generated and be used to relate with the past geographical events in Southeast Asia.

3.3 Results

Thirty-two individuals of shrew from genus *Crocidura* were captured from 13 out of 25 sites selected for shrew sampling. These specimens were mainly captured in montane and primary forest, with little to no anthropogenic activities present. Only two species were recorded in this study. *Crocidura foetida* recorded the highest number of species captured with 28 individuals and four other individuals recorded are *C. malayana*. All of *C. foetida* individuals were captured from ten sites across Borneo while *C. malayana* were recorded from three sites across Peninsular Malaysia.

3.3.1 Phylogenetic tree

3.3.1.1 Cytochrome *b*

All 43 partial cytochrome *b* gene sequences were analysed using MEGA7.0 software. Total lengths of 934 base pairs of mitochondrial sequences were obtained. The final alignment consists of 601 conserved sites, 268 parsimony-informative sites, and 333 variable sites. The average nucleotide composition without outgroup for thymine (T), cytosine (C), adenine (A) and guanine (G) are 30.9%, 26.4%, 28.7% and 13.9% respectively (Table 3.7). Thymine (T) has the highest average composition of nucleotide wtith 32.7%, detected from species B while the lowest is guanine (G) with 13.6% from *C. foetida* and *C. nigripes.*

Corrected Kimura-2 parameter (K2P) pairwise genetic distances among genus *Crocidura* are shown in Table 3.8. They reveal noticeable intra-specific divergences among *C. foetida* (2.2-2.8%), which were collected in Sarawak. The highest inter-specific divergence (20.7-21.4%) was observed between *C. foetida* and *C. batakorum*. The data were further analysed by implying three models of phylogenetic tree and as the result, all four models showed trees with similar topology (Figure 3.3).

Table 3.7: Comparison (%) of nucleotide composition inferred from cytochrome *b* mtDNA gene sequence among small shrew species analysed in the phylogenetic tree with the outgroup. (T = Thymine, U = Uracil, C = Cytosine, A = Adenine, G = Guanine)

	Species (Genbank accession no/Specimen no)	T(U)	C	A	G	Total
1	*Crocidura foetida* (BH15-063)	31.4	25.9	29.0	13.7	934
2	*Crocidura foetida* (BNP16-001)	31.4	25.9	29.0	13.7	934
3	*Crocidura foetida* (DKB16-035)	31.4	25.9	29.0	13.7	934
4	*Crocidura foetida* (ENG16-133)	31.7	25.7	29.0	13.6	934
5	*Crocidura foetida* (SNP16-036)	31.3	25.9	29.0	13.7	933
6	*Crocidura foetida* (GGNP15-001)	31.3	26.0	28.9	13.8	934
7	*Crocidura foetida* (VM016-010)	31.3	26.0	28.9	13.8	934
8	*Crocidura foetida* (KWT15-007)	31.4	25.9	29.0	13.7	934
9	*Crocidura foetida* (DKB16-036)	31.4	25.9	28.9	13.8	934
10	*Crocidura foetida doriae* (FJ814053)	30.7	26.7	28.7	13.9	934
11	*Crocidura foetida doriae* (FJ814055)	30.6	26.8	28.7	13.9	934
12	*Crocidura foetida* (NB14-002)	31.2	26.2	28.7	13.9	934
13	*Crocidura foetida* (MNP17-050)	30.7	26.7	28.8	13.8	934
14	*Crocidura mindorus* (FJ813843)	30.1	27.0	28.9	14.0	934
15	*Crocidura grayi* (FJ813874)	30.0	27.0	28.9	14.1	934
16	*Crocidura fuliginosa* (FJ813924)	31.8	25.6	28.3	14.3	934
17	*Crocidura fuliginosa* (FJ813925)	31.7	25.7	28.4	14.1	933
18	*Crocidura fuliginosa* (GU358522)	32.0	25.5	28.5	14.0	934
19	*Crocidura fuliginosa* (AB175079)	31.8	25.7	28.3	14.2	934
20	*Crocidura fuliginosa* (GU981271)	32.1	25.3	28.1	14.6	934
21	*Crocidura palawanensis* (FJ813978)	29.3	27.5	29.1	14.0	934
22	*Crocidura nigripes* (FJ813926)	30.6	27.0	28.8	13.6	934
23	*Crocidura panayensis* (FJ813950)	30.4	26.9	28.6	14.1	934
24	*Crocidura negrina* (FJ813962)	30.1	27.1	28.5	14.3	934
25	*Crocidura batakorum* (FJ813977)	31.8	26.8	27.7	13.7	934
26	*Crocidura lepidura* (FJ814022)	30.3	27.0	28.7	14.0	934
27	*Crocidura lepidura* (FJ814023)	30.4	26.9	28.8	13.9	934
28	*Crocidura orientalis* (FJ814029)	29.9	27.2	28.8	14.1	934
29	*Crocidura malayana* (PPS15-043)	30.5	26.6	29.0	13.9	934
30	*Crocidura malayana* (SD15-015)	30.4	26.7	29.1	13.8	934
31	*Crocidura malayana* (GI15-047)	30.4	26.7	29.1	13.8	934
32	*Crocidura malayana* (DQ630381)	30.6	26.4	29.1	13.8	934
33	*Crocidura malayana* (EF524619)	30.6	26.4	29.1	13.8	934
34	*Crocidura umbra* (KF283233)	29.1	28.7	28.4	13.8	934
35	*Crocidura monticola* (KF283271)	30.6	27.2	28.4	13.8	934
36	*Crocidura brunnea* (KF283272)	30.9	26.1	29.0	13.9	934
37	*Crocidura beccarii* (KX469583)	30.4	26.8	28.8	14.0	934
38	*Crocidura paradoxura* (KF801079)	30.8	26.4	28.9	13.8	934
39	*Crocidura neglecta* (KX469629)	31.7	26.0	28.1	14.2	934
40	Species A (TK16 001)	31.6	26.1	28.2	14.1	934
41	Species B (GGNP16 006)	32.7	24.8	28.4	14.1	934
42	Species C (KWT15 019)	30.8	26.9	28.1	14.2	934
43	*Suncus murinus* (LU14191)	32.3	25.7	27.7	14.2	934
	Average (In group)	30.9	26.4	28.7	13.9	934
	Average (outgroup included)	31.0	26.4	28.7	14.0	934

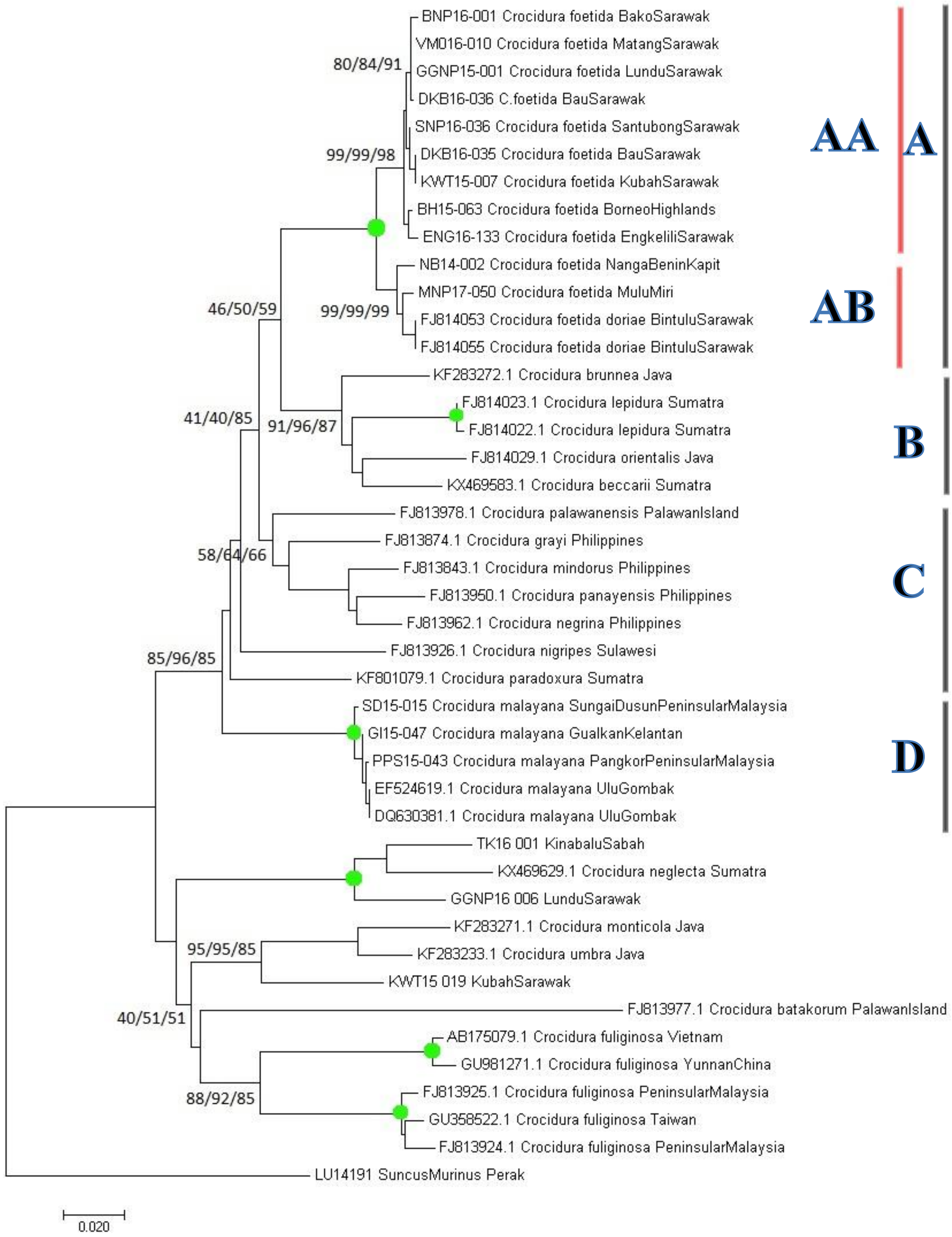

Figure 3.3: Consensus of three phylogenetic tress for cytochrome *b* with node support for all analyses performed (NJ/ML/MP/). Green dot indicates 100/100/100.

Table 3.8: Cytochrome *b* genetic distance between studied species.

		1	2	3	4	5	6	7	8	9
1	*C. foetida*									
2	*C. foetida doriae*	0.0243								
3	*C. mindorus*	0.0872	0.0937							
4	*C. grayi*	0.0853	0.0843	0.0651						
5	*C. fuliginosa*	0.1557	0.1576	0.1613	0.1572					
6	*C. palawanensis*	0.0904	0.0907	0.0757	0.0759	0.1605				
7	*C. nigripes*	0.0962	0.1037	0.0959	0.0786	0.1464	0.0926			
8	*C. panayensis*	0.1002	0.1044	0.0355	0.0678	0.1671	0.0786	0.0929		
9	*C. negrina*	0.0911	0.0950	0.0379	0.0663	0.1716	0.0756	0.0957	0.0366	
10	*C. batakorum*	0.2124	0.2110	0.2070	0.2001	0.1911	0.2022	0.1876	0.2090	0.2274
11	*C. lepidura*	0.0960	0.0960	0.1116	0.1025	0.1580	0.1003	0.1109	0.1148	0.1098
12	*C. orientalis*	0.0966	0.0971	0.1100	0.1056	0.1550	0.1127	0.1254	0.1100	0.1146
13	*C. malayana*	0.1039	0.1029	0.1063	0.0874	0.1585	0.1021	0.0926	0.0952	0.0981
14	*C. umbra*	0.1425	0.1472	0.1458	0.1503	0.1476	0.1333	0.1484	0.1493	0.1472
15	*C. monticola*	0.1690	0.1616	0.1788	0.1503	0.1485	0.1469	0.1519	0.1674	0.1652
16	*C. brunnea*	0.0864	0.0870	0.0981	0.0834	0.1547	0.1038	0.1020	0.0981	0.0963
17	*C. beccarii*	0.0930	0.0887	0.1045	0.0970	0.1508	0.0963	0.1069	0.1045	0.1042
18	*C. paradoxura*	0.0938	0.0933	0.0891	0.0893	0.1451	0.0858	0.0856	0.0981	0.0874
19	*C. neglecta*	0.1733	0.1684	0.1885	0.1649	0.1489	0.1858	0.1557	0.1769	0.1862
20	Species C	0.1461	0.1430	0.1467	0.1458	0.1201	0.1325	0.1441	0.1364	0.1412
21	Species B	0.1658	0.1695	0.1578	0.1624	0.1469	0.1718	0.1380	0.1762	0.1759
22	Species A	0.1712	0.1705	0.1897	0.1570	0.1642	0.1774	0.1569	0.1839	0.1835
23	*S.murinus*	0.2140	0.2099	0.1985	0.2141	0.2327	0.2241	0.2120	0.2064	0.2054

Table 3.8: continued

		10	11	12	13	14	15	16	17	18	19
1	*C. foetida*										
2	*C. foetida doriae*										
3	*C. mindorus*										
4	*C. grayi*										
5	*C. fuliginosa*										
6	*C. palawanensis*										
7	*C. nigripes*										
8	*C. panayensis*										
9	*C. negrina*										
10	*C. batakorum*										
11	*C. lepidura*	0.1997									
12	*C. orientalis*	0.1785	0.0743								
13	*C. malayana*	0.1985	0.1140	0.1077							
14	*C. umbra*	0.1866	0.1344	0.1447	0.1630						
15	*C. monticola*	0.1886	0.1517	0.1626	0.1564	0.0469					
16	*C. brunnea*	0.1938	0.0663	0.0623	0.0899	0.1447	0.1517				
17	*C. beccarii*	0.1677	0.0597	0.0584	0.0945	0.1467	0.1574	0.0613			
18	*C. paradoxura*	0.1873	0.0946	0.1100	0.0852	0.1327	0.1412	0.1011	0.0937		
19	*C. neglecta*	0.2254	0.1657	0.1449	0.1610	0.1530	0.1622	0.1609	0.1649	0.1720	
20	Species C	0.1887	0.1398	0.1403	0.1453	0.0933	0.0874	0.1455	0.1338	0.1455	0.1285
21	Species B	0.1990	0.1490	0.1342	0.1481	0.1608	0.1700	0.1461	0.1570	0.1566	0.0705
22	Species A	0.2376	0.1669	0.1359	0.1428	0.1633	0.1652	0.1478	0.1624	0.1808	0.0612
23	*S.murinus*	0.2452	0.2110	0.2117	0.1929	0.2224	0.2203	0.1921	0.2021	0.1790	0.2164

Table 3.8: continued

		20	21	22	23
1	*C. foetida*				
2	*C. foetida doriae*				
3	*C. mindorus*				
4	*C. grayi*				
5	*C. fuliginosa*				
6	*C. palawanensis*				
7	*C. nigripes*				
8	*C. panayensis*				
9	*C. negrina*				
10	*C. batakorum*				
11	*C. lepidura*				
12	*C. orientalis*				
13	*C. malayana*				
14	*C. umbra*				
15	*C. monticola*				
16	*C. brunnea*				
17	*C. beccarii*				
18	*C. paradoxura*				
19	*C. neglecta*				
20	Species C				
21	Species B	0.1307			
22	Species A	0.1450	0.0688		
23	*S.murinus*	0.2382	0.2177	0.2164	

3.3.2 Age of divergence estimation

The phylogeny with estimation time of divergence is produced in which these species are grouped into several clades (Figure 3.4). Divergence within family Soricidae between *Suncus murinus* and other *Crocidura* is estimated to occur about 8.56 Mya (7.99 Mya - 9.35 Mya). Within genus *Crocidur*a, the earliest divergence can be observed between *C. fuliginosa* and other *Crocidura* which is dated about 8 Mya (7.99 Mya – 9.35 Mya). *Crocidura foetida* and *C. f. doriae* is estimated to diverge as early as 0.73 Mya (0.44 Mya – 1.44 Mya), indicating recent speciation. The separation of *C. foetida* and other *Crocidura* from Java and Sumatra is estimated to separate at about 3.09 Mya (2.39 Mya – 3.2 Mya). Some of the recent speciation are between *C. mindorus* and *C. panayensis* that occurred about 0.99 Mya (0.67 Mya – 1.25 Mya) and also between *C. umbra and C. monticola* at about 1.2 Mya (0.86 Mya – 1.56 Mya). All of the divergence time for the species happened within the Pleistocene, Pliocene, and Miocene time period.

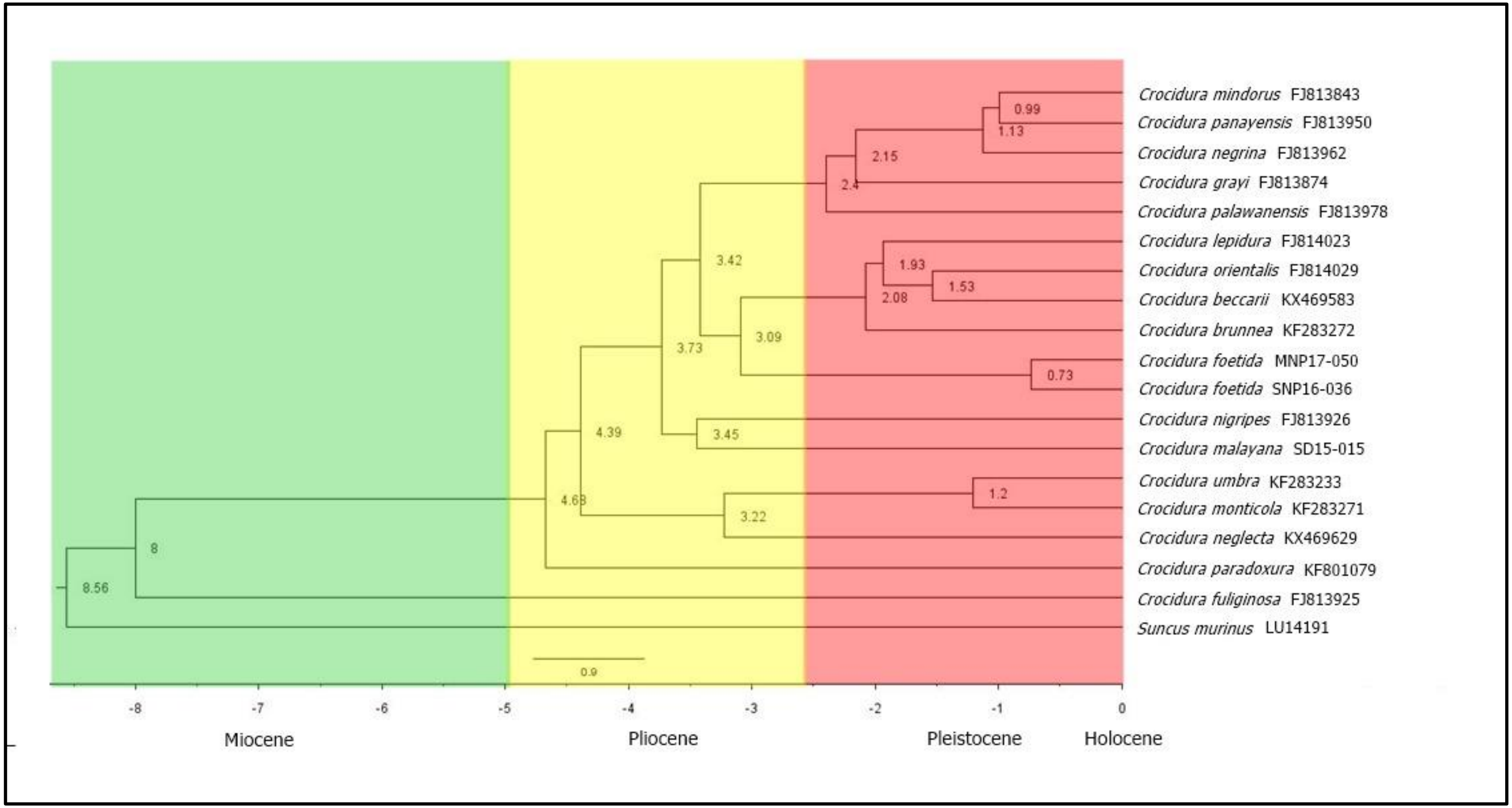

Figure 3.4: Single chronogram with divergence date estimates from 986 bp mtDNA sequences. The estimated mean node ages are labelled at each node.

3.3.3 Principal component analysis (PCA) on craniodental measurements

Principal component analysis conducted on the craniodental measurements of 15 samples revealed no distinct grouping between localities (Figure 3.5) (Table 3.10). All 14 craniodental measurements do not exhibit apparent differences and the localities overlapped with each other. One-way ANOVA analysis was carried out to observe any difference between the sexes of collected samples (Omar et al., 2013). The analysis revealed no significant difference, thus no sexual dimorphism observed.

The total variance for Factor 1 is 21.87%, contributed the most by PM3, M2B, and GLS (Table 3.9). PM3 has the highest factor loading value with 0.804641 followed by M2B with 0.601714. Factor 2 contributes 19.75% of the variable which most related with IM3S, IM3I, and GLS. The variable with the highest factor loading value is IM3S with 0.808766 followed by IM3I with 0.801350.

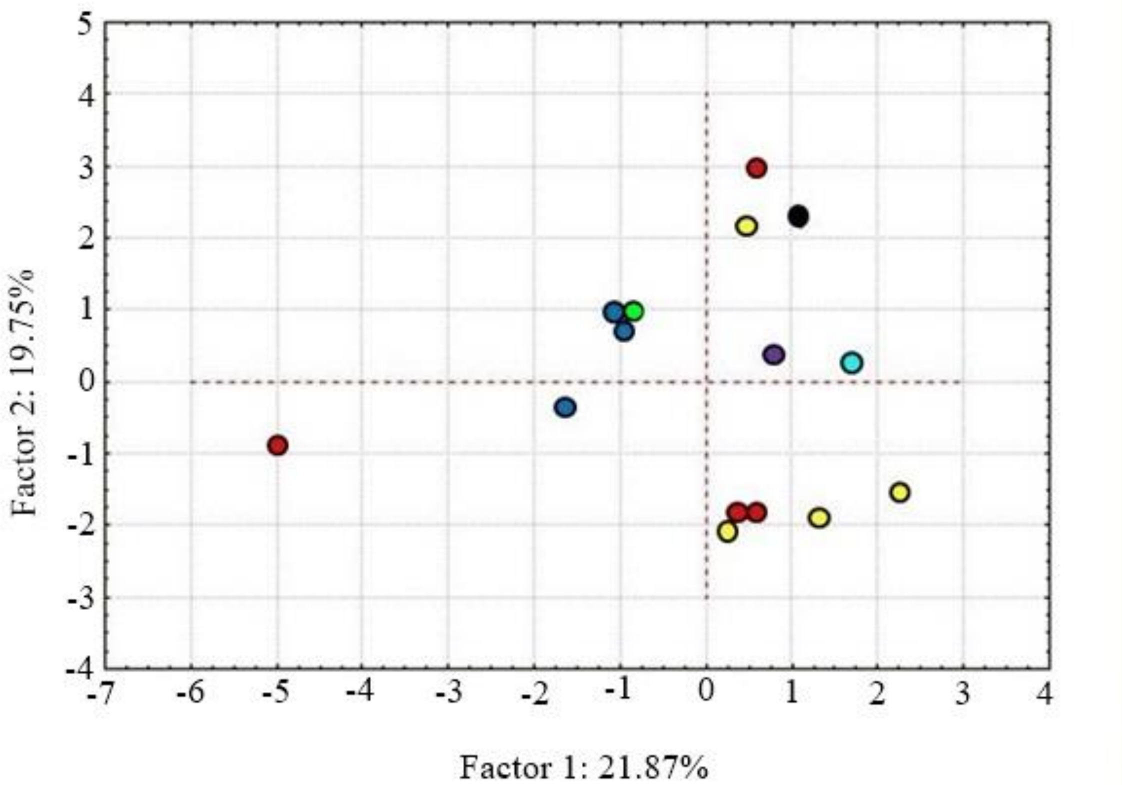

Figure 3.5: Scatter plot produced by PCA based on 14 cranio-dental measurements of *Crocidura foetida* collected across Sarawak. **Red**: Gunung Gading NP; **Blue**: Santubong NP; **Green**: Nanga Benin, Kapit; **Black**: Mulu NP; **Yellow**: Dered Krian NP; **Purple**: Kubah NP; **Turqoise**: Bungo Range NP.

Table 3.9: The PC1 and PC2 of factor-variable correlations (factor loadings) from the principle component analyses based on 14 cranio-dental measurements of studied species.

Variable	Factor coordinates based on correlations	
	PC1	PC2
Greatest length of skull (GLS)	0.557890	0.567597
Length of upper tooth row (IM3S)	0.092447	0.808766
Post-palatal length (PPL)	0.129691	-0.358920
Length of upper molariform (PM3)	0.804641	0.406403
Rostral breadth (ROB)	0.569781	0.035216
Breadth at third molars (M3B)	0.414540	-0.375225
Breadth at second molars (M2B)	0.601714	-0.439244
Braincase breadth (BB)	0.284856	-0.066061
Interorbital breadth (IOB)	0.284856	-0.169669
Rostral length (ROL)	-0.411804	0.476997
Post-palatal depth (PPD)	-0.009049	-0.039103
Condyle to glenoid length (CTG)	0.404071	0.497679
Lower tooth row length excluding first incisor (IM3I)	-0.313241	0.801350
Mandibular length	0.603303	0.090885
Eigenvalue	3.061545	21.765533
% Total variance	21.86818	19.75381

Table 3.10: Craniodental measurements of studied species.

	GLS	IM3S	PPL	PM3	ROB	M3B	M2B
SNP16-036	23.88	11.04	10.27	5.78	2.37	2.62	7.3
GGNP15-002	22.24	10.99	10.36	5.12	2.78	2.4	6.91
SNP16-043	23.23	11.73	9.96	5.87	2.77	2.6	7.05
NB14-002	23.21	11.62	9.68	5.74	3.34	2.73	7.06
DKB16-041	23.61	10.47	10.72	5.49	3.52	2.57	7.3
DKB16-039	23.76	11.63	9.87	6.19	3.85	2.69	6.95
BRNP17-052	23.47	11.27	9.79	6.78	3.39	2.78	7.21
SNP16-037	23.52	11.83	9.25	5.98	3.78	2.99	7.25
GGNP15-098	23.38	11.26	10.46	6.02	3.51	2.8	7.24
DKB16-036	23.3	11.1	10.82	6.26	3.63	2.85	7.33
GGNP15-001	22.97	11.31	10.32	5.82	3.8	3.1	7.12
DKB16-035	23.51	11.11	10.02	6.35	3.46	2.85	7.38
GGNP16-001	24.53	11.77	10.56	6.43	3.67	2.29	7.1
KWT15-021	23.5	11.37	10.57	6.07	3.5	2.83	7.28
MNP17-050	24.2	11.88	10.38	6.61	3.18	2.7	7.2

Table 3.10: continued

	BB	IOB	ROL	PPD	CTG	IM3I	MAL	Sex
SNP16-036	9.56	5.11	10.54	4.34	9	7.62	9.2	Male
GGNP15-002	8.54	4.79	10.53	4.14	9.02	7.55	9.22	Male
SNP16-043	10.57	5.34	10.7	4.45	8.92	7.66	9.83	Male
NB14-002	9.66	4.56	9.96	4.12	9.27	7.72	9.66	Female
DKB16-041	10.39	5.18	10.6	4.96	9.14	7.27	9.8	Male
DKB16-039	9.71	5.13	10.38	4.36	9.38	7.77	10.01	Male
BRNP17-052	10.07	5	10.21	4.15	9.3	7.36	9.97	Male
SNP16-037	9.1	4.9	10.71	4.14	9.1	7.53	8.99	Female
GGNP15-098	9.86	4.75	10.18	4.01	8.89	6.97	9.83	Female
DKB16-036	9.69	5.22	9.72	3.92	9.01	7.41	9.79	Male
GGNP15-001	9.29	4.69	9.59	4.24	9.14	7.17	9.87	Male
DKB16-035	10.19	5.3	9.69	4.25	9.39	7.13	9.61	Male
GGNP16-001	9.73	4.54	10.38	4.16	9.63	7.61	9.53	Male
KWT15-021	9.71	4.99	10.52	4.12	9.54	7.56	9.71	Male
MNP17-050	9.52	5.17	10.65	4.38	9.15	7.82	10.26	Female

3.3.4 RASP Analysis

The S-Diva analysis highlights six major dispersal events among these species in genus *Crocidura* (Node: 25, 32, 33, 34, 35, and 37) (Figure 3.6). Five major groups can be categorised out of these six events according to the arrangement of the clades. For clade 1, the route begins from node 37 to node 35, 34, and 21. The ancestor lineage started from Peninsular Malaysia and Sumatra and travelled to Java before colonising Java.

For second clade (37-35-34-33-32-22), the route started from Peninsular Malaysia and Sumatra, before moving to Java and then to Sulawesi. The route then returns back to Peninsular Malaysia. Clade 3 (37-35-34-33-32-23) shows similar route to clade 2, but with different destination. The route begins in Peninsular Malaysia and moves to Sumatra before leaving to Java. From Java, the route continues to Borneo which then split into three routes; first route continues to the Philippines, second route to Java and third route ends in Borneo.

For Clade 4 (37-35-34-33-32-26) and Clade 5 (37-35-34-33-32-31), the routes are similar to Clade 3. Clade 4 started at Peninsular Malaysia and Sumatra and moves to Java. The route continues to Borneo before back to Java. For Clade 5, the route begins in Peninsular Malaysia and Sumatra and moves to Java. From Java, the route continues to Borneo before going to the Philippines.

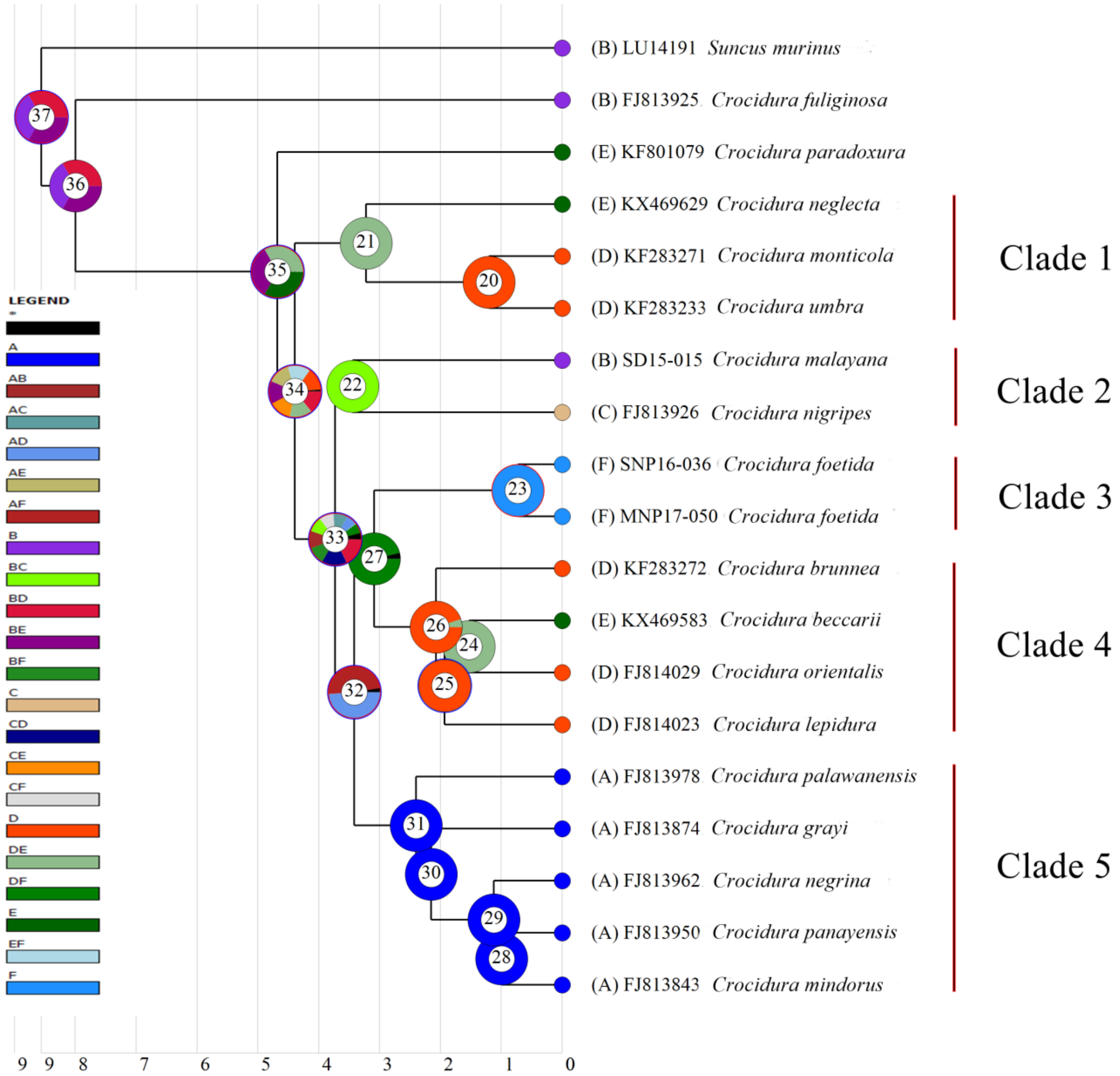

Figure 3.6: The possible dispersal routes for each of the nodes

3.4 Discussion

3.4.1 Phylogenetic relationship of *Crocidura foetida*

Molecular data obtained may provide information on the diversity and reveal latent phylogenetic structure (Avise 1994). This study, based on samples from northern Sarawak, enable us to define two clades within *C. foetida*. The phylogeographic split can be seen between Clade A, B, C and D according to their region (Clade A: Borneo Island; Clade B: Sumatra and Java; Clade C: Philippines Island; Clade D: Peninsular Malaysia) (Figure 3.3). In Clade A, two minor clades can be observed between *C. foetida* (Clade AA) and *C. foetida doriae* (Clade AB) (Figure 3.3). *Crocidura foetida doriae* is recognised as subspecies *to C. foetida* based on morphometric data (Ruedi, 1995). Using molecular approach, this study also supports the study by Ruedi (1995), as the genetic distance between *C. foetida* group and *C. f. doriae* group is 2.2.-2.8%, indicating close genetic distance. Genetic distance of less than 2% indicates intraspecific variation; 2% - 11% may need additional research involving the status of studied species; and values more than 11% indicates species recognition (Bradley & Baker, 2001).

Measurements of the teeth of the lower jaw of *C. f. doriae* were larger compared to recent specimens of *C. foetida* (Ruedi, 1995, Cranbrook, 2010). The difference is adequate to assign the population to a subspecies *C. f. doriae*, believed to adapt to a cooler temperature on the submontane area (Cranbrook, 2010). Cranbrook & Piper (2008), suggested that these two subspecies may be single species during the late Pleistocene (45-35 Kya). The specimens MNP17-050 and NB14-002 collected from Mulu National Park and Nanga

Benin respectively were grouped together with specimens identified as *C. f. doriae* (FJ814053 and FJ814055), taken from Genbank.

3.4.2 Biogeographic radiation of *Crocidura foetida*

The S-Diva analysis highlighted the route taken by *Crocidura foetida* to disperse across Southeast Asia. Various geological events occurred in Sundaland area especially the subsequent uplifts of mountains and land erosions shapes the geographical diversities in the area that happened in the early Miocene (Morley, 2012).

In this study, the most ancient dispersal time occurs at node 37 approximately 9 mya (Figure 3.6). According to Sheldon (2016), the climatic condition at this region is optimum for tropical birds and is accountable for shrew species as well. No apparent speciation event can be observed in the analysis. Then, the next important event occurred at node 34, 33, 32, 27, 26, and 25 with mostly occurred during the Pliocene (5 mya – 2.6 mya). During the Pliocene era, the temperature starts to decrease and resulted in rainforest extinction (Morley, 2012; Sheldon, 2016). The mountain ranges in Borneo, Sumatra and Java helps in maintaining the rainforest patches along northeast and southwest of Sundaland (Sheldon, 2016). The climatic conditions may force the movement of shrew species towards the patches of rainforest and is supported by this study which these shrew species disperse to northeast and southwest.

Focusing on *C. foetida* in Clade 3, the route was initiated from Peninsular Malaysia and Sumatra and moves to Java before continuing the journey to Borneo. The route then split into three different destinations; the Philippines, Java, and Borneo. Several speciation events happened during the Pleistocene era, as various climatic changes occurs in this time period (Tougard, 2001). The divergence of *C. foetida* and *C. f. doriae* occurred approximately 0.73 mya, in the late Pleistocene time period. The increase in temperature during Pleistocene era resulted in the increase of forest area and there are some periods of time which the rainforest flourished in the area (Heaney, 1991; Morley, 2000; Voris, 2000; Bird, 2005; Cannon et al., 2009). These are the environmental factors that may promotes the speciation event that occurs during Pleistocene.

3.4.3 Morphometric analysis

The principal component analysis does not revealed any distinct grouping within *C. foetida* species. All 14 craniodental measurements used in the analysis are unable to distinguish between localities of *C. foetida* and *C. f. doriae*. This indicates that the skull of *C. foetida* may not be suitable to be used for species identification. This result also similar to the genetic data which depicts close genetic distance between *C. foetida* and *C.f. doriae*. Due to small sample size, no apparent grouping can be observed. *Crocidura foetida doriae* were labelled as their locality, which are Nanga Benin (**GREEN**) and Mulu NP (**BLACK**). Sample from Nanga Benin overlapped with the populations from Santubong NP while Mulu NP does not overlap with any population. Overall, the skull size for *C. foetida* is very wide. The skull of *C. foetida* has a wide braincase with narrow interorbital breadth. The average breadth of braincase is 9.71 mm while the average breadth of interorbital is 4.98 mm. The average greatest length of skull is 23.48 mm. The age of the individuals and the elevation should be noted to give clearer information.

Reduction in size that differentiates *C. foetida* and *C. f. doriae* was completed during mid-Holocene (Cranbrook & Piper, 2008). Occurrence at lowlands means high abundance of prey and higher temperature than highlands may be the main factors in size reduction of *C. foetida*. Bergmann's rule indicated that species from climate with low temperature are generally larger than close relatives from climates with high temperature (Meiri et al., 2004).

Crocidura foetida distributed almost entirely in Sarawak. Divergence within this species identifies two groups that correspond to the western part of Sarawak and the northern part of Sarawak. This division may be related to geographic isolation due to climatic swing during the late Pleistocene. According to Mayr, (1963) and Pounds and Jackson (1981), the river system can be a barrier to the dispersal event. In Borneo, the river system of Rajang is a possible barrier to the dispersal of this species. However, study by Lugon-Moulin et al (1999) showed that river does not appear as strong geographic barrier and shrews may cross the river more often than expected.

3.5 Conclusion

This study had conducted various analyses on the genetic data and craniodental measurements of the studied individuals. The finding through molecular analysis suggests that there are visible but close genetic distance between *C. foetida* and its subspecies, *C. f. doriae*. However, craniodental analysis does not show any distinct grouping between localities. This study revealed that *C. f. doriae* is a subspecies of *C. foetida* in which this two subspecies was once a single species but later diverged due to geographical factors. Larger sample size with more extent distribution across Sarawak may help to clarify the phylogenetic relationship of *C. foetida*.

CHAPTER 4

SPECIES DISTRIBUTION MODELING OF THREE SHREWS FROM MALAYSIA USING MAXIMUM ENTROPY APPROACH

4.1 Introduction

Shrew in Malaysia has never been studied intensively in the wild due to the difficulty of trapping them (Omar et al., 2013). However, they are widely distributed across Southeast Asia and may represent a recent arrival to the region (Esselstyn et al., 2009). The increasing anthropogenic activities in the region had led to habitat loss and fragmentation that resulted in changes in the geographical extent of the species (Cowlishaw & Dunbar, 2000). The data on geographical ranges play an important role in describing the conservation status of a species and to evaluate the current levels of threat as presented in some of the major assessment list such as IUCN and CITES (Anderson & Martinez-Meyer, 2004; Hernandez et al., 2006).

Malaysian shrews are classified as either Least Concern, Data Deficient or Endangered under the IUCN status. Only *Chimarrogale phaeur*a is listed as Endangered while *Suncus ater* and *S. hosei* are listed as Data Deficient. Recent revision by the IUCN shows that most of the shrew species in Malaysia that are listed under Least Concern has no major threat and can be found in protected areas (IUCN, 2017). However, there is no information on population size and population trend if they are increasing or decreasing due to the lack of ecological and distributional studies. The geographical range of shrews in Malaysia remains unclear and an updated range map for these species is needed to aid in conservation planning (Loiselle et al., 2003; Clements et al., 2012), to improve assessment of risk status (Solano & Feria, 2007), to highlight unknown populations (Pearson et al., 2007), and to identify key areas for fieldwork (Papes & Gaubert, 2007).

Vertebrate species distributions have been tested widely with different species distribution modelling study. Various modelling tools are available to model the species distribution, including generalised regression analysis and spatial prediction (GRASP) (Lehmann et al., 2002), DIVA-GIS (Hijmans et al., 2001), and Maximum Entropy (MaxEnt) (Philips et al., 2006). Each of these models implemented different methods that depend on the type of response variables and predictors (Guisan & Thuiller, 2005). GRASP uses generalised linear model (GLM) and generalised additive model (GAM) to create statistical relationship between the environmental predictors and species abundance (Lehmann et al., 2002). DIVA-GIS implemented climatic envelop (CE) approach to be used for spatial analysis of data associated with genetic resource collections (Hijmans et al., 2001).

Maximum Entropy (MaxEnt) modelling is an exemplar of such algorithm that provide tools to predict wildlife distribution and habitat selection based on wildlife presence location, MaxEnt ecological niche modelling also have been demonstrated as a great tool to predict with high accuracy models of wildlife with a limited datasets (i.e. < 25 localities) (Philips et al., 2006; Hernandez et al., 2006; Pearson et al., 2007; Thorn et al., 2009). MaxEnt is able to generate deductions or predictions from partial data and only demand a presence-only data, using a random selection of background pixels from the study area as pseudo-absences (Philips et al., 2006). Based on the environmental conditions of the targeted species, the probabilities of species occurrence can be generated across the entire study area (Thorn et al., 2009). MaxEnt is used in this study as it is able to predict the distribution of shrew species that is poorly known in terms of its distribution and home range with limited samples or data (Nazeri et al., 2012). Thus, we will be able to understand comprehensively the shrew species habitat preferences and distribution and to plan conservation management. Thus, the current distribution of the shrews will be described, and its potential habitat occupancy will be predicted by applying a MaxEnt model throughout its range. Key areas that are suitable for these species will be identified to contribute in the long-term survival of the species.

4.2 Materials and Method

4.2.1 Sample collection

The samplings were conducted in 25 sites across Malaysia between 2014 and 2017. Sites selected in Sarawak were Kumpang Langgir in Engkelili, Kubah National Park (NP), Gunung Gading NP, Sematan, Mount Penrissen, Dered Krian NP, Santubong NP, Mulu NP, Samunsan Wildlife Sanctuary (WS), Bako NP, Gunung Lesung NP, Long Banga, and Bungoh Range NP. Two sites were chosen from Sabah, namely Kinabalu Park and Tawau Hills Park. In Peninsular Malaysia, the chosen sites were Ulu Gombak Forest Reserve, Sungai Dusun, Gua Ikan, Gunung Stong, Lawit in Tasik Kenyir, Bidong Island, Wang Kelian State Park, Pangkor Island and Penang Island. Most of the selected sites were montane and mixed dipterocarp forest (Table 4.1; Figure 4.1).

One hundred pitfall traps (height = 248mm, width = 232 mm) were used in this study and were set up every five metres in a grid formation. Traps were checked once daily in the morning around 1000 across the sampling period. Species identification was carried out following Philips and Philips, 2016.

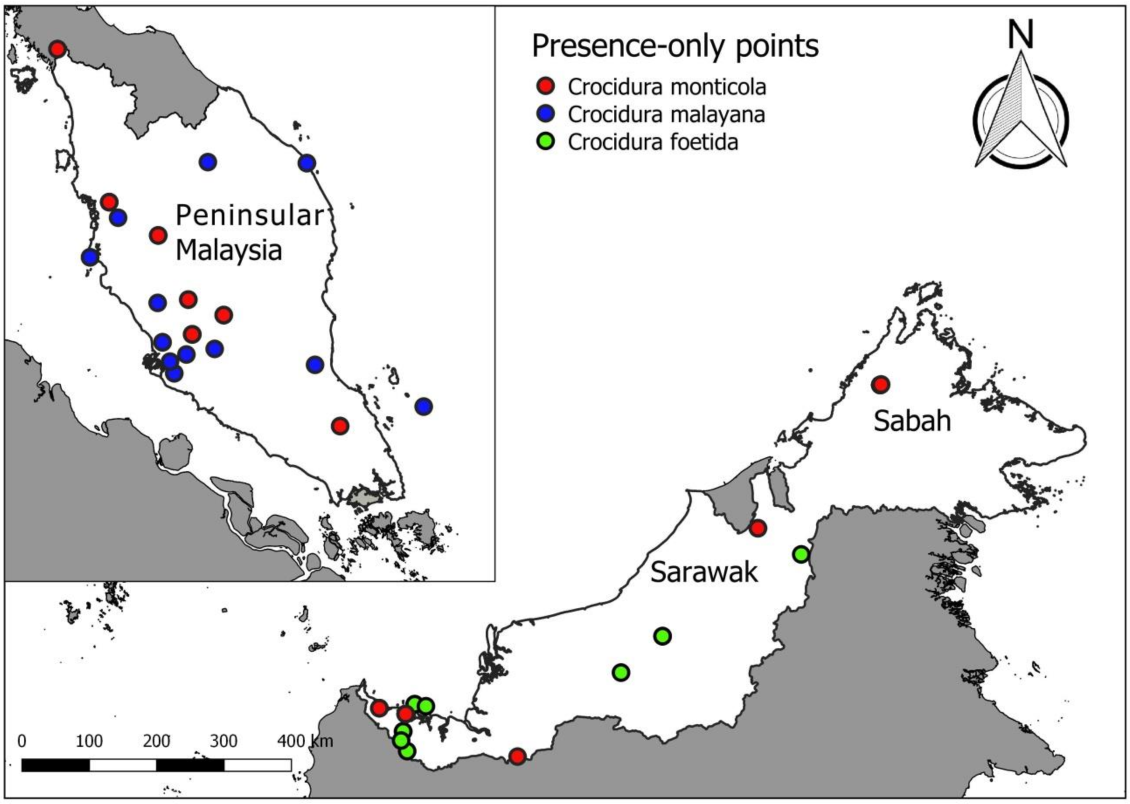

Figure 4.1: The location of the presence-only points used in the MaxEnt modelling. Scale is applied to both Peninsular Malaysia and Borneo Island.

Table 4.1: The selected study sites with habitat type and number of samples per locality captured in this study

Study sites	Habitat type	*Crocidura foetida*	*Crocidura malayana*	*Crocidura monticola*
Peninsular Malaysia				
Ulu Gombak Forest Reserve, Selangor	Mixed dipterocarp forest, semi-urban area	-	-	**1**
Sungai Dusun, Selangor	Riverine forest, mixed dipterocarp forest	-	**1**	-
Gua Ikan, Dabong, Kelantan	Limestone forest	-	**1**	-
Gunung Stong, Kelantan	Montane forest, mixed dipterocarp	-	-	-
Lawit, Tasik Kenyir, Terengganu	Mixed dipterocarp forest	-	-	-
Pulau Bidong, Terengganu	Beach forest	-	-	-
Wang Kelian State Park, Perlis	Limestone forest	-	-	-
Pulau Pangkor, Perak	Secondary forest, semi-urban area	-		-
Penang Island	Secondary forest, semi-urban area	-	**2**	-
Sarawak				
Kumpang Langgir, Engkelili	Mixed dipterocarp forest	**1**	-	**1**
Kubah National Park, Matang	Montane forest	**5**	-	**12**
Mount Gading National Park, Lundu	Montane forest	**2**	-	**1**
Sematan, Lundu	Secondary forest, semi-urban area	-	-	-
Mount Penrissen, Padawan	Montane forest	**1**	-	-
Dered Krian National Park, Bau	Limestone forest, mixed dipterocarp forest	**7**	-	-
Santubong National Park, Kuching	Montane forest, mixed dipterocarp forest	**3**	-	-
Mulu National Park, Miri	Montane forest, limestone forest	**1**	-	**4**
Samunsam Wildlife Sanctuary, Lundu	Mangrove forest, riverine forest, mixed dipterocarp forest	-	-	-
Bako National Park, Kuching	Mangrove forest, riverine forest, mixed dipterocarp forest, cliff	**1**	-	-
Gunung Lesung National Park	Montane forest, secondary forest	-	-	-
Long Banga, Miri	Montane forest, mixed dipterocarp forest	-	-	-

Table 4.1: continued

Bungoh Range NP	Montane forest, mixed dipterocarp forest	**1**	-	-
Nanga Benin, Kapit	Montane forest, mixed dipterocarp forest	**2**	-	-
Sabah				
Taman Kinabalu	Mixed dipterocarp forest, semi-urban area	-	-	**4**
Taman Bukit Tawau	Riverine forest, mixed dipterocarp forest	-	-	-

4.2.2 Environmental and species occurrence data

A database consists of 194 presence points recorded between 1948 and 2017 on Peninsular Malaysia and Malaysian Borneo was compiled (Table 4.2). A total of 60 presence-only points for *C. foetida* were obtained from Universiti Malaysia Sarawak (UNIMAS) Zoological Museum, the National Museum of Natural History (NMNH), United States of America database and samplings conducted by the author. An endemic to the Borneo Island, no records were found for this species from Kalimantan except for its type locality. However, the type locality is not included as it is not considered in recent times. The records for *C. f. doriae* were included in *C. foetida* database for this study as it has very few presence-points (n=7) to be modelled as single species and the points were only from one site. Sixty presence-points for *C. malayana* were also compiled, with 47 of the points were taken from Universiti Malaya (UM) zoological museum record, nine presence-points obtained from NMNH database, and the rest from this study. *Crocidura monticola* has the most presence-points with 74 points collected from this study and UM zoological museum records.

Table 4.2: The number of presence points taken from various source.

Species	*Crocidura foetida*	*C. malayana*	*C. monticola*
Universiti Malaysia Sarawak Zoological Museum	2	-	-
Universiti Malaya Zoological Museum	-	47	51
National Museum of Natural History database	34	9	-
This study	24	4	23
Total	60	60	74

Twenty-one environmental predictors used in the final model including 19 bioclimatic variables, an altitude layer, and a land cover layer. The 19 bioclimatic variables were considered as the “core variables” because they only require temperature and precipitation data for the analysis (Fick & Hijmans, 2017). The bioclimatic variables include annual mean temperature, mean diurnal range, isothermality, temperature seasonality, maximum temperature of warmest month, minimum temperature of coldest month, temperature annual range, mean temperature of wettest quarter, mean temperature of driest quarter, mean temperature of warmest quarter, mean temperature of coldest quarter, annual precipitation, precipitation of wettest month, precipitation of driest month, precipitation seasonality, precipitation of wettest quarter, precipitation of driest quarter, precipitation of warmest quarter and precipitation of coldest quarter (Table 4.3). The bioclimatic variables and altitude were obtained from WorldClim database version 1.4 (Hijmans et al., 2005) while the land cover layer were obtained from GLC2000. All environmental variables were re-sampled to the world geodetic system (WGS84) at a resolution of approximately 1 km^2 (0.008333 decimal degrees).

Table 4.3: The bioclimatic variables and the code used in modelling.

Code	Bioclimatic variables
BIO1	Annual mean temperature
BIO2	Mean diurnal range (Mean of monthly (maximum temp- minimum temp))
BIO3	Isothermality (BIO2/BIO7)(*100)
BIO4	Temperature seasonality (Standard deviation*100)
BIO5	Maximum temperature of warmest month
BIO6	Minimum temperature of coldest month
BIO7	Temperature annual range (BIO5 – BIO6)

Table 4.3: continued

BIO8	Mean temperature of wettest quarter
BIO9	Mean temperature of driest quarter
BIO10	Mean temperature of warmest quarter
BIO11	Mean temperature of coldest quarter
BIO12	Annual precipitation
BIO13	Precipitation of wettest month
BIO14	Precipitation of driest month
BIO15	Precipitation seasonality (Coefficient of Variation)
BIO16	Precipitation of wettest quarter
BIO17	Precipitation of driest quarter
BIO18	Precipitation of warmest quarter
BIO19	Precipitation of coldest quarter

4.2.3 Maximum Entropy

Maximum Entropy modelling is based on presence-only points; the coordinate of a site will be recorded if the shrews were recorded. All coordinates were recorded in decimal degrees. A database of 194 shrews' presence-only points was compiled based on samples caught during samplings, additional records from existing scientific literature (Omar et al., 2013) and museums data (National Museum of Natural History, United States of America; Universiti Malaysia Sarawak, Universiti Malaya). Observation and direct sightings data were not included as shrews does not have a distinctive appearance and its movement is very agile and fast, which may lead to inaccurate identification.

In MaxEnt, the gain of the variable is defined as the average log probability of the presence samples. It starts at zero and increases towards an asymptote during the run. According to

Philips et al (2010), the gain indicates how closely the model is concentrated around the presence samples. There are several methods to determine which variable contributes the most to the modelled species. A jackknife test can be used to obtain the estimate of which variable is the most important (Philips et al., 2010). The test produces a number of models where each of the variables is excluded in turn, creating a model with remaining variables. Then, a model using each variable in isolation is created. The results of the jackknife will be produced in bar charts type. The blue coloured chart indicates an important and informative variable while the turquoise coloured chart indicates unique variable (Philips, 2010). If the variable obtain zero or almost no gain, it is not useful for estimating the distribution of the modelled species. Analysis of variable contribution can also be used to determine the environmental variables that make the greatest contribution to the model. In MaxEnt, as each step of the algorithm increases the gain of the model, the program also assigns the increase in gain to the variables (Philips et al., 2010).

The area under the receiver operating curve (ROC) or the AUC is given in the receiver operating curve for training data (Philips, 2010). It is normal for the red (training) line to give out a higher AUC. The red line indicates how "fit" the model is to the training data. Phillips and Dudik, 2008, stated that a model with value more than 0.75 are potentially useful to the data. Shrew is a widespread species, thus the species prevalence can be deducted as 0.5, with a minimum record of three to ensure accurate species distribution model (Elith et al., 2011). Hinge feature implemented in the software was used as it allows a change in gradient of response, and is able to form a relatively smooth model with fitted functions (Elith et al., 2011). Other than the feature used, all other settings were set to default.

4.2.4 IUCN Distribution Map

The distribution map for the three modelled species appears to have wider range according to the range map established by the IUCN Red List (Figure 4.2; Figure 4.3; Figure 4.4) (Cassola, 2016; Chiozza, 2016). However, based on previous studies, *C. foetida* occupies undisturbed and dense forest from the lowland to the mid-montane forest (Ruedi, 1995; Cranbrook & Piper, 2008). *Crocidura malayana*, a widespread species and endemic to Peninsular Malaysia and to the adjacent island in the south of Isthmus of Kra, has been recorded from the lowland to montane forest up to 1200 m (Ruedi et al., 1990). The Sunda Shrew, *C. monticola* is widely spread across Malaysia with high preference on primary lowland and montane forest with a range of 100-1144 m a.s.l (Corbet & Hill, 1992; Davidson, 1984). These studies have indicated that the modelled species' true range is not as wide as the IUCN Red List suggests. The predictions of *C. foetida*, *C. malayana*, and *C. monticola* occurrence in Malaysia using MaxEnt can be used to update the IUCN range map to aid in local conservation management and conservation strategies.

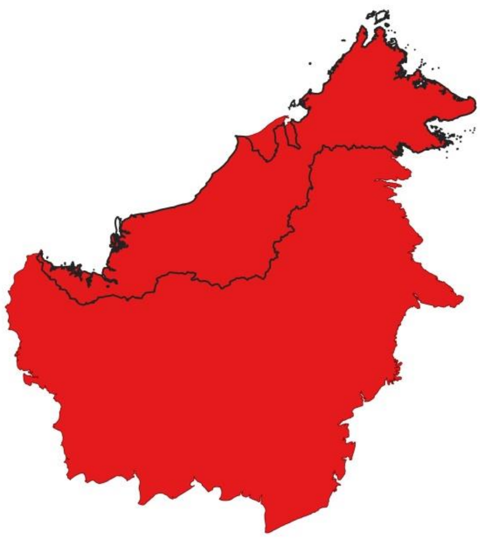

Figure 4.2: The distribution range map of *C. foetida* by IUCN Red List (Cassola, 2016)

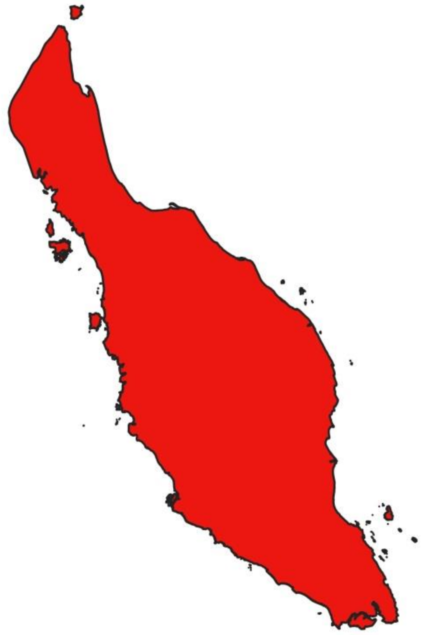

Figure 4.3: The distribution range map of *C. malayana* by IUCN Red List (Cassola, 2016)

Figure 4.4: The distribution range map of *C. monticola* by IUCN Red List (Chiozza, 2016)

4.2.5 Protected area

Protected area act as the site of in situ conservation strategies to reduce habitat degradation and ensuring species sustainability (Wilcox, 1984). Legal means such as passing an act, enactment or ordinance are used to guarantee the efficacy of protected area (Department of Wildlife and National Park, 2016). In Malaysia, there are almost 6 million hectares of forest area has been gazetted as protected area (Sarawak Forestry, 2006; Department of Wildlife and National Park, 2016; Sabah Forestry Department, 2017). Peninsular Malaysia has about 25% and 14% of lowland and hill dipterocarp forest respectively being classified as totally protected area (Department of Wildlife and National Park, 2016). Comparing the present protected area with the predicted distribution map of shrew species may help in identifying suitable habitat and to plan conservation strategies of shrew. The boundary map of protected area in Malaysia is extracted from the World Database on Protected Areas (WDPA).

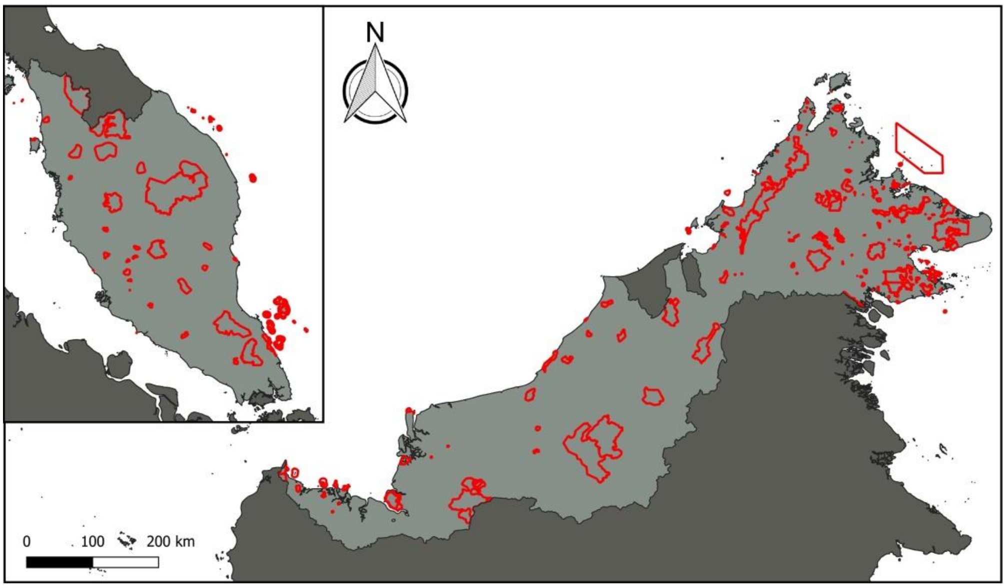

Figure 4.5: The map of protected area in Malaysia. Red line indicates the boundary of protected area.

4.3 Results

4.3.1 Distribution map

Modelling using Maximum Entropy for three different shrew species has resulted in three distribution maps models. The dark red colour indicates area with a high probability of occurrence for the species, and white indicates conditions that are not suitable for the species. The green dots show the test points used in this model.

Figure 4.6(a) is a map of *C. foetida* distribution generated using the MaxEnt model. Dark red colour can be seen accumulated in the western part of Sarawak and northern Sarawak with a lighter shade of red in the middle part. In Sabah, the northern part has the dark red shade with almost no red shade in other parts. The distribution of *C. malayana* is predicted and shown in Figure 4.6(b). This species has a wider range compared to *C. foetida*, with dark red shade can be observed in the west coast area of Peninsular Malaysia. Lighter red shade accumulated at the east coast, confining the occurrences to mainly on one side of Peninsular Malaysia. Figure 4.6(c) showed the predicted distribution of *C. monticola.* Dark red shades can be seen in the middle part of Peninsular Malaysia, the western part of Sarawak and northern part of Sabah. Patches of dark red shades can also be observed across the country.

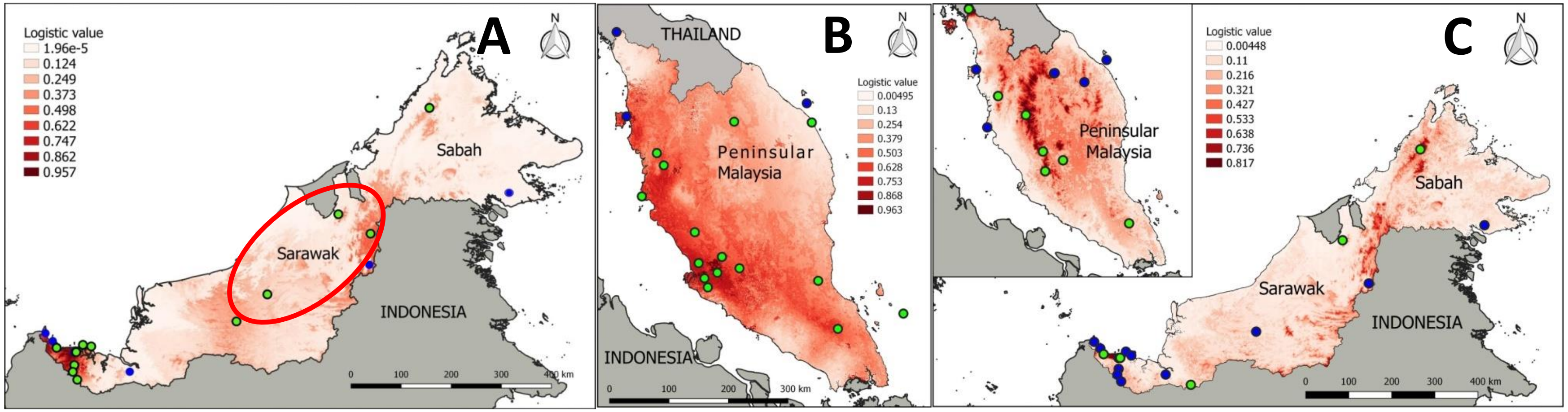

Figure 4.6: A: The distribution map of *Crocidura foetida* across Sabah and Sarawak generated using Maxent model. The points in the red circle indicate the points for *C. f. doriae*. **B:** The distribution map of *Crocidura malayana* across Peninsular Malaysia generated using Maxent model. **C:** The distribution map of *Crocidura monticola* across Malaysia generated using Maxent model. Green dots represent presence points and successful sampling while blue dots represent unsuccessful sampling.

4.3.2 Bioclimatic variables

For all three models on different shrew species, the mean area under the curve (AUC) of the receiver operating curve (ROC) was high, with mean values of 0.977, 0.921, and 0.916 for the training data of *C. foetida*, *C. malayana* and *C. monticola* respectively (Figure 4.8; Figure 4.10; Figure 4.12). Phillips and Dudik (2008), stated that the model with the value more than 0.75 is potentially useful. The red (training) lines for the three models are well above the black (random prediction) line indicating the models perform well than a random model (Philips, 2010). As the red line get further to the top left, the better the model is on predicting (Philips, 2010).

The variable that contributes the most to the *C. foetida* distribution model is BIO19 with 61.2 % (Table 4.4). This variable is similar to the jackknife test, proving that BIO19 will greatly decrease the gain of the model if omitted from the analysis (Figure 4.8). For *C. malayana*, BIO15 gained the most contribution to the model with 37.9%, different to the jackknife test which indicated BIO7 as the most importance variable (Figure 4.9). However, BIO7 gained the second most contribution behind BIO15 with 32.5% (Table 4.4). BIO16 contributes the most to the *C. monticola* distribution model with 40.8% (Table 4.4). The result is similar with the jackknife test of *C. monticola* (Figure 4.11). The variables that contributes zero percent for each model can be omitted and replace with other variables in future analysis (Table 4.3).

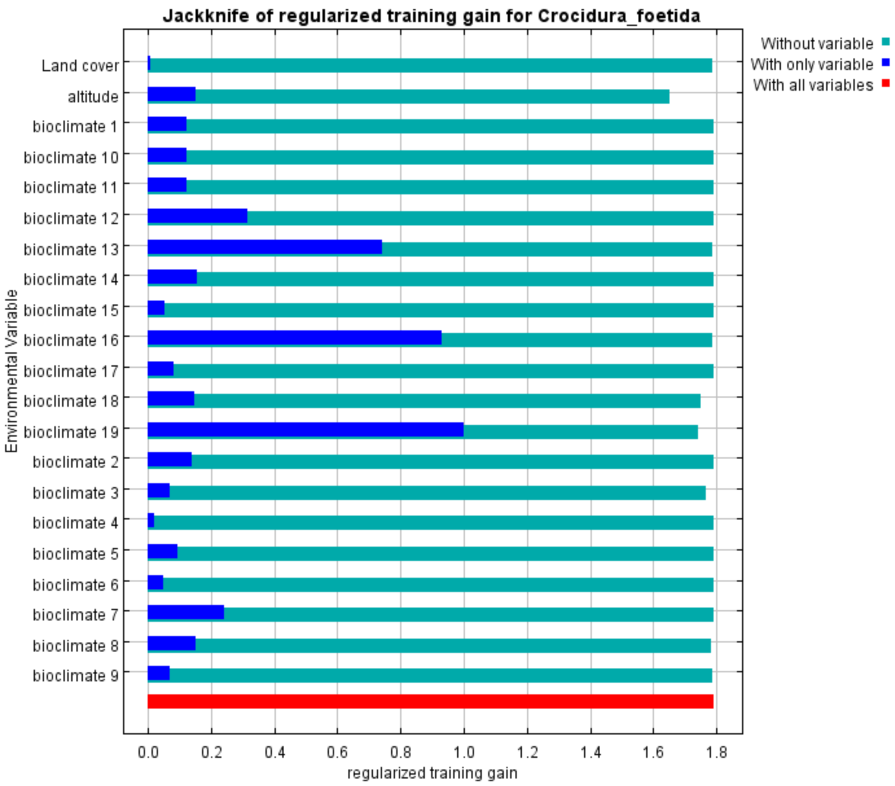

Figure 4.7: The jackknife test of variable importance of *C. foetida*

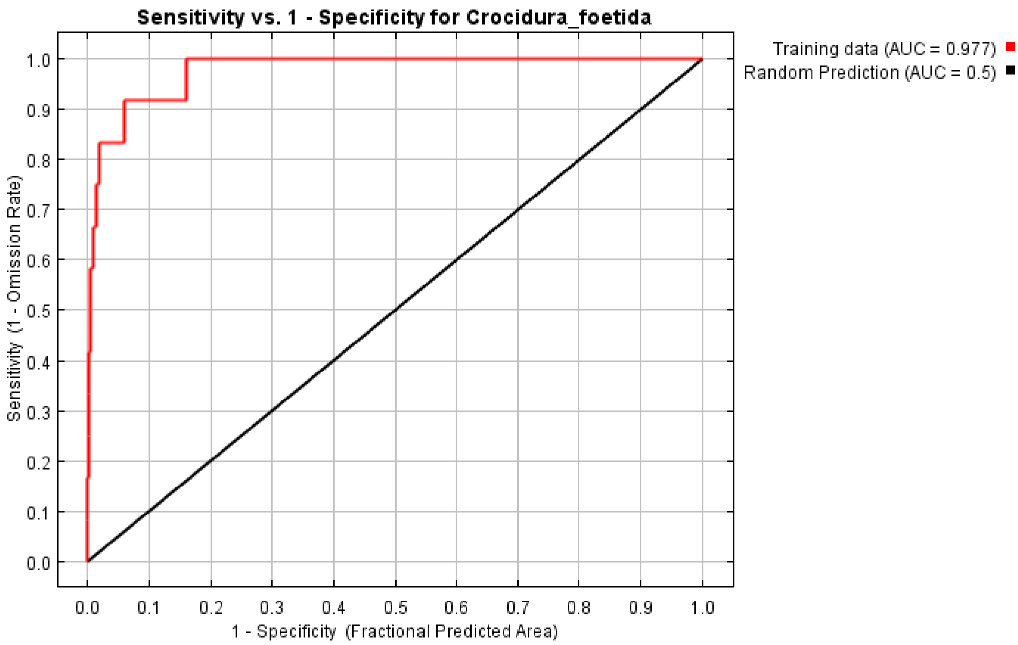

Figure 4.8: The receiver operating curve for training data of *C. foetida*

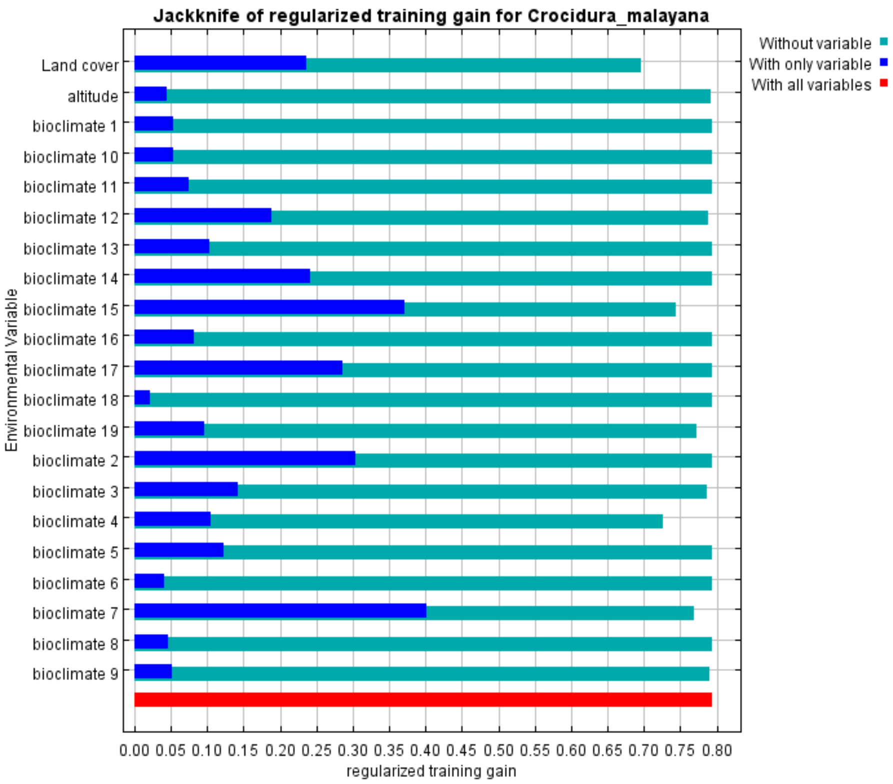

Figure 4.9: The jackknife test of variable importance of *C. malayana*

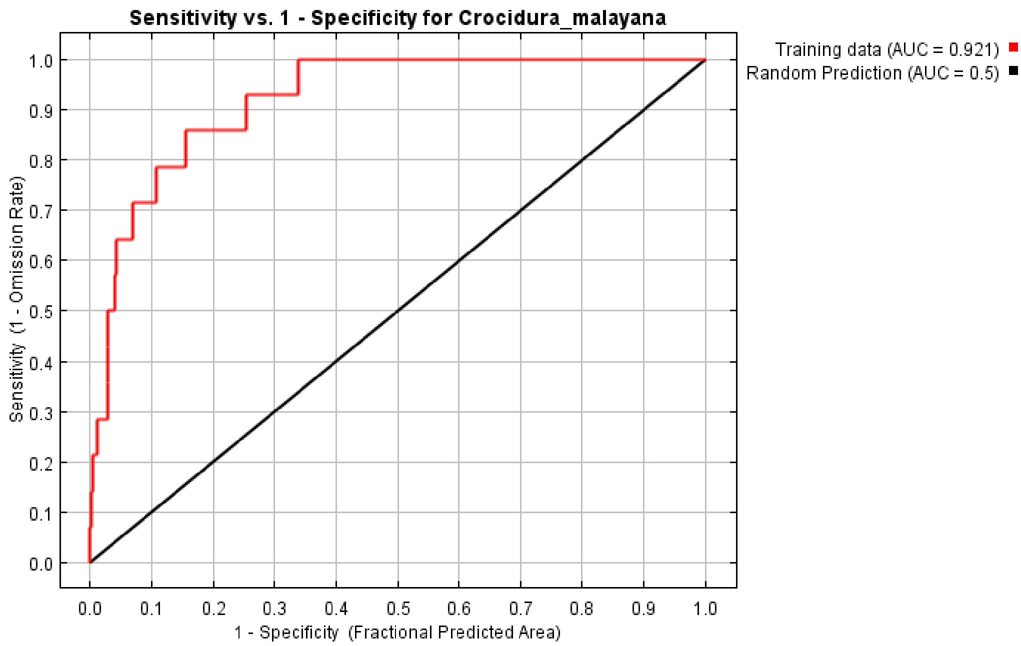

Figure 4.10: The receiver operating curve for training data of *C. malayana*

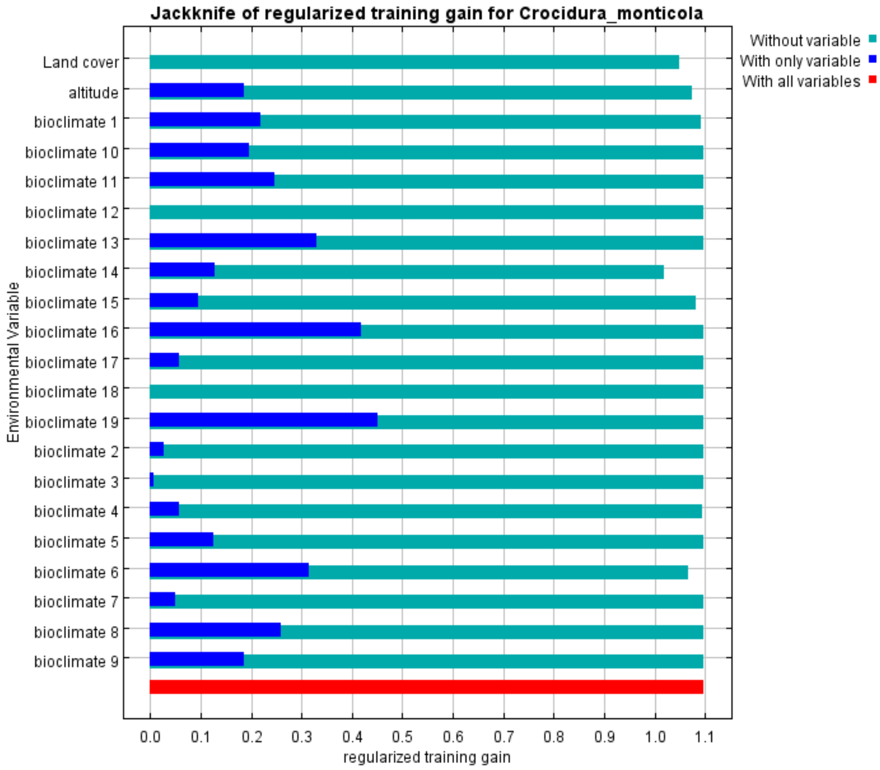

Figure 4.11: The jackknife test of variable importance of *C. monticola*

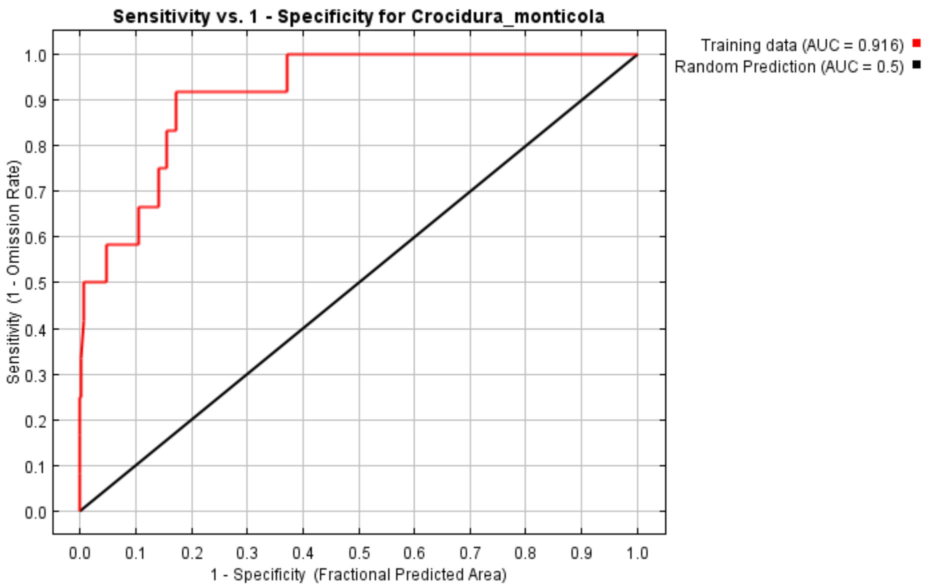

Figure 4.12: The receiver operating curve for training data of *C. monticola*

Table 4.4: The estimates of relative contributions of the environmental variables to the model. * indicates the highest percentage of contribution

Variable	*Crocidura foetida*	*Crocidura malayana*	*Crocidura monticola*
Land cover	0.3	5.2	3.4
Altitude	27.8	0.1	11.5
BIO1	0	0	0.3
BIO2	0	0	0
BIO3	0.6	0.7	0
BIO4	0	8.3	0.1
BIO5	0	0	0
BIO6	0	0.1	7
BIO7	1.4	32.5	0
BIO8	0.4	0	14.9
BIO9	0	0.4	0
BIO10	0	0	0
BIO11	0	0	0
BIO12	2.3	2.9	0
BIO13	0.8	6.1	2.2
BIO14	0	0	9.2
BIO15	0.1	37.9*	10.5
BIO16	0.9	0	40.8*
BIO17	0	0	0
BIO18	4.1	0	0
BIO19	61.2*	5.8	0

4.3.3 The comparison of protected area and predicted distribution

The predicted distribution map of the three modelled shrew species is compared with the boundary map of protected map in Malaysia. In Figure 4.13, the predicted distribution of *C. foetida* is observed to cover most of the protected area in Sarawak. In Sabah, light red shade covering most of the protected area in the middle and eastern part. Figure 4.14 shows the comparison between *C. malayana*'s distribution map with the protected area in Peninsular Malaysia. The red shade is observed to cover most of the protected area, but darker red shade can be seen outside of the protected area's boundaries, specifically in the west coast area. *Crocidura monticola* distribution covers most of the protected area in both Peninsular Malaysia and Borneo Island (Figure 4.15).

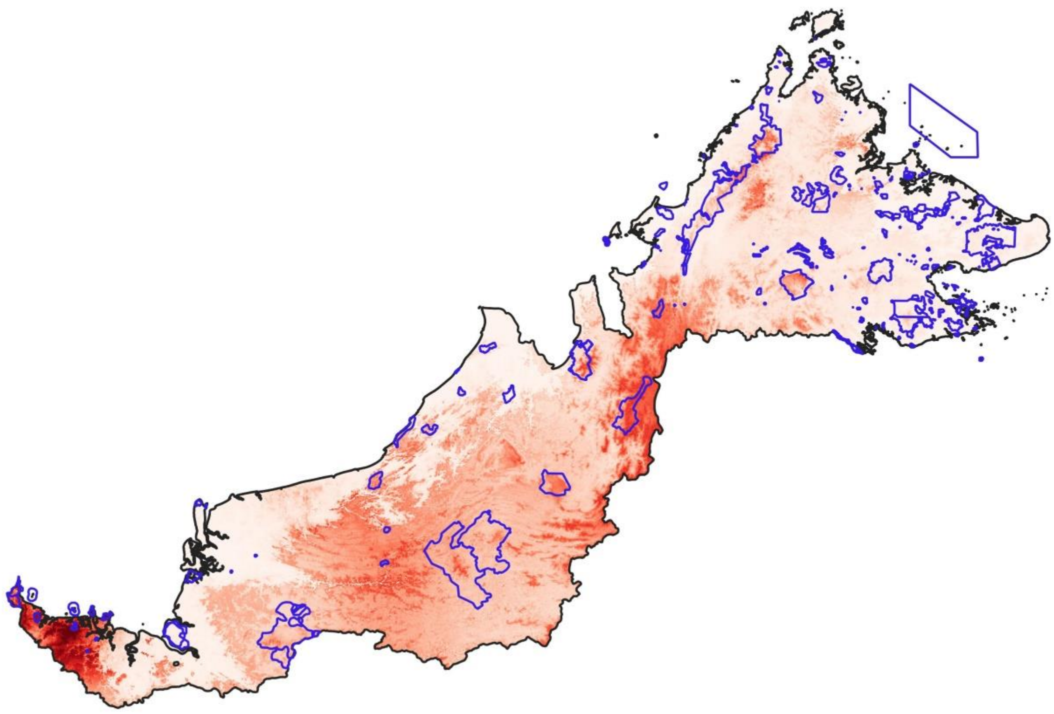

Figure 4.13: The comparison between the predicted distribution of *C. foetida* and the protected area in Sabah and Sarawak. The red shades indicate the predicted distribution and the blue area indicates the protected area.

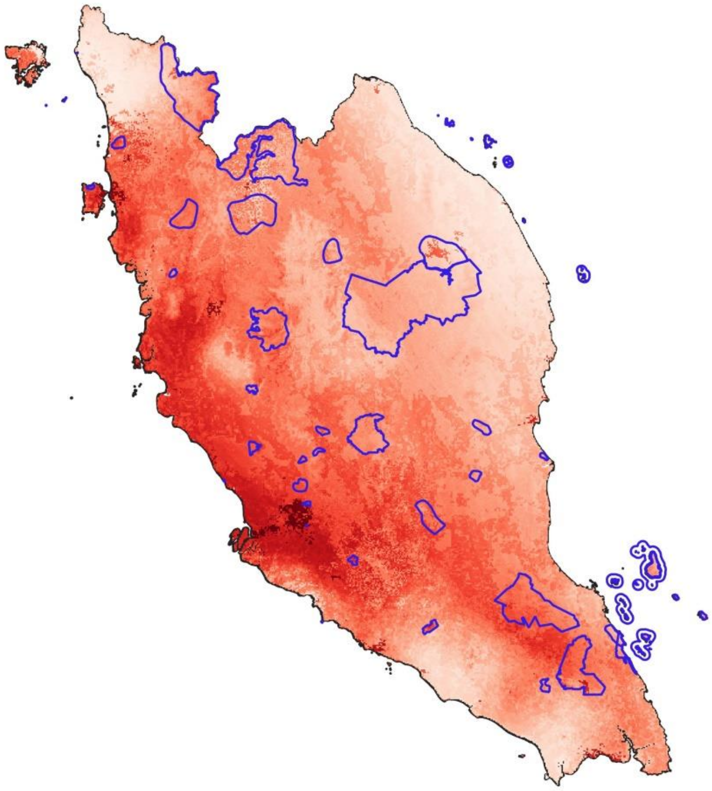

Figure 4.14: The comparison between the predicted distribution of *C. malayana* and the protected area in Peninsular Malaysia. The red shades indicate the predicted distribution and the blue area indicates the protected area.

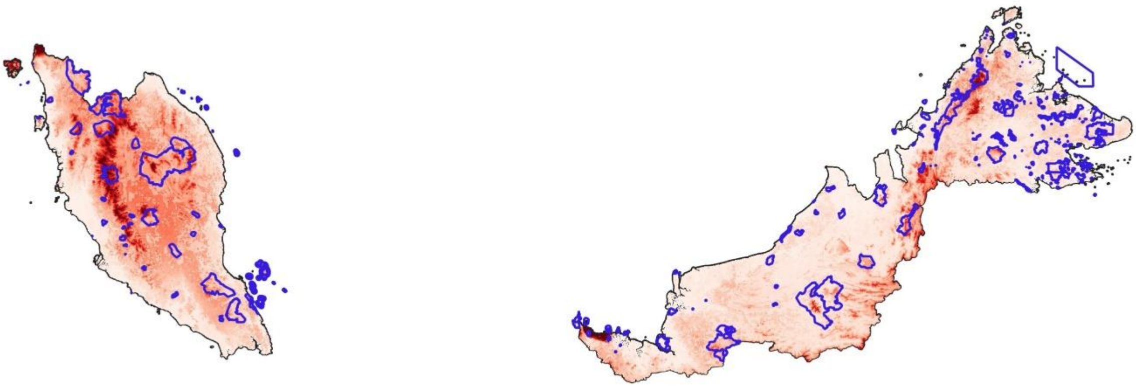

Figure 4.15: The comparison between the predicted distribution of *C. monticola* and the protected area in Malaysia. The red shades indicate the predicted distribution and the blue area indicates the protected area.

4.4 Discussion

4.4.1 Species distribution range

4.4.1.1 *Crocidura foetida*

The model suggests that *C. foetida* prefer areas with high elevation and dense forest, as documented by previous research (Ruedi, 1995; Cranbrook & Piper, 2008). The jackknife test and the analysis of variable contribution (Figure 4.7; Table 4.4) indicated that BIO19 (precipitation of coldest quarter) is the most important variable to the model. Precipitation of the coldest quarter refers to the three months period in a year that received the highest rainfall, which subsequently drop the surrounding temperature. With small body size and high metabolic rate, shrew depends on rainfall to decrease the metabolic rates to cope with the high humidity of Malaysian rainforest (Taylor et al., 2012). Water bodies are limited in montane forest, thus *C. foetida* that lives in high elevation depends on rainfall as water source as rainfall supports the application of small-sized water bodies (Wilting et al., 2010). Although scattered, mountain ranges and montane forest were predicted to have higher probability of *C. foetida*, whereas open and high-populated areas are least preferred by the species. These characteristics show the importance of protected area as a suitable habitat for this species (Figure 4.13). Western Sarawak predicted to be suitable for the habitat distribution of *C. foetida*. This is due to the occurrence record in some protected area which is also montane forests. Kubah NP, Gading NP, and Santubong NP were mountainous area that provide suitable conditions due to its dense forest and colder climate area. Central mountain ranges of Sarawak also have high probability of finding the distribution of *C. foetida*.

No apparent difference can be observed between the predicted distribution of *C. foetida* and *C. foetida doriae*. Both species and subspecies are predicted to occur on highland with only geographical factor separates them. *Crocidura foetida* is potentially distributed across highland in western Sarawak whereas *C. f. doriae* is predicted to distribute across highland in northern Sarawak (Figure 4.6(a)). Past climatic fluctuations were critical and could have resulted in the phylogeogprahic structure of the populations of *C. foetida* and its subspecies that can be observed today.

4.4.1.2 *Crocidura malayana*

For *C. malayana*, the model suggests a wide distribution across Peninsular Malaysia but is more concentrated at the west coast area (Figure 4.6(b)). Geographical barrier such as the mountain ranges may have limit its distribution to the south coast area. This species is not restricted in protected or low-populated area, indicating high adaptability. Based on the jackknife test and the analysis of variable contributions, two environmental variables are identified to contribute the most to the model, which are BIO7 and BIO5 (Figure 4.9; Table 4.4). BIO7 (temperature annual range) and BIO15 (precipitation seasonality) suggests that *C. malayana* is highly adaptable and also highly dependent on rainfall. Distributed widely across Peninsular Malaysia, *C. malayana* also depends on rainfall to cope with the high humidity and high temperature of Malaysian weather. The rainfall is able to lower the body temperature of *C. malayana* and subsequently decrease its metabolic rate (Taylor et al., 2012).

4.4.1.3 *Crocidura monticola*

Crocidura monticola is predicted to have high distribution on the Titiwangsa Range, according to the model (Figure 4.6(c)). In Sarawak and Sabah, this species is also predicted to be abundant in the mountainous area. Similar to *C. foetida*, montane forest provide suitable living conditions to *C. monticola* due to its low temperature and dense forest. Two environmental variables have been identified to be the most important for *C. monticola* distribution model, namely BIO19 (precipitation of coldest quarter) and BIO16 (precipitation of wettest quarter) (Figure 4.11; Table 4.4). The variables indicated that this species is also highly dependent on rainfall in the higher elevation area to decrease their metabolic rate and also as water source (Taylor et al., 2012).

4.4.2 IUCN Red List assesments

According to our predicted distribution model (Figure 4.4), *C. foetida* prefers dense, secluded and montane forest. The model however does not include record from Kalimantan as the occurrence record is not available. According to the IUCN distribution map, this species has a wider range with extent to Indonesia part of Borneo (Figure 4.2). The IUCN distribution map also includes coastal area, heavily populated area, and land use area. Known to have habitat preference on a much lower temperature, we can exclude the coastal area and also area with high anthropogenic activities. With such small body size, shrew species may not have a range that enables them to travel in a long distance and only reside in a particular area. Two other modelled species, *C. malayana* and *C. monticola* has a wider home range compared to *C. foetida*. The Malayan shrew, *C. malayana*, is predicted to occupy the west coast area compared to much larger distribution seen in the distribution map from IUCN (Figure 4.14). Geographical barrier such as the mountain range may have limit its distribution to the south coast area. The Sunda shrew, *C. monticola*, is predicted to occupy the mountainous area of Sabah and Sarawak and the Titiwangsa Range in Peninsular Malaysia. Similar to *C. foetida*, this species does not occupy coastal and highly populated area. The predicted distribution map for *C. monticola* is similar to the published map from IUCN Red List with the extent to Sumatra and Java (Figure 4.15).

Shrew species has limited information on their historical and current range, and MaxEnt is capable to assist conservation planning (Wilting et al., 2010). As one of the least known small mammals' species in Malaysia, its unique habitat preference makes it a suitable candidate for predictive modelling (Wilting et al., 2010). Comparing with the map of current habitat published by the IUCN Red List, the predicted distribution from this study provides a narrower range and specific result. Our maps suggest that these species have their own preferences in regards of temperature, elevation, humidity, and type of forest.

4.4.3 The importance of protected area

The predicted distribution map for the three modelled species indicated that these species has low preferences for cultivated landscapes, highly populated area, and coastal area compared to dense, primary forest. The model also predicted that the shrew species tend to avoid open areas. These characteristics are indicators of the importance of protected area as a reservoir for shrew population. There are also area of potentially highly suitable habitat patches that exists outside the boundary of protected area, peculiarly around the middle part of Peninsular Malaysia and Sarawak.

4.4.3.1 Peninsular Malaysia

According to the Department of Wildlife and National Park (2016), almost three million hectares of forest area in Peninsular Malaysia has been gazetted as protected area, covering approximately 23% of total area. Through recent findings of endemic and rare species, local authorities noticed the importance of gazetting forests as protected area as it may boost the animal species diversity in the said area (Francis et al., 2007; Jayaraj et al., 2013*). Crocidura malayana* is potentially found in most of the protected area in Peninsular Malaysia as its distribution range is wide and broad (Figure 4.6(b)). Another modelled species that can be found in Peninsular Malaysia is *C. monticola* which have a more patchy distribution (Figure 4.6(c)). This species has a narrower range, focusing on the middle part of Peninsular Malaysia, and potentially found at Taman Negara, Fraser's Hill and the Permanent Reserved Forests (PFRs).

4.4.3.2 Borneo

In Sabah and Sarawak, approximately three millions hectares of forest have been gazetted as protected area (Forest Department Sarawak, 2017; Sabah Forestry, 2017). Protected area is an effective tool in conserving animal species as recent findings suggested high animal diversity (Mount Kinabalu – Nor, 2001; Bako – Khan et al., 2007; Wind Cave NR – Rahman et al., 2011). There is high potential of capturing *C. foetida* in the western part of Sarawak in which is located the protected area of Gunung Gading NP, Gunung Santubong NP, Kubah NP, Dered Krian NP, and Bako NP. In Sabah, they can be potentially caught in the mountainous area of Kinabalu and Crocker Range which are also protected area. Shrew population in the northen part of Sarawak are well in the boundaries of Heart of Borneo (HoB) Initiative. The HoB Initiative is a programme aiming to conserve the biodiversity in Borneo Island for the benefit of the locals who rely upon it (WWF, 2017). This programme was initiated by the governments of Malaysia, Brunei, and Indonesia in 2007 (WWF, 2017).

The predicted distribution map of the three modelled species shows a large area of potential habitat that is not in the vicinity of protected area. Extensive studies can be conducted in the area outside of the protected area boundaries. Even though shrew is not being hunted and may have not high economic value, its role in the ecosystem is crucial. They control the population of insects by having its larvae and pupae as their diet and also a food source to a larger predator (Yoshino & Abe, 1984). The main threats for shrew are habitat degradation and anthropogenic activities (IUCN, 2018). Known also to be highly adaptable, lack of suitable habitat and decreasing food source may cause the species to decline in time.

4.4.4 Potential drawback of MaxEnt

MaxEnt does have a few limitations that can affect the performance of its model. Sample selection bias has a bigger impact on presence-only models than on presence-absence models (Phillips et al., 2009). Some areas may have been sampled more extensively than the others, thus the model will only combine the species distribution with the distribution of sampling effort (Soberon & Nakamura, 2009). To control the sample selection bias, Elith et al (2010) suggest creating sample bias grid by assigning greater weight to the species presence-only point with fewer neighbours in geographic space. The presence-only point compiled does not include temporal records, thus the area that is not suitable environmentally and under-sampled area cannot be distinguished (Clements et al., 2012). Sampling to be done equally across the study area can also be conducted.

With presence-only points, the occurrence records usually do not include temporal or spatial scale (Elith et al., 2011). The records only have the location or the coordinate of the species, and no information on the search area included. Information on the location where the species is found enables more detailed environmental variables (e.g more accurate and recent land cover for Malaysia) to be chosen and used in the model. This will help to increase the performance of the model and its predictive power (Elith et al., 2006; Elith et al., 2011).

4.5 Conclusion

This study used the Maximum Entropy model to predict the distribution and modelled potential habitat of three species of Malaysian shrews (*C. foetida, C. malayana, C. monticola*). The predicted model is the first step to plan conservation management and efforts. Known as common to lowland area, *C. foetida* and *C. monticola* are predicted to have high preferences on cooler climate and undisturbed montane forest. As expected, *C. malayana* is predicted to be distributed abundantly across Peninsular Malaysia, with the massive Titiwangsa Range is predicted to be their preference.

Detailed site-specific multiple year studies would be needed to improve the current knowledge on the habitat preference and requirements of the shrew species. There are plenty of potential areas for this purpose as predicted in this study. Based on our results, the IUCN Red List's range map for the three modelled species can be improved by eliminating the open and disturbed area and acknowledging the potential utility of SDMs. The distribution maps from this study are able to suggest a more specific distribution of the modelled species compared to those from IUCN. An intensive conservation of highly suitable areas identified from our model and the IUCN distribution map is recommended.

Protected area plays a major role in sustaining the animal species within in with the goals of reducing habitat loss (Wilcox, 1984). Protecting and conserving biological and genetic resources are critical and can be achieved by establishing protected areas on existing forest, where human disturbances are limited by law. However, non-protected area may also hold high animal diversity that is highly adaptable (Jayaraj, 2006). The predicted distribution of shrew outside the boundary of protected area can be explored to potentially found new population of shrew and records new occurrence data for shrew species.

Species distribution modelling can help in providing important information needed in preparing and planning conservation strategies as well to predict environmental changes and describing patterns of rare species diversity (Wilting et al., 2010; Clements et al., 2012). The application of species distribution models to conserve and manage little known and rare species are numerous, but a requirement for an effective wildlife and conservation policy is a continuous monitoring program on the state and extent of the habitat (Ferrer-Sanchez & Rodriguez-Estrella, 2016). Successful management for conservation of shrew species should focus on the areas with higher suitability as identified by our model where shrew species are extant. Conserving lowland tropical forests and preserving corridors within that habitat should help in the movement of remaining populations and lead to long term survival of shrew.

CHAPTER 5

GENERAL DISCUSSION AND CONCLUSIONS

5.1 General discussion

This study aims in understanding the phylogeographic and potential distribution of the Bornean shrew, *C. foetida* which has been poorly studied. This species has three subspecies, namely *C. f. foetida, C. f. doriae,* and *C. f. kelabit* which were described based on morphometric data (Ruedi, 1995). The subspecies, *C. foetida foetida, C. foetida doriae, C. foetida kelabit* occupy different elevations and area; *C. foetida foetida* in the lowlands, *C. foetida doriae* in the highlands, and *C. foetida kelabit* can only be found in Kelabit Highlands of Sarawak.

To achieve the research objectives, this study was divided into two major parts. The first part is using genetic data where a single mitochondrial DNA (Cytochrome *b*) was used. Partial DNA sequences were obtained from each captured specimen through molecular works. This study, based on samples from northern Sarawak, enable us to define two clades within *C. foetida*. These two clades however have close genetic distance (2.2%-2.8%). According to Bradley and Baker (2001), genetic distance less than 2% indicates intraspecific variation while 2% - 11% requires additional research to clarify the status of studied species. A value more than 11% indicates species recognition (Bradley & Baker, 2001). Craniodental analysis does not show any distinct grouping between localities, contrary with genetic data where noticeable grouping can be observed. This study revealed that *C. f. doriae* is a subspecies of *C. foetida* in which this two subspecies was once a single species but later diverged due to geographical factors.

The second part consists of modelling the potential distribution of three white-toothed shrews from Malaysia, namely *C. foetida*, *C. malayana*, and *C. monticola*. The ecological niche modelling, Maximum Entropy (MaxEnt) model is used in this study. MaxEnt model is widely used by ecologist in recent times due to its ability to run solely on presence-only points. Twenty-one environmental variables were used as the predictor alongside a compilation of shrews documented records from recent various sources. Based on the distribution model produced, *C. foetida* and *C. monticola* prefers a much cooler climate in the dense montane forest. These species were thought to be common in lowland but the distribution was predicted to be much abundance in higher ground and in primary undisturbed forest.

5.2 Recommendations

Due to the difficulty in catching shrew species, this study has limited sample size. A bigger sample size is needed to clarify more on the phylogenetic relationship of *C. foetida*. That being said, a more extensive sampling coverage across Borneo Island should be carried out in order to truly understand the systematic of *C. foetida* and to improve the accuracy of the species distribution model. Results on the craniodental analysis suggest a bigger sample size is needed. Genetic markers other than Cyt *b* such as BRCA, MCGf, RAG1 and vWF (adapted from Esselstyn et al., 2009) can be explored to provide better insight on the genetic information on these species.

5.3 Conclusion

This study had successfully answered all the research objectives which we are able to compare the phylogeography relationship of the Bornean shrew, *C. foetida* using mtDNA cytochrome *b*. The phylogenetic analysis of Bornean shrew samples collected from Sarawak reveals that *C. f. doriae* is a subspecies of *C. foetida*. Next, we presented three predicted distribution models of three shrew species from Malaysia. Two of the shrew species, *C. foetida* and *C. monticola* prefer a cooler climate in the dense montane forest. Another shrew species, *C. malayana* can be found abundantly across Peninsular Malaysia with Titiwangsa Range as their preferred area. Predicted distribution of these three species shows a large area of potential habitat that is not in the boundary of protected area. These models are critical in conservation planning and management strategies for these rare species.

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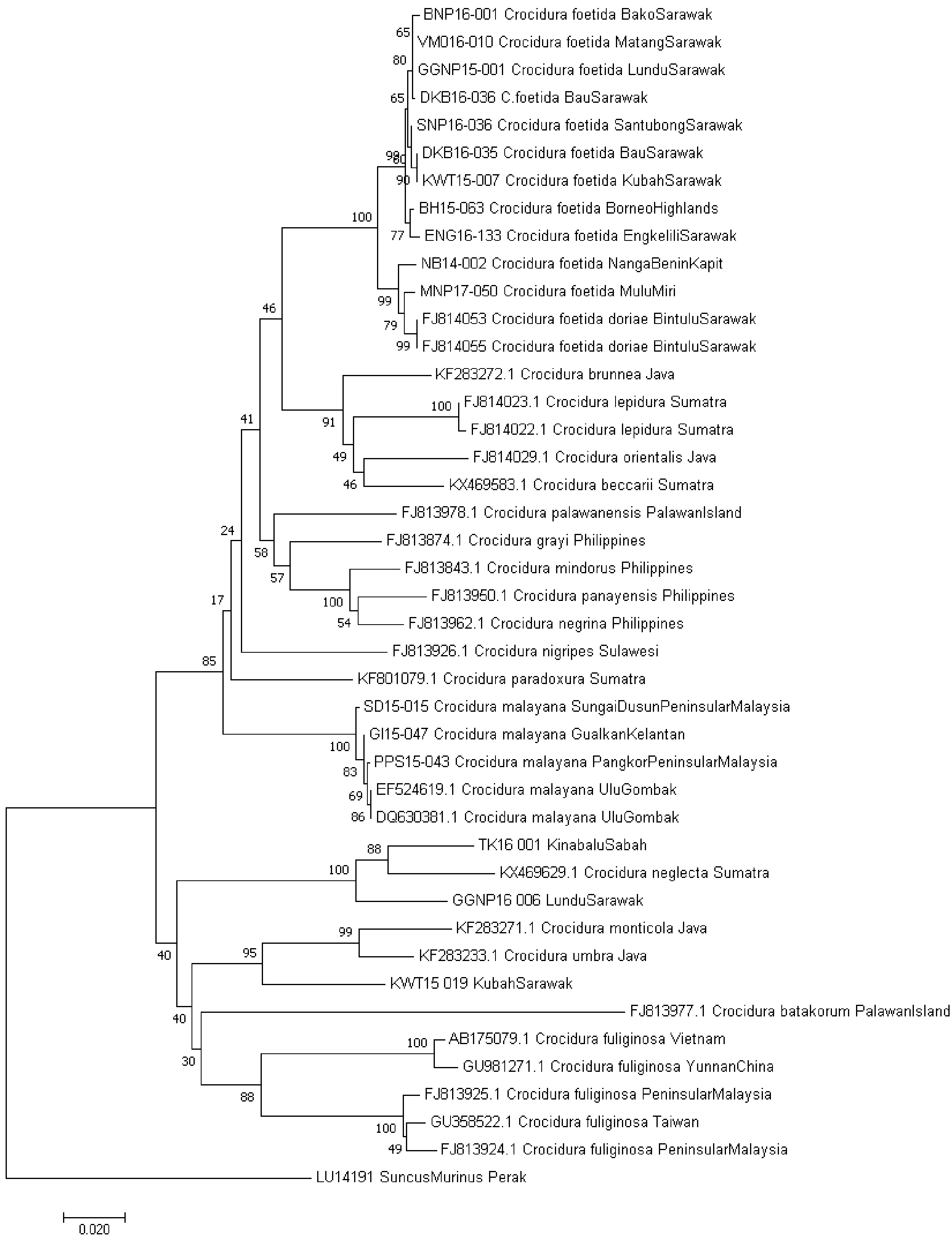
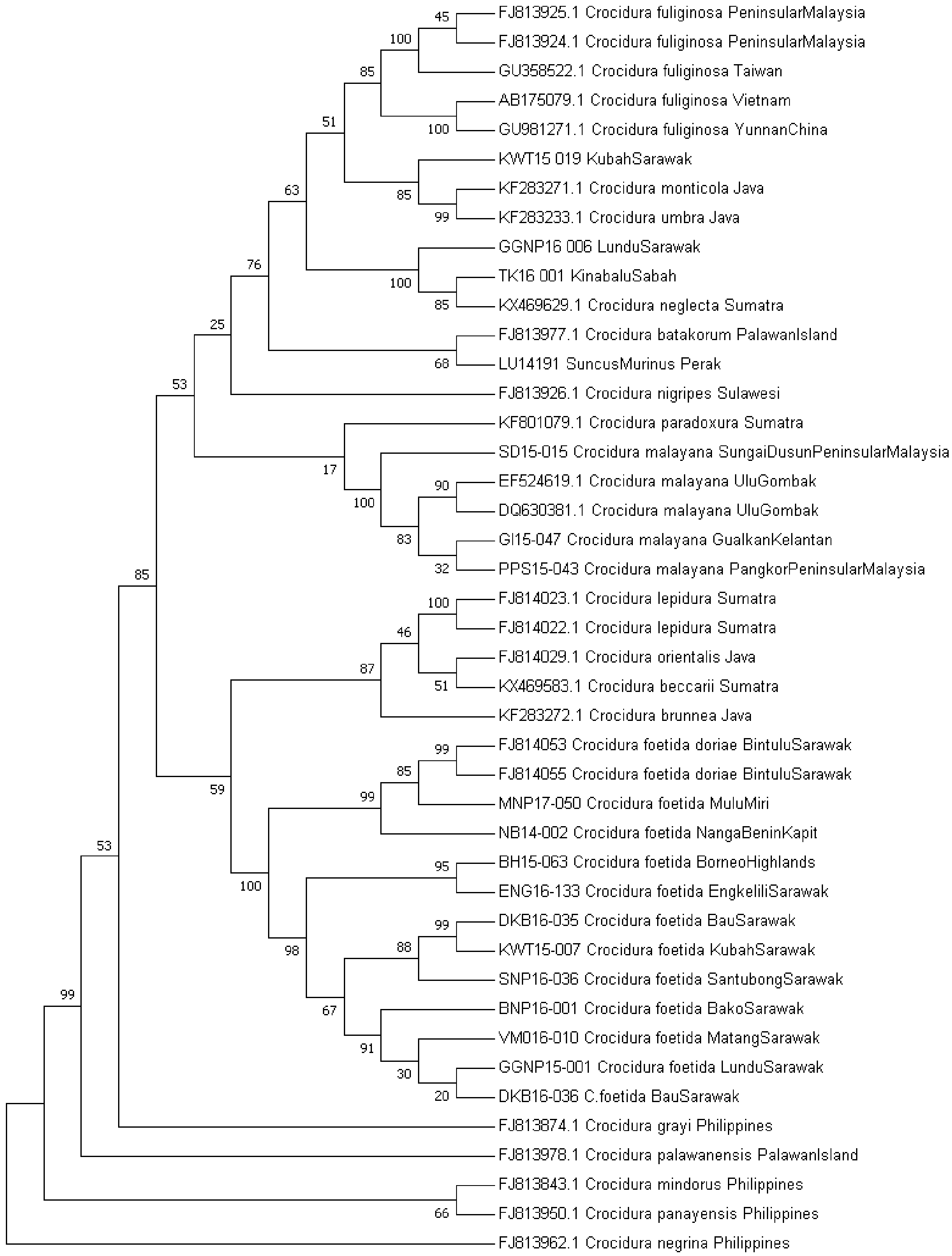
APPENDICES

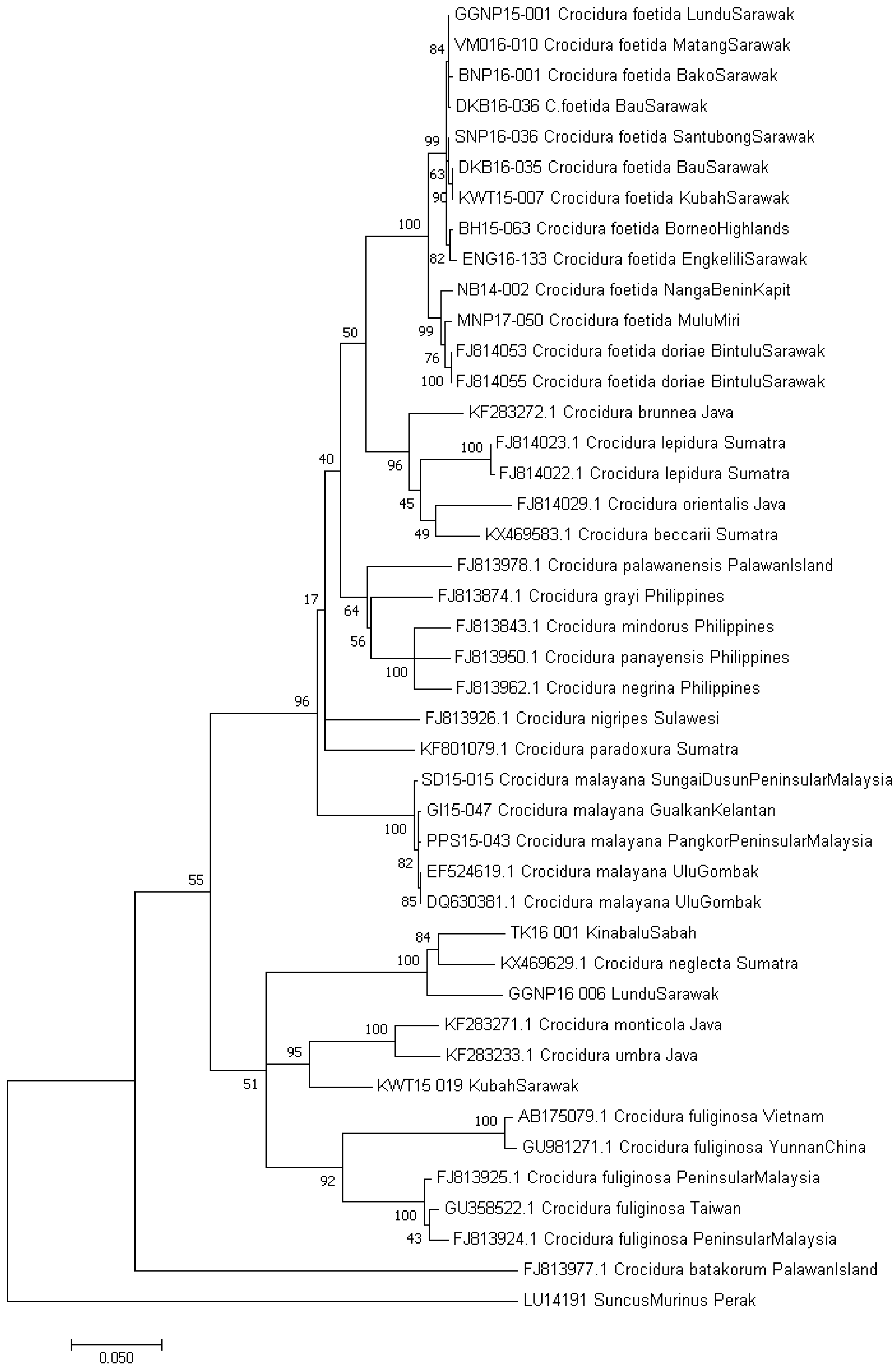
Appendix 1.0: Pylogenetic relationship of genus *Crocidura* inferred from mtDNA cytochrome *b* reconstructed using Neighbour-Joining method



Appendix 2.0: Pylogenetic relationship of genus *Crocidura* inferred from mtDNA cytochrome *b* reconstructed using Maximum Parsimony method



Appendix 3.0: Pylogenetic relationship of genus *Crocidura* inferred from mtDNA cytochrome *b* reconstructed using Maximum Likelihood method.



Appendix 4.0: The sequence used in the phylogenetic analysis

AB175079.1 Crocidura fuliginosa Vietnam	GCTTAATCGCACAAATCCTAACCGGACTATTTCTAGCAATACACTATACATCAGACACCATAACCGCCTTCTCCTCCG
GU981271.1 Crocidura fuliginosa YunnanChina	GCTTAATCGCACAAATCCTAACCGGGCTATTTCTAGCAATACACTATACATCAGACACCATAACCGCCTTCTCCTCCG
GU358522.1 Crocidura fuliginosa Taiwan	GCTTAATCGCACAAATCCTGACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCCTTCTCCTCCG
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	GCTTAATCGCACAAATCCTGACCGGACTATTTTTAGCCATACACTATACATCAGACACCATAACAGCCTTCTCCTCCG
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	GCTTAATAGCACAAATCCTGACCGGACTATTTTTAGCCATACACTATACATCAGACACCATAACAGCCTTCTCCTCCG
FJ814023.1 Crocidura lepidura Sumatra	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCCATACACTACACATCAGACACCATAACAGCCTTCTCCTCCG
FJ814022.1 Crocidura lepidura Sumatra	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCCATACACTACACATCAGACACCATAACAGCCTTCTCCTCCG
KF801079.1 Crocidura paradoxura Sumatra	GTTTAATCGCACAAATCTTAACCGGACTATTTTTAGCCATACACTATACATCAGACACCATAACAGCCTTCTCCTCCG
EF524619.1 Crocidura malayana UluGombak	GTCTAATCGCACAAATCCTAACTGGGTTATTTCTAGCTATACACTATACATCAGATACCATAACAGCTTTCTCCTCCG
FJ814053 Crocidura foetida doriae BintuluSarawak	GTTTAATTGCACAAATCCTAACCGGACTATTCTTAGCTATACACTATACATCAGACACCATAACAGCCTTCTCCTCCG
FJ814055 Crocidura foetida doriae BintuluSarawak	GTTTAATTGCACAAATCCTAACCGGACTATTCTTAGCTATACACTATACATCAGACACCATAACAGCCTTCTCCTCCG
KF283271.1 Crocidura monticola Java	GCTTAATCACACAAATCTTAACCGGACTATTTTTAGCTATACACTATACATCAGATACCATAACAGCCTTCTCCTCCG
BH15-063 Crocidura foetida BorneoHighlands	GTTTAATCGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCTTTCTCCTCCG
BNP16-001 Crocidura foetida BakoSarawak	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCTTTCTCCTCCG
DKB16-035 Crocidura foetida BauSarawak	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCTTTCTCCTCCG
ENG16-133 Crocidura foetida EngkeliliSarawak	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCTTTCTCCTCCG
GGNP15-001 Crocidura foetida LunduSarawak	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCTTTCTCCTCCG
DQ630381.1 Crocidura malayana UluGombak	GTCTAATCGCACAAATCCTAACTGGGTTATTTCTAGCTATACACTATACATCAGATACCATAACAGCTTTCTCCTCCG
GI15-047 Crocidura malayana GualkanKelantan	GTCTAATCGCACAAATCCTAACTGGGCTATTTCTAGCTATACACTATACATCAGATACCATAACAGCTTTCTCCTCCG
KWT15-007 Crocidura foetida KubahSarawak	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCTTTCTCCTCCG
MNP17-050 Crocidura foetida MuluMiri	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCCTTCTCCTCCG
NB14-002 Crocidura foetida NangaBeninKapit	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCTTTCTCCTCCG
DKB16-036 C.foetida BauSarawak	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCTTTCTCCTCCG
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	GTCTAATCGCACAAATCCTAACTGGGCTATTTCTAGCTATACACTATACATCAGATACCATAACAGCTTTCTCCTCCG
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	GTCTAATCGCACAAATCCTAACTGGGCTATTTCTAGCTATACACTATACATCAGACACCATAACAGCTTTCTCCTCCG
KF283272.1 Crocidura brunnea Java	GCTTAATTGCACAAATCCTAACCGGACTATTTTTAGCCATACATTATACATCAGACACTATAACAGCTTTCTCCTCCG
FJ813926.1 Crocidura nigripes Sulawesi	GTTTAATCGCTCAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGATACCATAACAGCTTTCTCCTCCG
FJ813874.1 Crocidura grayi Philippines	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCTATACACTACACATCAGACACCATAACAGCTTTTTCCTCCG
SNP16-036 Crocidura foetida SantubongSarawak	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCTTTCTCCTCCG
VM016-010 Crocidura foetida MatangSarawak	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGACACCATAACAGCTTTCTCCTCCG
KF283233.1 Crocidura umbra Java	GCTTAATCGCACAAATCCTAACCGGACTATTTTTAGCCATACACTACACATCAGACACCATAACAGCCTTCTCCTCCG
FJ814029.1 Crocidura orientalis Java	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCCATACATTACACATCAGACACCATAACAGCTTTCTCTTCCG
FJ813977.1 Crocidura batakorum PalawanIsland	GTTTAATTGCTCAAATTCTAACCGGATTATTTCTAGCCATACATTACACATCTGATACCATAACAGCCTTCTCCTCTG
FJ813978.1 Crocidura palawanensis PalawanIsland	GCTTAATTGCACAAATCCTAACCGGATTATTTTTAGCTATACACTACACATCAGACACCATAACAGCCTTCTCCTCCG
LU14191 SuncusMurinus Perak	GGTTAATTGCACAAATCCTTACCGGCCTATTCCTAGCCATACATTACACATCAGACACTATAACAGCTTTTTCCTCCG
TK16 001 KinabaluSabah	GCTTAATTGCACAAATCCTAACCGGATTATTTTTAGCTATACACTACACATCAGATACTATAACAGCTTTCTCTTCCG
GGNP16 006 LunduSarawak	GCCTAATTGCACAAATTCTAACCGGATTATTTCTAGCTATACACTACACATCAGATACTATAACAGCTTTTTCCTCCG
KWT15 019 KubahSarawak	GCTTAATCGCACAAATCCTAACCGGACTATTTTTAGCTATACACTATACATCAGATACCATAACAGCCTTCTCCTCCG
FJ813843.1 Crocidura mindorus Philippines	GCTTAATTGCACAAATTCTAACCGGACTATTTTTAGCCATACACTACACATCAGACACCATAACAGCTTTCTCCTCCG
FJ813950.1 Crocidura panayensis Philippines	GTTTAATTGCACAAATCCTAACCGGACTATTTTTAGCCATACACTACACATCAGATACCATAACAGCTTTCTCCTCCG
FJ813962.1 Crocidura negrina Philippines	GTTTAATCGCACAAATCCTAACCGGACTATTCTTAGCTATACACTACACATCAGATACCATAACAGCTTTCTCCTCCG
KX469583.1 Crocidura beccarii Sumatra	GTTTAATTGCACAAATCCTAACCGGACTATTTCTAGCCATGCACTATACATCAGACACCATAACAGCCTTCTCTTCCG
KX469629.1 Crocidura neglecta Sumatra	GCCTAATTGCACAAATCCTAACCGGATTATTTTTAGCTATACACTACACATCAGATACTATAACAGCTTTCTCCTCCG

AB175079.1 Crocidura fuliginosa Vietnam	TTACACACATCTGCCGCGAT GTAAATTACGGTTGATTAATTCGATATCTTCACGCTAACGGAGCCTCCATATTTTTTA
GU981271.1 Crocidura fuliginosa YunnanChina	TTACACACATCTGCCGCGAT GTAAATTACGGTTGATTAATTCGATATCTTCACGCTAACGGAGCCTCCATATTTTTTA
GU358522.1 Crocidura fuliginosa Taiwan	TTACGCACATTTGCCGAGAT GTAAACTACGGCTGATTAATTCGATATCTCCACGCTAACGGAGCCTCTATATTTTTTA
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	TTACACACATTTGCCGAGAT GTAAACTACGGCTGATTAATTCGATATCTCCACGCTAACGGAGCCTCTATATTTTTTA
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	TTACGCACATTTGCCGAGAT GTAAACTACGGCTGATTAATTCGATACCTCCACGCTAACGGGGCCTCTATATTTTTTA
FJ814023.1 Crocidura lepidura Sumatra	TCACCCACATCTGCCGAGAT GTAAATTACGGCTGATTAATCCGATACCTCCACGCCAACGGGGCCTCTATATTTTTCA
FJ814022.1 Crocidura lepidura Sumatra	TCACCCACATCTGCCGAGAT GTAAATTACGGCTGATTAATCCGATACCTCCACGCCAACGGGGCCTCTATATTTTTCA
KF801079.1 Crocidura paradoxura Sumatra	TCACACACATTTGCCGAGAC GTTAATTATGGCTGACTAATTCGATATCTCCACGCTAATGGGGCCTCTATATTCTTCA
EF524619.1 Crocidura malayana UluGombak	TCACACACATCTGCCGAGAC GTAAATTATGGCTGACTAATCCGTTATCTCCACGCCAATGGAGCCTCCATATTTTTCA
FJ814053 Crocidura foetida doriae BintuluSarawak	TCACACATATTTGCCGAGAT GTAAATTATGGTTGATTAATTCGATATCTTCACGCCAATGGAGCCTCCATATTCTTTA
FJ814055 Crocidura foetida doriae BintuluSarawak	TCACACATATTTGCCGAGAC GTAAATTATGGTTGATTAATTCGATATCTTCACGCCAATGGAGCCTCCATATTCTTTA
KF283271.1 Crocidura monticola Java	TCACACATATCTGTCGAGAT GTGAATTATGGCTGACTAATCCGATATCTCCACGCTAACGGAGCCTCCATATTTTTCA
BH15-063 Crocidura foetida BorneoHighlands	TCACACATATTTGCCGAGAT GTAAATTATGGCTGATTAATTCGATACCTTCACGCCAATGGAGCCTCTATATTCTTTA
BNP16-001 Crocidura foetida BakoSarawak	TCACACATATTTGCCGAGAT GTAAATTATGGCTGATTAATTCGATACCTTCACGCCAATGGAGCCTCTATATTCTTTA
DKB16-035 Crocidura foetida BauSarawak	TCACACATATTTGCCGAGAT GTAAATTATGGCTGATTAATTCGATACCTTCACGCCAATGGAGCCTCTATATTCTTTA
ENG16-133 Crocidura foetida EngkeliliSarawak	TCACACATATTTGCCGAGAT GTAAATTATGGCTGATTAATTCGTTACCTTCACGCCAATGGAGCCTCTATATTCTTTA
GGNP15-001 Crocidura foetida LunduSarawak	TCACACATATTTGCCGAGAT GTAAATTATGGCTGATTAATTCGATACCTTCACGCCAATGGAGCCTCTATATTCTTTA
DQ630381.1 Crocidura malayana UluGombak	TCACACACATCTGCCGAGAC GTAAATTATGGCTGACTAATCCGTTATCTCCACGCCAATGGAGCCTCCATATTTTTCA
GI15-047 Crocidura malayana GualkanKelantan	TCACACACATCTGCCGAGAC GTAAATTATGGCTGACTAATCCGTTATCTCCACGCCAATGGAGCCTCCATATTTTTCA
KWT15-007 Crocidura foetida KubahSarawak	TCACACATATTTGCCGAGAT GTAAATTATGGCTGATTAATTCGATACCTTCACGCCAATGGAGCCTCTATATTCTTTA
MNP17-050 Crocidura foetida MuluMiri	TCACACATATTTGCCGAGAT GTGAATTATGGTTGATTAATTCGATACCTTCACGCCAATGGAGCCTCCATATTCTTTA
NB14-002 Crocidura foetida NangaBeninKapit	TCACACATATTTGCCGAGAT GTAAATTATGGTTGATTAATTCGATACCTTCACGCCAATGGAGCCTCTATATTCTTTA
DKB16-036 C.foetida BauSarawak	TCACACATATTTGCCGAGAT GTAAATTATGGCTGATTAATTCGATACCTTCACGCCAATGGAGCCTCTATATTCTTTA
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	TCACACACATCTGCCGAGAC GTAAATTATGGCTGACTAATCCGTTATCTCCACGCCAATGGAGCCTCCATATTTTTCA
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	TCACACACATCTGCCGAGAC GTAAATTATGGCTGACTAATCCGTTATCTCCACGCCAATGGAGCCTCCATATTTTTCA
KF283272.1 Crocidura brunnea Java	TCACACATATCTGCCGAGAC GTAAATTATGGTTGATTAATCCGATACCTCCACGCCAACGGAGCCTCTATATTTTTCA
FJ813926.1 Crocidura nigripes Sulawesi	TCACACATATCTGCCGAGAC GTAAATTACGGCTGACTAATTCGATACCTCCATGCCAACGGAGCCTCTATATTCTTCA
FJ813874.1 Crocidura grayi Philippines	TCACACATATCTGCCGAGAT GTAAATTACGGCTGACTAATCCGATATCTCCACGCCAATGGAGCCTCTATATTCTTCA
SNP16-036 Crocidura foetida SantubongSarawak	TCACACATATTTGCCGAGAW GTAAATTATGGCTGATTAATTCGATACCTTCACGCCAATGGAGCCTCTATATTCTTTA
VM016-010 Crocidura foetida MatangSarawak	TCACACATATTTGCCGAGAT GTAAATTATGGCTGATTAATTCGATACCTTCACGCCAATGGAGCCTCTATATTCTTTA
KF283233.1 Crocidura umbra Java	TCACACATATCTGTCGAGAT GTAAATTATGGCTGACTAATTCGATATCTCCACGCTAACGGAGCCTCTATATTCTTCA
FJ814029.1 Crocidura orientalis Java	TCACACACATCTGCCGAGAT GTAAACTATGGCTGATTAATTCGATATCTCCACGCCAACGGAGCCTCCATATTTTTCA
FJ813977.1 Crocidura batakorum PalawanIsland	TTACACATATCTGCCGAGAT GTAAATTATGGTTGATTAATCCGATATCTTCATGCTAACGGCGCATCCATATTTTTCA
FJ813978.1 Crocidura palawanensis PalawanIsland	TCACACACATTTGCCGAGAT GTAAATTATGGTTGACTAATTCGATATCTCCACGCCAACGGAGCCTCAATATTCTTCA
LU14191 SuncusMurinus Perak	TAACACACATCTGCCGAGAC GTAAATTATGGCTGACTAATTCGTTATTTACACGCAAATGGCGCTTCCATATTTTTCA
TK16 001 KinabaluSabah	TCACACATATCTGCCGAGAT GTAAACTACGGCTGATTAATTCGATATCTTCACGCCAACGGAGCCTCTATATTTTTCA
GGNP16 006 LunduSarawak	TCACACATATCTGCCGAGAT GTAAACTACGGCTGATTAATTCGATATCTTCACGCCAACGGAGCCTCTATATTTTTCA
KWT15 019 KubahSarawak	TCACACATATCTGTCGAGAT GTAAATTATGGCTGACTAATTCGATATCTCCACGCCAACGGAGCCTCCATATTTTTCA
FJ813843.1 Crocidura mindorus Philippines	TCACACATATCTGCCGAGAT GTAAATTATGGTTGACTAATTCGATATCTACACGCCAATGGAGCCTCTATATTCTTCA
FJ813950.1 Crocidura panayensis Philippines	TCACACATATCTGCCGAGAT GTAAATTATGGTTGACTAATTCGATATCTCCATGCCAATGGAGCCTCTATATTTTTCA
FJ813962.1 Crocidura negrina Philippines	TCACACATATCTGCCGAGAT GTAAATTATGGTTGACTAATTCGATATCTCCACGCCAATGGAGCCTCTATATTCTTCA
KX469583.1 Crocidura beccarii Sumatra	TCACACACATCTGCCGAGAT GTAAATTATGGCTGATTAATCCGATACCTCCATGCCAACGGGGCCTCCATATTTTTCA
KX469629.1 Crocidura neglecta Sumatra	TCACACATATCTGCCGAGAC GTAAACTACGGTTGATTAATTCGATATCTCCACGCCAACGGAGCCTCTATATTCTTTA

AB175079.1 Crocidura fuliginosa Vietnam	TTTGCCTATTCCTCCATGTCGGACGAGGATTATATTATGGCTCCTATATATTCCTTGAAACATGAAACATTGGTGTTC
GU981271.1 Crocidura fuliginosa YunnanChina	TTTGCCTATTCCTCCATGTCGGACGAGGATTATATTATGGCTCCTATATATACCTTGAAACATGAAACATTGGTGTTC
GU358522.1 Crocidura fuliginosa Taiwan	TTTGCCTATTCCTTCATGTAGGACGAGGACTTTATTACGGCTCTTACATATATCTTGAAACATGAAACATTGGCGTTC
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	TTTGCCTATTCCTTCATGTAGGACGAGGACTTTATTACGGCTCTTACATATATCTTGAAACATGAAACATTGGCGTTC
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	TTTGCCTATTCCTTCATGTAGGACGAGGGCTTTATTACGGCTCTTATATATATCTTGAAACATGAAACATTGGCGTTC
FJ814023.1 Crocidura lepidura Sumatra	TTTGCTTATTTCTTCACGTAGGACGAGGACTCTACTATGGTTCCTATATATTTCTTGAAACATGAAACATTGGTGTCC
FJ814022.1 Crocidura lepidura Sumatra	TTTGCTTATTTCTTCACGTAGGACGAGGACTCTACTATGGTTCCTATATATTTCTTGAAACATGAAACATTGGTGTCC
KF801079.1 Crocidura paradoxura Sumatra	TTTGCCTATTCCTTCATGTAGGCCGAGGACTCTACTATGGCTCTTATATATTCCTTGAAACATGAAACATTGGCGTTC
EF524619.1 Crocidura malayana UluGombak	TTTGCCTATTCCTCCATGTAGGACGAGGACTCTATTATGGCTCTTATATATTCCTTGAAACATGAAATATTGGAGTTT
FJ814053 Crocidura foetida doriae BintuluSarawak	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
FJ814055 Crocidura foetida doriae BintuluSarawak	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
KF283271.1 Crocidura monticola Java	TCTGCCTGTTCCTTCACGTAGGCCGAGGACTCTATTATGGCTCCTACATATACCTTGAAACATGAAATATTGGTGTTC
BH15-063 Crocidura foetida BorneoHighlands	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
BNP16-001 Crocidura foetida BakoSarawak	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
DKB16-035 Crocidura foetida BauSarawak	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
ENG16-133 Crocidura foetida EngkeliliSarawak	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
GGNP15-001 Crocidura foetida LunduSarawak	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
DQ630381.1 Crocidura malayana UluGombak	TTTGCCTATTCCTCCATGTAGGACGAGGACTCTATTATGGCTCTTATATATTCCTTGAAACATGAAATATTGGAGTTT
GI15-047 Crocidura malayana GualkanKelantan	TTTGCCTATTCCTCCATGTAGGACGAGGACTCTATTATGGCTCTTATATATTCCTTGAAACATGAAATATTGGAGTTT
KWT15-007 Crocidura foetida KubahSarawak	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
MNP17-050 Crocidura foetida MuluMiri	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
NB14-002 Crocidura foetida NangaBeninKapit	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGTTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
DKB16-036 C.foetida BauSarawak	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	TTTGCCTATTCCTCCATGTAGGACGAGGACTCTATTATGGCTCTTATATATTCCTTGAAACATGAAATATTGGAGTTT
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	TTTGCCTATTCCTCCATGTAGGACGAGGACTCTATTATGGCTCTTATATATTCCTTGAAACATGAAATATTGGAGTTT
KF283272.1 Crocidura brunnea Java	TTTGCTTATTTCTTCATGTAGGACGAGGACTCTACTATGGCTCCTATATATTCCTTGAAACATGAAACATTGGTGTCC
FJ813926.1 Crocidura nigripes Sulawesi	TTTGCCTGTTCCTCCATGTAGGACGAGGACTCTACTATGGCTCCTATATATTTCTTGAAACATGAAACATTGGCGTCC
FJ813874.1 Crocidura grayi Philippines	TTTGCCTGTTCCTCCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTCC
SNP16-036 Crocidura foetida SantubongSarawak	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
VM016-010 Crocidura foetida MatangSarawak	TCTGCTTATTCCTTCATGTAGGACGAGGACTCTACTATGGCTCCTACATATTCCTTGAAACATGAAACATTGGTGTTC
KF283233.1 Crocidura umbra Java	TCTGCCTATTCCTTCACGTAGGCCGAGGACTCTACTATGGCTCCTACATGTACCTTGAAACATGAAATATTGGTGTTC
FJ814029.1 Crocidura orientalis Java	TTTGCTTATTCCTACACGTAGGACGAGGACTCTACTACGGCTCCTATATATTCCTCGAAACATGAAATATCGGTGTCC
FJ813977.1 Crocidura batakorum PalawanIsland	TCTGCCTTTTCCTCCATGTAGGACGAGGACTCTACTATGGCTCCTATATATACCTCGAAACATGAAATATCGGCGTTC
FJ813978.1 Crocidura palawanensis PalawanIsland	TTTGCCTATTCCTTCATGTAGGACGAGGGCTCTACTATGGCTCCTATATATTTCTTGAAACATGAAACATCGGTGTCC
LU14191 SuncusMurinus Perak	TTTGCCTTTTTCTTCATGTGGGCCGAGGACTTTATTATGGTTCTTATATATTTCTTGAAACATGGAACATTGGCGTAT
TK16 001 KinabaluSabah	TCTGCCTATTCCTTCACGTAGGCCGAGGACTCTACTACGGCTCTTACATATATCTCGAAACATGAAATATTGGTATCT
GGNP16 006 LunduSarawak	TTTGCCTATTCCTTCACGTAGGCCGAGGACTCTACTACGGCTCTTATATGTATCTCGAAACATGAAATATTGGCATTC
KWT15 019 KubahSarawak	TTTGCCTATTTCTTCATGGAGGCCGAGGACTCTATTATGGCTCCTACATATATCTTGAAACATGAAATATTGGTGTTC
FJ813843.1 Crocidura mindorus Philippines	TTTGCCTATTTCTCCATGTAGGACGAGGACTTTACTATGGCTCCTATATATTCCTTGAAACATGAAACATTGGTGTTC
FJ813950.1 Crocidura panayensis Philippines	TTTGCCTATTTCTCCATGTAGGACGGGGACTTTACTATGGCTCCTATATATTCCTTGAAACATGAAATATTGGTGTCC
FJ813962.1 Crocidura negrina Philippines	TTTGCCTATTTCTCCATGTAGGACGAGGACTCTACTATGGCTCCTATATATTCCTTGAAACATGAAACATTGGTGTCC
KX469583.1 Crocidura beccarii Sumatra	TTTGCTTATTTCTTCACGTAGGACGAGGACTCTACTATGGCTCCTATATATTTCTTGAAACATGAAACATCGGTGTCC
KX469629.1 Crocidura neglecta Sumatra	TTTGCTTATTCCTTCACGTAGGCCGAGGACTTTATTACGGCTCTTACATATATCTTGAAACATGAAATATTGGCGTCC

AB175079.1 Crocidura fuliginosa Vietnam	TACTTCTATTTGCAGTTATAGCTACTGCCTTTATAGGGTATGTTCTTCCCTGAGGTCAAATATCATTCTGAGGCGCGA
GU981271.1 Crocidura fuliginosa YunnanChina	TACTTCTATTTGCAGTTATAGCTACTGCCTTTATAGGGTATGTTCTTCCCTGAGGTCAAATGTCATTCTGAGGCGCGA
GU358522.1 Crocidura fuliginosa Taiwan	TACTCCTATTTGCAGTCATAGCTACCGCCTTTATAGGATACGTTCTTCCTTGAGGCCAAATATCATTCTGAGGCGCAA
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	TACTCCTATTTGCAGTCATAGCTACCGCCTTTATAGGGTACGTTCTTCCTTGAGGCCAAATATCATTCTGAGGCGCAA
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	TACTCCTATTTGCAGTCATAGCTACCGCCTTTATAGGGTATGTTCTTCCTTGAGGCCAAATATCATTCTGAGGCGCAA
FJ814023.1 Crocidura lepidura Sumatra	TACTTTTATTTGCAGTTATAGCCACTGCCTTTATAGGCTATGTACTCCCTTGAGGCCAAATATCATTCTGAGGAGCAA
FJ814022.1 Crocidura lepidura Sumatra	TACTTTTATTTGCAGTTATAGCCACTGCCTTTATAGGCTATGTACTCCCTTGAGGCCAAATATCATTCTGAGGAGCAA
KF801079.1 Crocidura paradoxura Sumatra	TACTTTTATTTGCAGTTATAGCTACTGCTTTCATAGGCTACGTACTCCCTTGAGGCCAAATATCATTCTGAGGAGCAA
EF524619.1 Crocidura malayana UluGombak	TACTTTTATTTGCAGTCATAGCTACTGCCTTCATAGGCTACGTACTCCCTTGAGGCCAAATATCATTCTGAGGGGCAA
FJ814053 Crocidura foetida doriae BintuluSarawak	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
FJ814055 Crocidura foetida doriae BintuluSarawak	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
KF283271.1 Crocidura monticola Java	TCCTTTTATTTGCAGTTATAGCCACTGCCTTTATAGGATATGTTCTTCCCTGAGGCCAAATATCGTTTTGAGGCGCAA
BH15-063 Crocidura foetida BorneoHighlands	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
BNP16-001 Crocidura foetida BakoSarawak	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
DKB16-035 Crocidura foetida BauSarawak	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
ENG16-133 Crocidura foetida EngkeliliSarawak	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
GGNP15-001 Crocidura foetida LunduSarawak	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
DQ630381.1 Crocidura malayana UluGombak	TACTTTTATTTGCAGTCATAGCTACTGCCTTCATAGGCTACGTACTCCCTTGAGGCCAAATATCATTCTGAGGGGCAA
GI15-047 Crocidura malayana GualkanKelantan	TACTTTTATTTGCAGTCATAGCTACTGCCTTCATAGGCTACGTACTCCCTTGAGGCCAAATATCATTCTGAGGGGCAA
KWT15-007 Crocidura foetida KubahSarawak	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
MNP17-050 Crocidura foetida MuluMiri	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
NB14-002 Crocidura foetida NangaBeninKapit	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
DKB16-036 C.foetida BauSarawak	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	TACTTTTATTTGCAGTCATAGCTACTGCCTTCATAGGCTACGTACTCCCTTGAGGCCAAATATCATTCTGAGGGGCAA
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	TACTTTTATTTGCAGTCATAGCTACTGCCTTCATAGGCTATGTACTCCCTTGAGGCCAAATATCATTCTGAGGGGCAA
KF283272.1 Crocidura brunnea Java	TACTTTTATTTGCAGTTATAGCAACTGCCTTCATAGGCTATGTACTCCCTTGAGGCCAAATATCATTCTGAGGGGCAA
FJ813926.1 Crocidura nigripes Sulawesi	TACTCTTATTTGCAGTTATAGCTACTGCTTTCATAGGCTACGTACTTCCTTGAGGCCAAATATCATTCTGAGGAGCAA
FJ813874.1 Crocidura grayi Philippines	TACTTTTATTTGCAGTTATAGCTACTGCTTTTATAGGATACGTACTCCCTTGAGGCCAAATATCATTCTGAGGAGCAA
SNP16-036 Crocidura foetida SantubongSarawak	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
VM016-010 Crocidura foetida MatangSarawak	TACTTTTATTTACAGTCATAGCTACTGCTTTCATAGGCTATGTACTCCCTTGAGGTCAAATATCATTCTGAGGAGCAA
KF283233.1 Crocidura umbra Java	TCCTTTTATTCGCAGTTATGGCCACTGCCTTTATAGGATATGTTCTTCCCTGAGGTCAAATATCGTTTTGAGGCGCAA
FJ814029.1 Crocidura orientalis Java	TACTTCTATTTGCAGTTATAGCTACTGCCTTCATAGGCTATGTACTCCCTTGAGGCCAAATATCATTCTGAGGGGCAA
FJ813977.1 Crocidura batakorum PalawanIsland	TACTTCTACTTGCAGTTATAGCCACCGCTTTTATAGGATACGTCCTACCCTGAGGCCAAATATCATTCTGAGGCGCTA
FJ813978.1 Crocidura palawanensis PalawanIsland	TACTTTTATTTGCCGTCATAGCCACTGCTTTCATAGGCTACGTACTCCCTTGAGGACAAATATCATTCTGAGGAGCAA
LU14191 SuncusMurinus Perak	TACTTTTATTTGCAGTAATAGCTACCGCATTCATAGGATATGTCCTCCCCTGAGGACAAATATCATTCTGAGGTGCAA
TK16 001 KinabaluSabah	TACTTTTATTTGCGGTTATAGCTACCGCCTTTATAGGATATGTTCTTCCTTGAGGTCAAATATCATTCTGAGGTGCAA
GGNP16 006 LunduSarawak	TACTTTTATTTGCAGTTATAGCTACCGCCTTTATAGGGTATGTTCTTCCTTGAGGTCAAATATCATTCTGAGGCGCAA
KWT15 019 KubahSarawak	TCCTTTTATTTGCAGTTATAGCCACTGCCTTTATAGGGTATGTTCTTCCTTGAGGCCAAATATCATTCTGAGGCGCAA
FJ813843.1 Crocidura mindorus Philippines	TACTTTTATTTGCAGTCATAGCTACTGCTTTCATAGGTTACGTACTCCCTTGAGGTCAAATATCATTCTGAGGGGCAA
FJ813950.1 Crocidura panayensis Philippines	TACTCTTATTTGCAGTCATAGCTACTGCTTTCATAGGTTACGTACTTCCTTGAGGTCAGATATCATTCTGAGGGGCAA
FJ813962.1 Crocidura negrina Philippines	TACTTTTATTTGCAGTCATAGCTACTGCTTTCATAGGCTACGTACTCCCTTGAGGTCAAATATCATTCTGAGGGGCAA
KX469583.1 Crocidura beccarii Sumatra	TACTTTTATTTGCAGTTATAGCTACTGCCTTCATAGGCTACGTACTCCCTTGAGGCCAAATATCATTCTGAGGGGCAA
KX469629.1 Crocidura neglecta Sumatra	TACTTTTATTTGCAGTTATAGCTACCGCCTTTATAGGGTATGTTCTTCCTTGAGGTCAAATATCATTCTGAGGTGCAA

AB175079.1 Crocidura fuliginosa Vietnam	CAGTCATTACTAATTTACTCTCAGCCATCCCTTACATTGGCACTAATCTTGTAGAATGAATCTGAGGGGGGTTTTCCG
GU981271.1 Crocidura fuliginosa YunnanChina	CAGTTATTACTAATTTACTCTCAGCCATCCCTTATATTGGCACTAATCTTGTAGAATGAATCTGAGGAGGGTTTTCCG
GU358522.1 Crocidura fuliginosa Taiwan	CAGTTATTACTAATTTACTTTCAGCCATCCCTTACATCGGAACTAACCTCGTAGAATGAATCTGAGGAGGATTTTCCG
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	CAGTTATTACCAATTTACTTTCAGCCATCCCTTACATCGGAACTAACCTCGTAGAATGAATCTGAGGGGGATTTTCCG
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	CAGTTATTACCAATTTACTTTCAGCCATCCCTTACATCGGAACTAACCTCGTAGAATGAATCTGAGGAGGATTTTCCG
FJ814023.1 Crocidura lepidura Sumatra	CAGTCATTACTAACCTACTTTCAGCTATTCCCTATATCGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
FJ814022.1 Crocidura lepidura Sumatra	CAGTCATTACTAACCTACTTTCAGCTATTCCCTATATCGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
KF801079.1 Crocidura paradoxura Sumatra	CAGTCATCACTAACTTACTTTCAGCTATCCCCTATATTGGTACTAATCTCGTAGAATGAATCTGAGGGGGTTTTTCTG
EF524619.1 Crocidura malayana UluGombak	CAGTCATCACCAATTTACTTTCAGCTATCCCCTATATCGGCACTAACCTTGTAGAATGAATCTGAGGAGGTTTCTCTG
FJ814053 Crocidura foetida doriae BintuluSarawak	CAGTCATCACCAATCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
FJ814055 Crocidura foetida doriae BintuluSarawak	CAGTCATCACCAATCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
KF283271.1 Crocidura monticola Java	CAGTTATTACTAATCTACTCTCAGCCATCCCTTACATTGGCACTAATCTTGTAGAATGAATCTGAGGAGGCTTCTCCG
BH15-063 Crocidura foetida BorneoHighlands	CAGTCATCACCAATCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
BNP16-001 Crocidura foetida BakoSarawak	CAGTCATCACCAATCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
DKB16-035 Crocidura foetida BauSarawak	CAGTCATCACCAACCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
ENG16-133 Crocidura foetida EngkeliliSarawak	CAGTCATCACCAATCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
GGNP15-001 Crocidura foetida LunduSarawak	CAGTCATCACCAATCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
DQ630381.1 Crocidura malayana UluGombak	CAGTCATCACCAATTTACTTTCAGCTATCCCCTATATCGGCACTAACCTTGTAGAATGAATCTGAGGAGGTTTCTCTG
GI15-047 Crocidura malayana GualkanKelantan	CAGTCATCACCAATTTACTTTCAGCTATCCCCTATATCGGCACTAACCTTGTAGAATGAATCTGAGGAGGTTTCTCTG
KWT15-007 Crocidura foetida KubahSarawak	CAGTCATCACCAACCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
MNP17-050 Crocidura foetida MuluMiri	CAGTCATCACCAATCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
NB14-002 Crocidura foetida NangaBeninKapit	CAGTCATCACCAATCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
DKB16-036 C.foetida BauSarawak	CAGTCATCACCAATCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	CAGTCATCACCAATTTACTTTCAGCTATCCCCTATATCGGCACTAACCTTGTAGAATGAATCTGAGGAGGTTTCTCTG
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	CAGTCATCACCAATTTACTTTCAGCTATCCCCTATATCGGCACTAACCTTGTAGAATGAATCTGAGGAGGTTTCTCTG
KF283272.1 Crocidura brunnea Java	CAGTTATCACCAATTTACTTTCAGCTATCCCCTATATCGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
FJ813926.1 Crocidura nigripes Sulawesi	CAGTCATCACTAATCTACTTTCAGCTATCCCCTATATTGGCACTAACCTCGTAGAATGAATCTGAGGAGGTTTCTCTG
FJ813874.1 Crocidura grayi Philippines	CAGTCATCACCAATCTACTTTCAGCTATCCCCTATATCGGTACTAACCTCGTAGAATGAATCTGAGGAGGTTTCTCTG
SNP16-036 Crocidura foetida SantubongSarawak	CAGTCATCACCAATCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
VM016-010 Crocidura foetida MatangSarawak	CAGTCATCACCAATCTCCTTTCAGCTATCCCCTATATTGGTACTAACCTCGTAGAATGAATCTGAGGAGGCTTCTCTG
KF283233.1 Crocidura umbra Java	CAGTTATTACCAACCTACTCTCAGCCATCCCTTACATTGGCACTAATCTTGTAGAATGAATCTGAGGAGGCTTCTCCG
FJ814029.1 Crocidura orientalis Java	CAGTTATTACTAATTTACTTTCAGCTATTCCCTATATCGGTACTAACCTAGTAGAATGAATCTGAGGGGGCTTCTCTG
FJ813977.1 Crocidura batakorum PalawanIsland	CAGTCATTACTAACTTACTCTCAGCTATCCCTTATATTGGTACTACCCTCGTCGAATGAATCTGAGGAGGTTTCTCTG
FJ813978.1 Crocidura palawanensis PalawanIsland	CAGTCATCACCAATCTACTTTCAGCTATCCCCTATATTGGTACAAATCTCGTAGAATGAATCTGAGGAGGTTTCTCTG
LU14191 SuncusMurinus Perak	CAGTTATTACCAATCTCTTATCAGCTATCCCCTATATCGGCACAAACCTCGTAGAATGAATCTGAGGCGGCTTCTCCG
TK16 001 KinabaluSabah	CAGTTATTACTAATTTACTTTCAGCCATTCCTTACATCGGAACTAACCTTGTAGAGTGAATCTGAGGAGGCTTCTCTG
GGNP16 006 LunduSarawak	CAGTTATTACTAATTTACTTTCAGCCATTCCTTATATTGGTTCTAACCTTGTAGAATGAATCTGAGGAGGTTTCTCTG
KWT15 019 KubahSarawak	CAGTTATTACCAATTTACTTTCAGCCATTCCTTACATTGGTACTAATCTTGTAGAGTGAATCTGAGGAGGCTTCTCCG
FJ813843.1 Crocidura mindorus Philippines	CAGTCATTACCAACCTACTTTCAGCTATCCCCTATATCGGTACTAATCTCGTAGAATGAATCTGAGGCGGTTTCTCTG
FJ813950.1 Crocidura panayensis Philippines	CAGTCATTACCAATCTACTTTCAGCTATCCCCTATATCGGTACTAATCTCGTAGAATGAATCTGAGGCGGTTTCTCTG
FJ813962.1 Crocidura negrina Philippines	CAGTCATTACCAATCTACTTTCAGCTATCCCCTATATCGGTACTAATCTCGTAGAATGAATCTGAGGCGGTTTCTCTG
KX469583.1 Crocidura beccarii Sumatra	CAGTCATTACCAATTTACTTTCAGCTATTCCCTATATCGGTACTAACCTCGTAGAATGAATCTGAGGGGGTTTCTCTG
KX469629.1 Crocidura neglecta Sumatra	CAGTTATTACTAATTTACTTTCAGCCATTCCTTACATTGGTACTAACCTTGTAGAGTGAATCTGAGGGGGTTTCTCTG

AB175079.1 Crocidura fuliginosa Vietnam	TCGATAAGGCCACTTTAACTCGGTTTTTTGCTTTTCACTTTATTCTTCCTTTCATCGTAGCCGCACTAGCAGGAGTTC
GU981271.1 Crocidura fuliginosa YunnanChina	TCGATAAGGCCACTTTAACTCGGTTTTTTGCTTTTCACTTTATTCTTCCTTTCATCGTAGCCGCACTAGCAGGAGTTC
GU358522.1 Crocidura fuliginosa Taiwan	TTGATAAAGCCACTTTAACTCGCTTTTTTGCTTTCCACTTTATCCTCCCCTTTATCGTAGCCGCACTCGCAGGAGTCC
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	TTGATAAAGCCACTTTAACTCGCTTTTTTGCTTTCCACTTTATCCTCCCCTTTATCGTAGCCGCACTCGCAGGAGTCC
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	TTGATAAAGCCACTTTAACTCGCTTTTTTGCTTTCCACTTTATCCTCCCCTTTATCGTAGCCGCACTCGCAGGAGTTC
FJ814023.1 Crocidura lepidura Sumatra	TTGACAAAGCTACTTTAACCCGCTTTTTTGCCTTCCACTTCATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTTC
FJ814022.1 Crocidura lepidura Sumatra	TTGACAAAGCTACTTTAACCCGCTTTTTTGCCTTCCACTTCATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTTC
KF801079.1 Crocidura paradoxura Sumatra	TTGATAAAGCCACCTTAACCCGCTTTTTCGCTTTCCACTTCATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
EF524619.1 Crocidura malayana UluGombak	TTGATAAAGCCACCTTAACTCGCTTTTTCGCCTTTCACTTTATTCTCCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
FJ814053 Crocidura foetida doriae BintuluSarawak	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTCC
FJ814055 Crocidura foetida doriae BintuluSarawak	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTCC
KF283271.1 Crocidura monticola Java	TTGATAAAGCCACTCTGACCCGCTTCTTCGCCTTCCACTTCATTCTTCCCTTTATTGTAACCGCACTCGCAGGAGTCC
BH15-063 Crocidura foetida BorneoHighlands	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTTC
BNP16-001 Crocidura foetida BakoSarawak	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCTTTCATCGTAGCCGCACTCGCAGGAGTTC
DKB16-035 Crocidura foetida BauSarawak	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTTC
ENG16-133 Crocidura foetida EngkeliliSarawak	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTTC
GGNP15-001 Crocidura foetida LunduSarawak	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTTC
DQ630381.1 Crocidura malayana UluGombak	TTGATAAAGCCACCTTAACTCGCTTTTTCGCCTTTCACTTTATTCTCCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
GI15-047 Crocidura malayana GualkanKelantan	TTGATAAAGCCACCTTAACTCGCTTTTTCGCCTTTCACTTTATTCTCCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
KWT15-007 Crocidura foetida KubahSarawak	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTTC
MNP17-050 Crocidura foetida MuluMiri	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTCC
NB14-002 Crocidura foetida NangaBeninKapit	TTGATAAAGCTACCTTAACTCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTCC
DKB16-036 C.foetida BauSarawak	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTTC
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	TTGATAAAGCCACCTTAACTCGCTTTTTCGCCTTTCACTTTATTCTCCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	TTGATAAAGCCACCTTAACTCGCTTTTTCGCCTTTCACTTTATTCTCCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
KF283272.1 Crocidura brunnea Java	TTGATAAAGCCACTTTAACCCGCTTCTTTGCCTTCCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
FJ813926.1 Crocidura nigripes Sulawesi	TTGATAAAGCCACCCTAACCCGCTTTTTCGCTTTCCATTTTATTCTCCCCTTCATCGTAGCTGCACTCGCAGGAGTAC
FJ813874.1 Crocidura grayi Philippines	TTGATAAGGCCACTTTAACCCGCTTTTTCGCCTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
SNP16-036 Crocidura foetida SantubongSarawak	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTTC
VM016-010 Crocidura foetida MatangSarawak	TTGATAAAGCTACCTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTTC
KF283233.1 Crocidura umbra Java	TTGACAAAGCCACTCTAACCCGCTTCTTCGCTTTCCACTTCATTCTTCCCTTTATTGTAGCCGCACTCGCAGGAGTCC
FJ814029.1 Crocidura orientalis Java	TTGACAAGGCCACTTTAACCCGCTTCTTTGCCTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
FJ813977.1 Crocidura batakorum PalawanIsland	TTGACAAAGCCACTTTAACTCGTTTCTTCGCTTTTCACTTTATCCTCCCCTTCATTGTAGCCGCCCTGGCAGGAGTTC
FJ813978.1 Crocidura palawanensis PalawanIsland	TCGATAAGGCCACTCTAACCCGCTTTTTCGCTTTCCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
LU14191 SuncusMurinus Perak	TTGATAAAGCTACCTTGACCCGCTTCTTCGCTTTCCATTTTATCCTCCCTTTTATCGTTGCTGCCCTTGCAGGAGTAC
TK16 001 KinabaluSabah	TCGATAAAGCCACCCTAACCCGATTCTTTGCCTTTCACTTTATTCTCCCTTTTATCGTAGCTGCACTCGCAGGAGTAC
GGNP16 006 LunduSarawak	TTGACAAAGCCACCTTAACCCGATTCTTTGCCTTCCACTTTATTCTCCCTTTCATCGTAGCTGCACTCGCAGGAGTAC
KWT15 019 KubahSarawak	TTGATAAAGCCACTTTAACTCGCTTCTTTGCTTTTCACTTCATTCTCCCCTTCATTGTAGCCGCACTCGCAGGAGTAC
FJ813843.1 Crocidura mindorus Philippines	TTGATAAAGCCACTTTAACCCGCTTCTTCGCTTTCCACTTTATTCTTCCCTTCATCGTAGCTGCACTCGCAGGAGTAC
FJ813950.1 Crocidura panayensis Philippines	TTGATAAAGCCACTTTAACCCGCTTTTTCGCTTTCCACTTTATTCTTCCTTTCATCGTAGCCGCACTCGCAGGAGTAC
FJ813962.1 Crocidura negrina Philippines	TTGATAAAGCCACTTTAACCCGCTTTTTCGCTTTCCACTTCATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
KX469583.1 Crocidura beccarii Sumatra	TTGATAAAGCTACTTTAACCCGCTTTTTTGCTTTTCACTTTATTCTTCCCTTCATCGTAGCCGCACTCGCAGGAGTAC
KX469629.1 Crocidura neglecta Sumatra	TTGACAAAGCTACCTTAACCCGATTCTTTGCCTTTCACTTTATTCTCCCTTTTATCGTAGCTGCACTTGCAGGAGTAC

AB175079.1 Crocidura fuliginosa Vietnam	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	G	G	A	C	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	C	C	A	T	C
GU981271.1 Crocidura fuliginosa YunnanChina	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	T	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	G	G	A	C	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	C	C	A	T	C
GU358522.1 Crocidura fuliginosa Taiwan	A	T	C	T	C	T	T	A	T	T	T	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	T	A	A	T	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	G	G	A	T	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	C	C	A	C	C
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	A	T	C	T	C	T	T	A	T	T	Y	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	T	A	A	T	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	G	G	A	T	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	C	C	A	C	C
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	A	T	C	T	C	T	T	A	T	T	T	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	T	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	G	G	A	T	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	C	C	A	C	C
FJ814023.1 Crocidura lepidura Sumatra	A	C	C	T	C	T	T	A	T	T	T	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	G	A	A	C	T	C	A	G	A	C	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
FJ814022.1 Crocidura lepidura Sumatra	A	C	C	T	C	T	T	A	T	T	T	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	G	A	A	C	T	C	A	G	A	C	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
KF801079.1 Crocidura paradoxura Sumatra	A	C	C	T	C	T	T	A	T	T	T	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	T	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	T	A	A	A	A	T	T	C	C	C	T	T	T	C	A	C	C
EF524619.1 Crocidura malayana UluGombak	A	C	C	T	C	T	T	A	T	T	C	T	T	A	C	A	C	G	A	A	A	C	C	G	G	C	T	C	A	A	A	T	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	T	A	A	A	A	T	C	C	C	C	T	T	T	C	A	C	C
FJ814053 Crocidura foetida doriae BintuluSarawak	A	C	C	T	C	T	T	A	T	T	C	T	T	G	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
FJ814055 Crocidura foetida doriae BintuluSarawak	A	C	C	T	C	T	T	A	T	T	C	T	T	G	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
KF283271.1 Crocidura monticola Java	A	C	C	T	T	C	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	T	A	A	T	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	G	G	A	T	A	T	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
BH15-063 Crocidura foetida BorneoHighlands	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	T	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
BNP16-001 Crocidura foetida BakoSarawak	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	T	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
DKB16-035 Crocidura foetida BauSarawak	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	T	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
ENG16-133 Crocidura foetida EngkeliliSarawak	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	T	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
GGNP15-001 Crocidura foetida LunduSarawak	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	T	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
DQ630381.1 Crocidura malayana UluGombak	A	C	C	T	C	T	T	A	T	T	C	T	T	A	C	A	C	G	A	A	A	C	C	G	G	C	T	C	A	A	A	T	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	T	A	A	A	A	T	C	C	C	C	T	T	T	C	A	C	C
GI15-047 Crocidura malayana GualkanKelantan	A	C	C	T	C	T	T	A	T	T	C	T	T	A	C	A	C	G	A	A	A	C	C	G	G	C	T	C	A	A	A	T	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	T	A	A	A	A	T	C	C	C	C	T	T	T	C	A	C	C
KWT15-007 Crocidura foetida KubahSarawak	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	T	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
MNP17-050 Crocidura foetida MuluMiri	A	C	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	T	A	A	A	A	T	T	C	C	T	T	T	C	C	A	C	C
NB14-002 Crocidura foetida NangaBeninKapit	A	C	C	T	C	T	T	A	T	T	C	T	T	G	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
DKB16-036 C.foetida BauSarawak	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	T	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	A	C	C	T	C	T	T	A	T	T	C	T	T	A	C	A	C	G	A	A	A	C	C	G	G	C	T	C	A	A	A	T	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	T	A	A	A	A	T	C	C	C	C	T	T	T	C	A	C	C
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	A	C	C	T	C	T	T	A	T	T	C	T	T	A	C	A	C	G	A	A	A	C	C	G	G	C	T	C	A	A	A	T	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	T	A	A	A	A	T	C	C	C	C	T	T	T	C	A	C	C
KF283272.1 Crocidura brunnea Java	A	C	C	T	C	T	T	A	T	T	T	T	T	A	C	A	T	G	A	A	A	C	T	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
FJ813926.1 Crocidura nigripes Sulawesi	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	T	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	T	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
FJ813874.1 Crocidura grayi Philippines	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	T	T	C	A	A	A	T	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
SNP16-036 Crocidura foetida SantubongSarawak	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	T	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
VM016-010 Crocidura foetida MatangSarawak	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	T	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
KF283233.1 Crocidura umbra Java	A	C	C	T	T	C	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	G	G	A	T	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
FJ814029.1 Crocidura orientalis Java	A	C	C	T	C	T	T	A	T	T	T	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
FJ813977.1 Crocidura batakorum PalawanIsland	A	C	C	T	C	C	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	T	A	A	T	A	A	T	C	C	G	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	T	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
FJ813978.1 Crocidura palawanensis PalawanIsland	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	T	T	C	A	A	A	T	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	T	A	C	A	G	A	C	A	A	A	A	T	T	C	C	C	T	T	T	C	A	C	C
LU14191 SuncusMurinus Perak	A	C	C	T	A	C	T	A	T	T	T	C	T	G	C	A	C	G	A	A	A	C	T	G	G	C	T	C	A	A	A	C	A	A	C	C	C	C	T	C	T	G	G	A	T	T	A	A	A	C	T	C	A	G	A	T	A	C	A	G	A	T	A	A	A	A	T	T	C	C	C	T	T	T	C	A	T	C
TK16 001 KinabaluSabah	A	C	C	T	C	T	T	A	T	T	T	T	T	A	C	A	C	G	A	A	A	C	T	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	G	G	A	C	A	C	A	G	A	T	A	A	A	A	T	C	C	C	C	T	T	T	C	A	C	C
GGNP16 006 LunduSarawak	A	C	C	T	C	T	T	A	T	T	T	T	T	A	C	A	T	G	A	A	A	C	T	G	G	C	T	C	A	A	A	C	A	A	C	C	C	G	T	C	C	G	G	A	T	T	A	A	A	C	T	C	G	G	A	T	A	C	A	G	A	T	A	A	A	A	T	T	C	C	C	T	T	T	C	A	C	C
KWT15 019 KubahSarawak	A	C	C	T	T	T	T	A	T	T	C	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	T	A	A	T	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	G	G	A	T	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	C	C	A	C	C
FJ813843.1 Crocidura mindorus Philippines	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	C	G	A	A	A	C	C	G	G	T	T	C	A	A	A	T	A	A	C	C	C	G	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	C	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
FJ813950.1 Crocidura panayensis Philippines	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	C	G	A	A	A	C	C	G	G	T	T	C	A	A	A	T	A	A	C	C	C	C	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	C	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
FJ813962.1 Crocidura negrina Philippines	A	T	C	T	C	T	T	A	T	T	C	T	T	A	C	A	C	G	A	A	A	C	C	G	G	T	T	C	A	A	A	T	A	A	C	C	C	G	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	G	G	A	C	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
KX469583.1 Crocidura beccarii Sumatra	A	C	C	T	C	C	T	A	T	T	T	T	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	A	G	A	C	A	C	A	G	A	C	A	A	A	A	T	T	C	C	T	T	T	T	C	A	C	C
KX469629.1 Crocidura neglecta Sumatra	A	C	C	T	C	T	T	A	T	T	T	C	T	A	C	A	T	G	A	A	A	C	C	G	G	C	T	C	A	A	A	C	A	A	C	C	C	A	T	C	C	G	G	A	T	T	A	A	A	C	T	C	G	G	A	C	A	C	A	G	A	T	A	A	A	A	T	C	C	C	C	T	T	T	C	A	C	C

AB175079.1 Crocidura fuliginosa Vietnam	CCTACTATACTATCAAAGATATTTTAGGAGCTTTAATTATAATTACCGCCCTATCTTCCTTAGTCTTATTCTCTCCAG
GU981271.1 Crocidura fuliginosa YunnanChina	CCTACTATACTATCAAAGATATTTTAGGAGCTTTAATTATAATTACCGCCCTATCTTCCTTAGTCTTATTCTCTCCAG
GU358522.1 Crocidura fuliginosa Taiwan	CTTACTATACTATTAAAGATATTTTAGGAGCTTTAATTATGATTACCGCCTTATCTTCCCTAGTCCTATTCTCCCCAG
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	CTTATTATACTATTAAAGATATTTTAGGAGCTTTAATTATGATCACCGCCTTATCTTCCCTAGTCCTATTCTCCCCAG
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	CTTACTATACTATTAAAGATATTTTAGGAGCTTTAATTATGATCACCGCCTTATCTTCCCTAGTCCTATTCTCCCCAG
FJ814023.1 Crocidura lepidura Sumatra	CCTACTACACTATTAAAGATATTTTAGGAGCTCTAATCATAATCACCACTTTATCCTCCTTAGTTCTATTCTCCCCAG
FJ814022.1 Crocidura lepidura Sumatra	CCTACTACACTATTAAAGATATCTTAGGAGCTCTAATCATAATCACCACTTTATCCTCCTTAGTTCTATTCTCCCCAG
KF801079.1 Crocidura paradoxura Sumatra	CCTATTATACTATTAAAGATATCCTAGGAGCTCTAATTATAATTACCACTTTATCTTCCCTAGTCCTATTTACCCCAG
EF524619.1 Crocidura malayana UluGombak	CTTATTATACTATTAAAGATATTCTAGGAGCATTAATTATAATCACCACTTTATCCTCCCTAGTCCTATTTACCCCAG
FJ814053 Crocidura foetida doriae BintuluSarawak	CCTACTACACTATTAAGGATATTCTAGGGGCTTTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACCCCAG
FJ814055 Crocidura foetida doriae BintuluSarawak	CCTACTACACTATTAAGGATATTCTAGGGGCTTTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACCCCAG
KF283271.1 Crocidura monticola Java	CTTATTACACTATTAAAGATATCTTAGGAGCTTTAATCATAATCACCGCTTTATCCTCCCTAGTCCTATTCTCCCCAG
BH15-063 Crocidura foetida BorneoHighlands	CCTATTACACTATTAAAGATATTCTAGGGGCTTTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACACCAG
BNP16-001 Crocidura foetida BakoSarawak	CCTACTACACTATTAAAGATATTCTAGGGGCTTTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACACCAG
DKB16-035 Crocidura foetida BauSarawak	CCTACTACACTATTAAAGATATTCTAGGGGCTTTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACACCAG
ENG16-133 Crocidura foetida EngkeliliSarawak	CCTATTACACTATTAAAGATATTCTAGGAGCTTTAATCATAATTACCACCTTATCCTCCTTAGTTCTATTTACACCAG
GGNP15-001 Crocidura foetida LunduSarawak	CCTACTACACTATTAAAGATATTCTAGGGGCTTTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACACCAG
DQ630381.1 Crocidura malayana UluGombak	CTTATTATACTATTAAAGATATTCTAGGAGCATTAATTATAATCACCACTTTATCCTCCCTAGTCCTATTTACCCCAG
GI15-047 Crocidura malayana GualkanKelantan	CCTATTATACTATTAAAGATATTCTAGGAGCATTAATTATAATCACCACTTTATCCTCCCTAGTCCTATTTACCCCAG
KWT15-007 Crocidura foetida KubahSarawak	CCTACTACACTATTAAAGATATTCTAGGGGCTTTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACACCAG
MNP17-050 Crocidura foetida MuluMiri	CCTACTACACTATTAAGGATATTCTAGGGGCTTTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACCCCAG
NB14-002 Crocidura foetida NangaBeninKapit	CCTACTACACTATTAAGGATATTCTAGGGGCTCTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACCCCAG
DKB16-036 C.foetida BauSarawak	CCTACTACACTATTAAAGATATTCTAGGGGCTTTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACACCAG
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	CTTATTATACTATTAAAGATATTCTAGGAGCATTAATTATAATCACCACTTTATCCTCCCTAGTCCTATTTACCCCAG
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	CTTACTATACTATTAAAGATATTCTAGGAGCATTAATTATAATCACCACTTTATCCTCCCTAGTCCTATTTACCCCAG
KF283272.1 Crocidura brunnea Java	CCTACTATACTATTAAAGATATTCTAGGAGCTTTAATCATAATTACCATTTTATCCTCTTTAGTCCTATTCTCCCCAG
FJ813926.1 Crocidura nigripes Sulawesi	CTTACTATACTATTAAAGATATCCTAGGAGCTTTAATTATAATCACCACTTTATCCTCCCTAGTCTTATTCACCCCAG
FJ813874.1 Crocidura grayi Philippines	CTTATTATACTATCAAAGATATTCTAGGGGCCTTAATCATAATTACCACTCTATCCTCCCTAGTCCTATTTGCCCCAG
SNP16-036 Crocidura foetida SantubongSarawak	CCTACTACACTATTAAAGATATTCTAGGGGCTTTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACACCAG
VM016-010 Crocidura foetida MatangSarawak	CCTACTACACTATTAAAGATATTCTAGGGGCTTTAATCATAATTACCACCTTATCCTCCTTAGTCCTATTTACACCAG
KF283233.1 Crocidura umbra Java	CTTATTACACTATCAAAGACATCCTAGGAGCTTCAATCATAATCACCGCTTTATCCTCCCTAGTTTTATTCTCCCCAG
FJ814029.1 Crocidura orientalis Java	CCTACTACACCATTAAAGATATCCTAGGAGCTTTAATCATGATTACCACTTTATCCTCTTTAGTCCTATTCTCCCCAG
FJ813977.1 Crocidura batakorum PalawanIsland	CCTACTACACCATTAAAGACATCTTAGGAGTACTAATTTTGATTACTATATTACTTCTTCTAGTCCTATTCTCCCCAG
FJ813978.1 Crocidura palawanensis PalawanIsland	CTTATTATACTATTAAAGATATTCTAGGAGCCCTAATCATAATCACCACTCTATCCTCCCTAGTTCTATTTACCCCAG
LU14191 SuncusMurinus Perak	CCTACTACACTATCAAAGATATCCTTGGAGCACTAATTATAATTTCCACATTATCCTCTTTAGTCCTATTTTCCCCAG
TK16 001 KinabaluSabah	CTTACTATACTATTAAAGATATCCTAGGAGCTTTAATTATAATCACCGCTCTATCCTCATTAGTCCTATTCTCCCCCG
GGNP16 006 LunduSarawak	CTTATTATACTATTAAAGATATCTTAGGAGCTTTAATTATAATAACCGCTTTATCCTCATTAGTCCTATTCTCTCCCG
KWT15 019 KubahSarawak	CTTACTACACTATTAAAGATATCTTAGGAGCTTTAATCATAATTACCGCTCTATCCTCCCTAGTTCTATTTTCCCCAG
FJ813843.1 Crocidura mindorus Philippines	CCTATTATACTATCAAAGATATTCTAGGAGCCTTAATCATAATTACCACCCTATCCTCCCTAGTTCTATTTACTCCAG
FJ813950.1 Crocidura panayensis Philippines	CTTATTATACTATCAAAGATATTCTAGGAGCCTTAATCATAATTACCACTCTATCCTCCCTAGTTCTATTTACCCCAG
FJ813962.1 Crocidura negrina Philippines	CTTATTATACTATCAAAGATATTCTAGGAGCCTTAATCATAATTACCGCTCTATCCTCCTTAGTTCTATTTACCCCAG
KX469583.1 Crocidura beccarii Sumatra	CCTACTACACTATTAAAGATATTCTAGGAGCTTTAATCATAATTACTACTTTATCCTCCCTAGTCCTATTCTCCCCAG
KX469629.1 Crocidura neglecta Sumatra	CTTACTATACTATCAAAGATATCTTAGGGGCTTTAATTATAATCACCGCTCTATCCTCATTAGTCTTATTCTCCCCCG

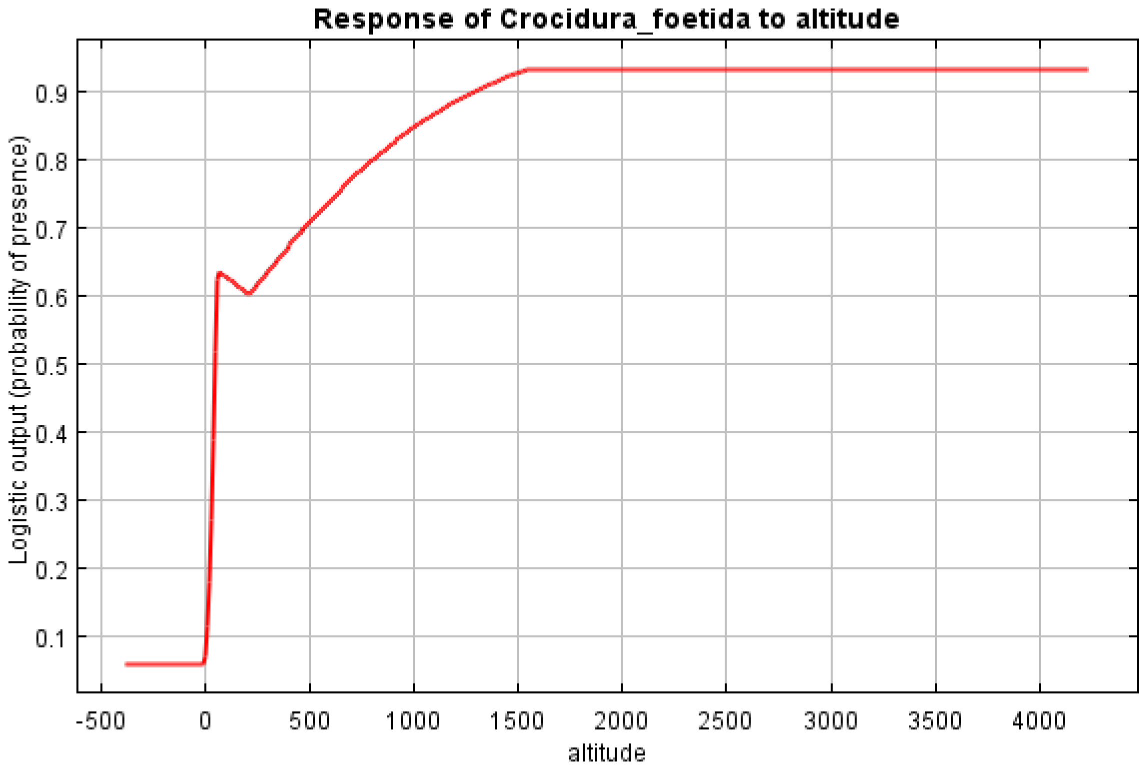
AB175079.1 Crocidura fuliginosa Vietnam	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	T	C	C	C	C	T	C	A	A	C	A	C	A	C	C	A	C	C	A	C	A	T	A	T	C	A	A	A	C	C	A	G	A	A	T	G	A	T	A	C	T
GU981271.1 Crocidura fuliginosa YunnanChina	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	T	C	C	C	C	T	C	A	A	C	A	C	A	C	C	A	C	C	A	C	A	T	A	T	C	A	A	A	C	C	A	G	A	A	T	G	A	T	A	C	T
GU358522.1 Crocidura fuliginosa Taiwan	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	T	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	C	C	T	T	A	A	C	A	C	A	C	C	A	C	C	A	C	A	T	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	A	T	A	T	A	T	T	A	G	G	A	G	A	T	C	C	A	G	A	C	A	A	T	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	C	A	C	A	C	C	A	C	C	A	C	A	T	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	A	T	A	T	A	T	T	A	G	G	A	G	A	T	C	C	A	G	A	C	A	A	T	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	C	C	T	T	A	A	C	A	C	A	C	C	A	C	C	A	C	A	T	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T
FJ814023.1 Crocidura lepidura Sumatra	A	T	A	T	A	C	T	A	G	G	A	G	A	T	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	T	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	G	T	A	T	T
FJ814022.1 Crocidura lepidura Sumatra	A	T	A	T	A	C	T	A	G	G	A	G	A	T	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	T	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	G	T	A	T	T
KF801079.1 Crocidura paradoxura Sumatra	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	T	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	C	C	T	T	A	A	T	A	C	A	C	C	A	C	C	T	C	A	T	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T
EF524619.1 Crocidura malayana UluGombak	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	T	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	T	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	C	T
FJ814053 Crocidura foetida doriae BintuluSarawak	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	G	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
FJ814055 Crocidura foetida doriae BintuluSarawak	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	G	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
KF283271.1 Crocidura monticola Java	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	T	T	A	C	A	T	C	C	C	C	G	C	A	A	A	C	C	C	C	C	T	T	A	A	T	A	C	A	C	C	A	C	C	A	C	A	T	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T
BH15-063 Crocidura foetida BorneoHighlands	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	T	T
BNP16-001 Crocidura foetida BakoSarawak	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
DKB16-035 Crocidura foetida BauSarawak	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
ENG16-133 Crocidura foetida EngkeliliSarawak	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	T	T
GGNP15-001 Crocidura foetida LunduSarawak	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
DQ630381.1 Crocidura malayana UluGombak	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	T	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	T	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	C	T
GI15-047 Crocidura malayana GualkanKelantan	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	T	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	T	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	C	T
KWT15-007 Crocidura foetida KubahSarawak	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
MNP17-050 Crocidura foetida MuluMiri	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	G	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
NB14-002 Crocidura foetida NangaBeninKapit	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	G	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	T	T
DKB16-036 C.foetida BauSarawak	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	T	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	T	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	C	T
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	T	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	T	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	C	T
KF283272.1 Crocidura brunnea Java	A	T	A	T	A	T	T	G	G	G	A	G	A	C	C	C	A	G	A	C	A	A	T	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	T	C	A	C	A	T	C	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
FJ813926.1 Crocidura nigripes Sulawesi	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	C	C	C	C	C	G	C	T	A	A	C	C	C	T	C	T	T	A	A	C	A	C	G	C	C	A	C	C	T	C	A	C	A	T	T	A	A	A	C	C	A	G	A	G	T	G	A	T	A	T	T
FJ813874.1 Crocidura grayi Philippines	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	T	C	C	T	C	T	T	A	A	C	A	C	A	C	C	A	C	C	T	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
SNP16-036 Crocidura foetida SantubongSarawak	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
VM016-010 Crocidura foetida MatangSarawak	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	C	T
KF283233.1 Crocidura umbra Java	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	T	T	A	C	A	T	C	C	C	C	G	C	A	A	A	C	C	C	C	C	T	T	A	A	T	A	C	A	C	C	A	C	C	A	C	A	T	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T
FJ814029.1 Crocidura orientalis Java	A	T	A	T	G	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	T	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	C	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	G	C	C	A	G	A	A	T	G	A	T	A	T	T
FJ813977.1 Crocidura batakorum PalawanIsland	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	T	A	A	T	T	A	C	A	T	C	C	C	T	G	C	C	A	A	C	C	C	T	C	T	T	A	A	C	A	C	C	C	C	A	C	C	A	C	A	T	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T
FJ813978.1 Crocidura palawanensis PalawanIsland	A	T	A	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	G	T	A	T	T
LU14191 SuncusMurinus Perak	A	T	A	T	A	T	T	A	G	G	C	G	A	C	C	C	A	G	A	T	A	A	T	T	A	T	A	T	T	C	C	C	G	C	A	A	A	C	C	C	C	C	T	A	A	A	C	A	C	A	C	C	C	C	C	T	C	A	T	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T
TK16 001 KinabaluSabah	A	T	A	T	A	T	T	A	G	G	T	G	A	T	C	C	A	G	A	C	A	A	T	T	A	T	A	T	T	C	C	C	G	C	A	A	A	T	C	C	C	C	T	C	A	A	C	A	C	A	C	C	G	C	C	A	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	C	T
GGNP16 006 LunduSarawak	A	C	A	T	A	T	T	A	G	G	A	G	A	C	C	C	G	G	A	C	A	A	C	T	A	T	A	T	T	C	C	C	G	C	A	A	A	C	C	C	C	C	T	C	A	A	C	A	C	A	C	C	A	C	C	A	C	A	C	A	T	T	A	A	A	C	C	A	G	A	G	T	G	A	T	A	T	T
KWT15 019 KubahSarawak	A	C	T	T	A	T	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	C	C	T	T	A	A	C	A	C	A	C	C	A	C	C	A	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T
FJ813843.1 Crocidura mindorus Philippines	A	C	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	C	A	A	C	A	C	A	C	C	A	C	C	T	C	A	C	A	T	T	A	A	A	C	C	A	G	A	G	T	G	A	T	A	T	T
FJ813950.1 Crocidura panayensis Philippines	A	C	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	C	T	A	C	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	C	A	C	A	C	C	A	C	C	T	C	A	C	A	T	C	A	A	G	C	C	A	G	A	A	T	G	A	T	A	T	T
FJ813962.1 Crocidura negrina Philippines	A	C	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	C	A	A	T	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	T	A	A	C	A	C	A	C	C	A	C	C	T	C	A	C	A	T	C	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T
KX469583.1 Crocidura beccarii Sumatra	A	T	A	T	A	C	T	A	G	G	A	G	A	C	C	C	A	G	A	T	A	A	T	T	A	T	A	T	C	C	C	C	G	C	A	A	A	C	C	C	T	C	T	C	A	A	T	A	C	A	C	C	A	C	C	C	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T
KX469629.1 Crocidura neglecta Sumatra	A	C	A	T	A	T	T	A	G	G	A	G	A	T	C	C	A	G	A	C	A	A	T	T	A	C	A	T	T	C	C	T	G	C	A	A	A	C	C	C	C	C	T	C	A	A	C	A	C	A	C	C	A	C	C	A	C	A	C	A	T	T	A	A	A	C	C	A	G	A	A	T	G	A	T	A	T	T

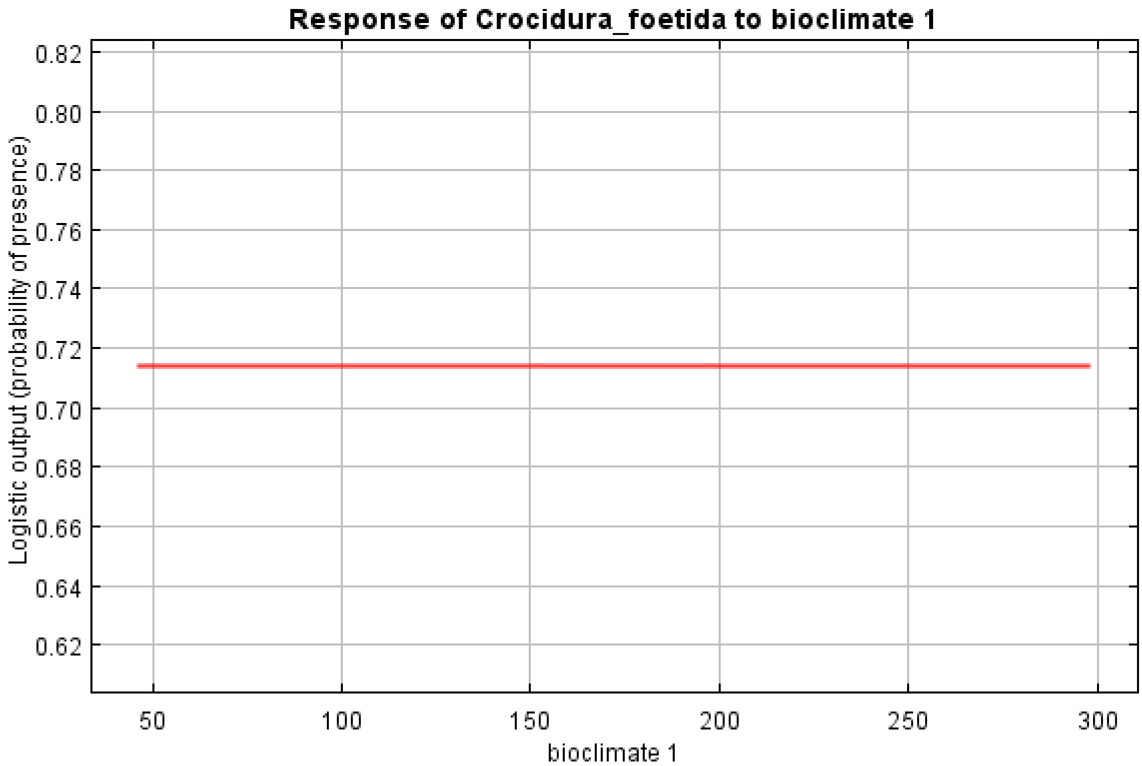
AB175079.1 Crocidura fuliginosa Vietnam	TTTTATTTGCCTACGCAATTTTACGATCAATCCCTAATAAACTTGGAGGAGTCTTAGCCCTCGTTCTATCAATCGCTA
GU981271.1 Crocidura fuliginosa YunnanChina	TTTTATTTGCCTACGCAATTTTACGATCAATTCCTAATAAACTTGGAGGAGTCTTAGCCCTCGTTCTATCAATCGCTA
GU358522.1 Crocidura fuliginosa Taiwan	TCTTATTTGCCTATGCAATTTTACGATCAATTCCCAATAAACTTGGAGGAGTCTTAGCCCTTGTCCTATCAATTGCTA
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	TCTTATTTGCCTATGCAATTTTACGATCAATTCCCAATAAACTTGGAGGAGTCTTAGCCCTTGTCCTATCAATTGCTA
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	TCTTATTTGCCTATGCAATTTTACGATCAATTCCCAATAAACTTGGAGGAGTCTTAGCCCTTGTCCTATCAATTGCCA
FJ814023.1 Crocidura lepidura Sumatra	TCCTATTTGCCTACGCAATCTTACGATCAATCCCTAATAAACTTGGAGGAGTTATAGCACTTGTTTTATCAATCGCAA
FJ814022.1 Crocidura lepidura Sumatra	TCCTATTTGCCTACGCAATCTTACGATCAATCCCTAATAAACTTGGAGGGGTTATAGCACTTGTTTTATCAATCGCAA
KF801079.1 Crocidura paradoxura Sumatra	TCCTATTTGCCTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTTATAGCACTTGTTTTATCAATTGCGA
EF524619.1 Crocidura malayana UluGombak	TTCTATTTGCCTATGCAATCCTACGATCAATCCCTAATAAACTTGGAGGAGTTATAGCTCTTGTCTTATCAATCGCAA
FJ814053 Crocidura foetida doriae BintuluSarawak	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATCGCAA
FJ814055 Crocidura foetida doriae BintuluSarawak	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATCGCAA
KF283271.1 Crocidura monticola Java	TCCTATTCGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCCTAGCCCTCGTCCTATCAATCGCAA
BH15-063 Crocidura foetida BorneoHighlands	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATTGCAA
BNP16-001 Crocidura foetida BakoSarawak	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATTGCAA
DKB16-035 Crocidura foetida BauSarawak	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATTGCAA
ENG16-133 Crocidura foetida EngkeliliSarawak	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATTGCAA
GGNP15-001 Crocidura foetida LunduSarawak	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATTGCAA
DQ630381.1 Crocidura malayana UluGombak	TTCTATTTGCCTATGCAATCCTACGATCAATCCCTAATAAACTTGGAGGAGTTATAGCTCTTGTCTTATCAATCGCAA
GI15-047 Crocidura malayana GualkanKelantan	TTCTATTTGCCTATGCAATCCTACGATCAATCCCTAATAAACTTGGAGGAGTTATAGCTCTTGTCTTATCAATCGCAA
KWT15-007 Crocidura foetida KubahSarawak	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATTGCAA
MNP17-050 Crocidura foetida MuluMiri	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATCGCAA
NB14-002 Crocidura foetida NangaBeninKapit	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTCGTCTTATCAATCGCAA
DKB16-036 C.foetida BauSarawak	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTTATAGCACTTGTCTTATCAATTGCAA
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	TTCTATTTGCCTATGCAATCCTACGATCAATCCCTAATAAACTTGGAGGAGTTATAGCTCTTGTCTTATCAATCGCAA
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	TTCTATTTGCCTATGCAATCCTACGATCAATCCCTAATAAACTTGGAGGAGTTATAGCTCTTGTCTTATCAATCGCAA
KF283272.1 Crocidura brunnea Java	TCCTATTTGCCTATGCAATCTTACGATCAATCCCTAACAAACTTGGAGGAGTTATAGCACTTGTCTTATCAATCGCAA
FJ813926.1 Crocidura nigripes Sulawesi	TCCTCTTTGCCTATGCAATCCTACGATCAATTCCTAACAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATCGCAA
FJ813874.1 Crocidura grayi Philippines	TCCTATTTGCCTATGCAATCCTACGATCAATTCCTAACAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATCGCAA
SNP16-036 Crocidura foetida SantubongSarawak	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATTGCAA
VM016-010 Crocidura foetida MatangSarawak	TCCTATTTGCTTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTCATAGCACTTGTCTTATCAATTGCAA
KF283233.1 Crocidura umbra Java	TCCTATTTGCTTATGCAATCCTACGATCAATCCCTAATAAACTTGGAGGAGTCCTAGCCCTCGTCCTATCAATCGCAA
FJ814029.1 Crocidura orientalis Java	TCCTATTTGCCTATGCAATCTTACGATCAATCCCTAATAAACTTGGAGGAGTTTTAGCACTTGTCTTATCAATCGCAA
FJ813977.1 Crocidura batakorum PalawanIsland	TTTTATTTGCCTACGCAATCTTACGATCAATTCCCAATAAACTTGGAGGAGTCCTAGCTCTCCTCCTATCAATCCTAA
FJ813978.1 Crocidura palawanensis PalawanIsland	TCCTATTTGCTTATGCAATCCTACGATCAATTCCCAATAAACTTGGAGGAGTCATAGCACTTGTCCTATCAATCGCGA
LU14191 SuncusMurinus Perak	TCCTATTCGCCTATGCAATTCTACGATCTATTCCTAATAAATTAGGTGGAGTTCTGGCACTTGTTCTATCGATTTTAA
TK16 001 KinabaluSabah	TCCTATTTGCCTATGCAATCCTACGATCAATTCCTAATAAACTCGGGGGAGTCTTAGCTCTTGTCTTATCAATCGCCA
GGNP16 006 LunduSarawak	TCCTATTTGCCTACGCAATCCTACGATCAATTCCTAATAAACTCGGAGGAGTCTTAGCGCTTGTTTTATCAATCGCTA
KWT15 019 KubahSarawak	ACCTATTTGCCTACGCAATCCTACGATCAATTCCCAATAAACTTGGAGGAGTCTTAGCCCTCGTCCTATCAATCGCTA
FJ813843.1 Crocidura mindorus Philippines	TCCTATTTGCCTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTTATAGCACTTGTCTTATCAATCGCAA
FJ813950.1 Crocidura panayensis Philippines	TTCTATTTGCCTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTTATAGCACTTGTCTTATCAATCGCAA
FJ813962.1 Crocidura negrina Philippines	TCCTATTTGCCTATGCAATCCTACGATCAATTCCTAATAAACTTGGAGGAGTAATAGCACTTGTCTTATCAATCGCAA
KX469583.1 Crocidura beccarii Sumatra	TCCTATTTGCCTATGCAATCTTACGATCAATCCCCAATAAACTTGGAGGAGTCATAGCACTCGTCTTATCAATCGCAA
KX469629.1 Crocidura neglecta Sumatra	TCCTGTTTGCCTATGCAATCCTACGATCAATTCCTAATAAACTCGGAGGAGTCTTAGCCCTTGTCCTATCAATCGCTA

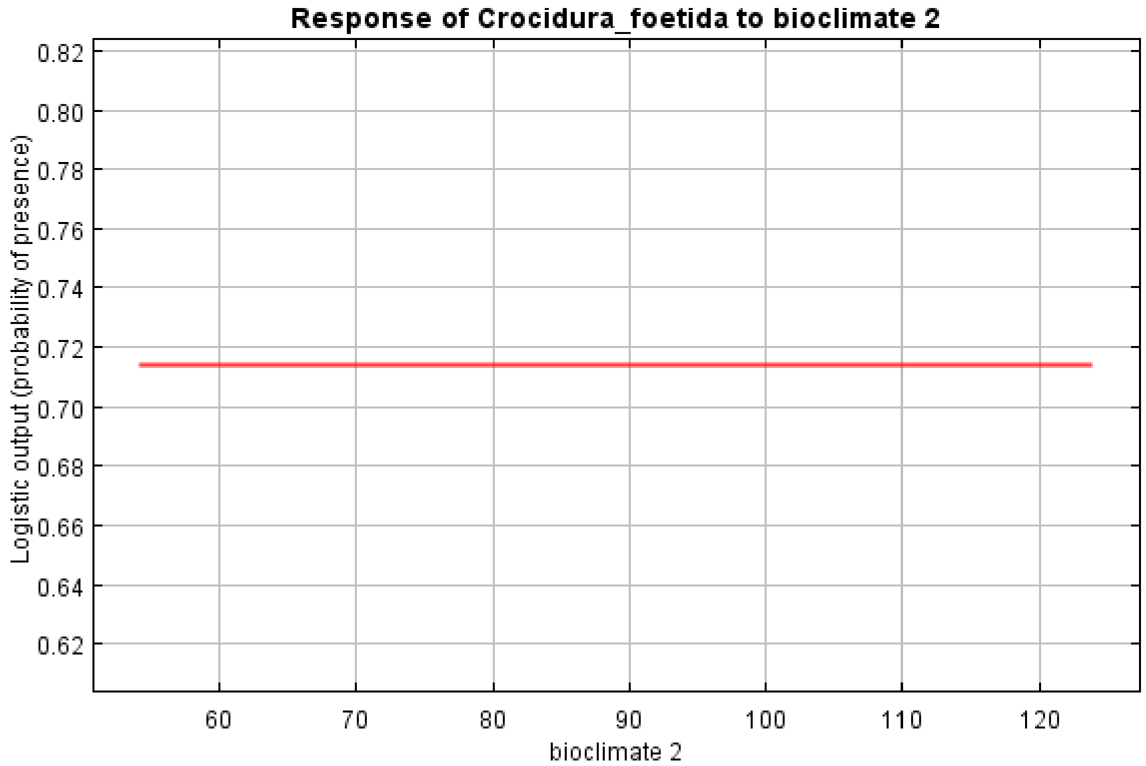
AB175079.1 Crocidura fuliginosa Vietnam	TTCTAATAATTATTCCACTC	CTCCATACAGCCAAACAACGAAGCATAATATTTCGACCAATAAGCCAATGTATATTCT
GU981271.1 Crocidura fuliginosa YunnanChina	TTCTAATAATTATTCCACTC	CTCCATACAGCCAAACAACGAAGCATGATATTTCGACCAATAAGCCAATGTATATTCT
GU358522.1 Crocidura fuliginosa Taiwan	TCCTAATAATTATTCCCCTA	CTCCATACAGCTAAACAACGAAGTATAATATTTCGACCAATAAGCCAATGTCTATTCT
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	TCCTAATAATTATTCCCCTA	CTCCATACAGCTAAACAACGAAGTATAATATTTCGACCAATAAGCCAATGTCTATTCT
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	TCCTAATAATTATTCCCCTA	CTCCATACAGCTAAACAACGAAGTATAATATTTCGACCAATAAGCCAATGTCTATTCT
FJ814023.1 Crocidura lepidura Sumatra	TCCTAGTAATCATCCCACTA	CTCCATACAGCCAAACAACGAAGCATAATATTCCGACCAATAAGTCAATGTGTATTCT
FJ814022.1 Crocidura lepidura Sumatra	TCCTAGTAATCATCCCACTA	CTCCATACAGCCAAACAACGAAGCATAATATTCCGACCAATAAGTCAATGTGTATTCT
KF801079.1 Crocidura paradoxura Sumatra	TCCTAATAATCATCCCACTC	CTCCACACAGCCAAACAACGAAGCATAATATTCCGGCCAATAAGTCAATGTATATTCT
EF524619.1 Crocidura malayana UluGombak	TCCTAATAATCATCCCACTT	CTCCATACAGCTAAACAACGAAGCATAATATTCCGACCGATAAGTCAATGTATATTCT
FJ814053 Crocidura foetida doriae BintuluSarawak	TCCTAATAATCATCCCACTC	CTCCACACAGCCAAACAACGAAGCATAATGTTTCGACCAATAAGTCAATGTTTATTCT
FJ814055 Crocidura foetida doriae BintuluSarawak	TCCTAATAATCATCCCACTC	CTCCACACAGCCAAACAACGAAGCATAATGTTTCGACCAATAAGTCAATGTTTATTCT
KF283271.1 Crocidura monticola Java	TCTTAATAATCATTCCACTC	CTTCATACAGCCAAACAACGAAGTATAATATTCCGACCAATAAGCCAATGCTTATTTT
BH15-063 Crocidura foetida BorneoHighlands	TCCTAATAATTATCCCACTC	CTCCATACAGCCAAACAACGAAGCATAATATTCCGACCAATGAGTCAATGTTTATTCT
BNP16-001 Crocidura foetida BakoSarawak	TCCTAATAATTATCCCACTC	CTCCATACAGCCAAACAACGAAGCATGATATTCCGACCAATGAGTCAATATTTATTCT
DKB16-035 Crocidura foetida BauSarawak	TCCTAATAATTATCCCACTC	CTCCATACAGCCAAACAACGAAGCATAATATTTCGACCAATGAGTCAATGTTTATTCT
ENG16-133 Crocidura foetida EngkeliliSarawak	TCCTAATAATTATCCCACTC	CTCCATACAGCCAAACAACGAAGCATAATATTCCGACCAATGAGTCAATGTTTATTCT
GGNP15-001 Crocidura foetida LunduSarawak	TCCTAATAATTATCCCACTC	CTCCATACAGCCAAACAACGAAGCATGATATTCCGACCAATGAGTCAATGTTTATTCT
DQ630381.1 Crocidura malayana UluGombak	TCCTAATAATCATCCCACTT	CTCCATACAGCTAAACAACGAAGCATAATATTCCGACCGATAAGTCAATGTATATTCT
GI15-047 Crocidura malayana GualkanKelantan	TCCTAATAATCATCCCACTT	CTCCATACAGCTAAACAACGAAGCATAATATTCCGACCGATAAGTCAATGTATATTCT
KWT15-007 Crocidura foetida KubahSarawak	TCCTAATAATTATCCCACTC	CTCCATACAGCCAAACAACGAAGCATAATATTTCGACCAATGAGTCAATGTTTATTCT
MNP17-050 Crocidura foetida MuluMiri	TCCTAATAATCATCCCACTC	CTCCATACAGCCAAACAACGAAGCATAATGTTTCGACCAATAAGTCAATGTTTATTCT
NB14-002 Crocidura foetida NangaBeninKapit	TCCTAATAATCATCCCACTC	CTCCATACAGCCAAACAACGAAGCATAATGTTTCGACCAATAAGTCAATGTTTATTCT
DKB16-036 C.foetida BauSarawak	TCCTAATAATTATCCCACTC	CTCCATACAGCCAAACAACGAAGCATGATATTCCGACCAATGAGTCAATGTTTATTCT
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	TCCTAATAGTCATCCCACTT	CTCCATACAGCTAAACAACGAAGCATAATATTCCGACCGATAAGTCAATGTATATTCT
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	TCCTAATAATCATCCCACTT	CTCCATACAGCTAAACAACGAAGCATAATATTCCGACCGATAAGTCAATGTATATTCT
KF283272.1 Crocidura brunnea Java	TCCTAGTAATCATCCCACTT	CTCCATACAGCTAAACAACGAAGCATGATATTCCGACCAATAAGTCAATGTATATTCT
FJ813926.1 Crocidura nigripes Sulawesi	TCCTAATAATTATCCCACTC	CTCCATACAGCCAAACAACGAAGCATAATATTTCGACCAATAAGTCAATGTATATTCT
FJ813874.1 Crocidura grayi Philippines	TCCTAATAATCATTCCACTC	CTCCACACAGCTAAGCAACGAAGTATAATATTTCGACCAATAAGTCAATGTATATTCT
SNP16-036 Crocidura foetida SantubongSarawak	TCCTAATAATTATCCCACTC	CTCCATACAGCCAAACAACGAAGCATAATATTCCGACCAATGAGTCAATGTTTATTCT
VM016-010 Crocidura foetida MatangSarawak	TCCTAATAATTATCCCACTC	CTCCATACAGCCAAACAACGAAGCATGATATTCCGACCAATGAGTCAATGTTTATTCT
KF283233.1 Crocidura umbra Java	TCCTAATAATTATTCCACTC	CTCCATACAGCCAAACAACGAAGCATAATATTCCGACCAATAAGCCAATGCTTATTTT
FJ814029.1 Crocidura orientalis Java	TTCTAATAATCATCCCACTT	CTCCATACAGCCAAACAACGAAGCATAATATTCCGACCAATAAGTCAATGTATATTCT
FJ813977.1 Crocidura batakorum PalawanIsland	TCCTAATAGTTATTCCACTC	CTCCATACAGCTAAACAACGAAGCATAATATTCCGGCCCATAAGCCAATGCATATTCT
FJ813978.1 Crocidura palawanensis PalawanIsland	TCCTAATAATCATCCCACTC	CTCCATACAGCCAAGCAACGAAGCATAATATTCCGACCAATAAGTCAATGTATATTCT
LU14191 SuncusMurinus Perak	TCCTAATGGTCGTTCCACTT	CTTCACACAGCCAAACAACGAAGCATAATTTTCCGACCAATAAGCCAATGCATATTCT
TK16 001 KinabaluSabah	TTCTAACAGTCATCCCACTT	CTCCACACAGCTAAGCAACGAAGTATAATATTCCGTCCTATAAGCCAATGCCTATTCT
GGNP16 006 LunduSarawak	TTCTAACAGTTATACCACTT	CTCCATACAGCTAAACAACGAAGTATAATATTCCGTCCTATAAGTCAATGTCTATTCT
KWT15 019 KubahSarawak	TCCCGATAGTCATTCCACTC	CTCCATACAGCCAAACAACGAAGTATAATATTCTGACCAATAAGCCAATGCTTATTCT
FJ813843.1 Crocidura mindorus Philippines	TCCTGATAATTATCCCACTC	CTCCATACAGCCAAGCAACGAAGCATAATATTTCGACCAATAAGTCAATGTATATTCT
FJ813950.1 Crocidura panayensis Philippines	TCCTGATAATCATCCCACTC	CTCCATACAGCCAAGCAACGAAGCATAATATTCCGACCAATAAGTCAATGCATATTCT
FJ813962.1 Crocidura negrina Philippines	TCCTGATAATTATCCCACTC	CTTCACACAGCCAAGCAACGAAGCATAATGTTCCGACCAATGAGTCAATGTATGTTCT
KX469583.1 Crocidura beccarii Sumatra	TTCTAGTAGTCATCCCACTC	CTCCATACAGCTAAACAACGAAGCATAATATTCCGACCAATAAGTCAATGTATATTCT
KX469629.1 Crocidura neglecta Sumatra	TTCTAACAGCCATTCCACTT	CTCCACACAGCTAAACAACGAAGTATAATATTCCGTCCTATAAGCCAATGCCTATTCT

AB175079.1 Crocidura fuliginosa Vietnam	GAATCCTAGTAGCAGACCTATTTACATTAACTTGAATTGGAGGCCAACCAGTTGAGCACCCATTCGTAGTAATTGG
GU981271.1 Crocidura fuliginosa YunnanChina	GAATCCTAGTAGCAGACCTGTTTACATTAACTTGAATTGGAGGCCAACCAGTTGAGCACCCATTCGTAGTAATTGG
GU358522.1 Crocidura fuliginosa Taiwan	GAGTCCTAGTAGCAGACCTATTCACATTAACTTGAATTGGAGGTCAGCCAGTTGAACACCCATTTGTAGTAATTGG
FJ813925.1 Crocidura fuliginosa PeninsularMalaysia	GAGTCCTAGTAGCAGACCTATTCACACTAACTTGAATTGGAGGCCAGCCAGTTGAACACCCATTTGTAGTAATTGG
FJ813924.1 Crocidura fuliginosa PeninsularMalaysia	GAGTCCTAGTAGCAGACCTATTCACATTAACTTGAATTGGAGGTCAGCCAGTTGAACACCCATTTGTAGTAATTGG
FJ814023.1 Crocidura lepidura Sumatra	GAATTCTAGTAGCAGACCTAGCTACACTAACTTGAATTGGAGGCCAACCAGTTGAATATCCATTTGTAGTAATCGG
FJ814022.1 Crocidura lepidura Sumatra	GAATTCTAGTAGCAGACCTAGCTACACTAACTTGAATTGGAGGCCAACCAGTTGAATATCCATTTGTAGTAATCGG
KF801079.1 Crocidura paradoxura Sumatra	GAATCCTAGTAGCAGACCTAGCTACACTAACCTGAATTGGAGGCCAACCAGTCGAACATCCATTTGTAGTAATTGG
EF524619.1 Crocidura malayana UluGombak	GAATCCTAGTAGCAGATCTGGCTACACTAACTTGAATTGGAGGCCAACCAGTTGAACATCCATTTGTAGTAATCGG
FJ814053 Crocidura foetida doriae BintuluSarawak	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATTGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
FJ814055 Crocidura foetida doriae BintuluSarawak	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATTGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
KF283271.1 Crocidura monticola Java	GAATCCTAGTGGCAGACCTACTCACACTAACCTGAATTGGAGGTCAACCAGTTGAACATCCATTTGTAGTAATCGG
BH15-063 Crocidura foetida BorneoHighlands	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATCGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
BNP16-001 Crocidura foetida BakoSarawak	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATCGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
DKB16-035 Crocidura foetida BauSarawak	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATCGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
ENG16-133 Crocidura foetida EngkeliliSarawak	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATCGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
GGNP15-001 Crocidura foetida LunduSarawak	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATCGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
DQ630381.1 Crocidura malayana UluGombak	GAATCCTAGTAGCAGATCTGGCTACACTAACTTGAATTGGAGGCCAACCAGTTGAACATCCATTTGTAGTAATCGG
GI15-047 Crocidura malayana GualkanKelantan	GAATCCTAGTAGCAGATCTGGCTACACTAACTTGAATTGGAGGCCAACCAGTTGAACATCCATTTGTAGTAATCGG
KWT15-007 Crocidura foetida KubahSarawak	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATCGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
MNP17-050 Crocidura foetida MuluMiri	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATTGGAGACCAACCAGTTGAACACCCATTCGTAGTAATCGG
NB14-002 Crocidura foetida NangaBeninKapit	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATTGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
DKB16-036 C.foetida BauSarawak	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATCGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
PPS15-043 Crocidura malayana PangkorPeninsularMalaysia	GAATCCTAGTAGCAGATCTGGCTACACTAACTTGAATTGGAGGCCAACCAGTTGAACATCCATTTGTAGTAATCGG
SD15-015 Crocidura malayana SungaiDusunPeninsularMalaysia	GAATCCTAGTAGCAGATCTGGCTACACTAACTTGAATTGGAGGCCAACCAGTTGAACATCCATTTGTAGTAATCGG
KF283272.1 Crocidura brunnea Java	GAATTCTAGCAGCAGACCTAGCTACACTAACTTGAATTGGAGGTCAACCAGTTGAACATCCATTTGTAGTAATCGG
FJ813926.1 Crocidura nigripes Sulawesi	GAATCCTAGTAGCTGACCTAACTACATTAACTTGAATTGGAGGTCAACCAGTTGAACACCCATTTGTAGTAATTGG
FJ813874.1 Crocidura grayi Philippines	GAATTCTAGTAGCAGACCTAGCTACACTAACCTGAATTGGGGGTCAACCAGTCGAACACCCATTTGTAGTAATCGG
SNP16-036 Crocidura foetida SantubongSarawak	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATCGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
VM016-010 Crocidura foetida MatangSarawak	GAATTCTAGTAGCAGATCTAGTTACACTAACTTGAATCGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
KF283233.1 Crocidura umbra Java	GAATCCTAGTAGCAGACCTACTTACACTAACCTGAATCGGAGGCCAACCAGTTGAACATCCATTTGTAGTAATCGG
FJ814029.1 Crocidura orientalis Java	GGATTCTAGTAGCAGACCTAGCTACACTAACTTGAATCGGAGGCCAACCAGTTGAACACCCATTCGTAGTAATCGG
FJ813977.1 Crocidura batakorum PalawanIsland	GAATTTTAGTGGCAGACCTATTTACACTAACATGAATCGGCGGTCAACCAGTTGAACACCCATTTGTAGTAATTGG
FJ813978.1 Crocidura palawanensis PalawanIsland	GAATTCTAGTGGCAGACCTAGCCACACTAACTTGAATCGGAGGCCAACCAGTTGAACACCCATTTGTAGTAATCGG
LU14191 SuncusMurinus Perak	GAATCCTAGTTGCAGACCTATTTACATTAACATGAATTGGAGGTCAACCAGTCGAACATCCATTTGTTGTAATCGG
TK16 001 KinabaluSabah	GAATTCTAGTAGCAGATCTGCTTACATTAACTTGAATTGGAGGACAACCAGTTGAACACCCATTTGTAGTAATTGG
GGNP16 006 LunduSarawak	GAATTCTAGTAGCAGACCTATTTACATTAACTTGAATTGGAGGACAACCAGTTGAACACCCATTTGTAGTAATTGG
KWT15 019 KubahSarawak	GAATCCTAGTAGCGGACCTATTTACACTAACTTGAATCGGAGGCCAGCCAGTTGAACACCCATTCGTAGTAATTGG
FJ813843.1 Crocidura mindorus Philippines	GAATTCTAGTAGCAGACCTAGCCACACTAACCTGAATTGGAGGCCAACCAGTCGAACACCCATTCGTAGTAATCGG
FJ813950.1 Crocidura panayensis Philippines	GAATCCTAGTAGCAGACCTAGCCACACTAACTTGAATTGGAGGCCAACCAGTCGAACACCCATTCGTAGTAATCGG
FJ813962.1 Crocidura negrina Philippines	GAATTCTAGTAGCAGACCTCGCCACACTAACTTGAATTGGAGGCCAACCAGTCGAACATCCATTCGTAGTAATCGG
KX469583.1 Crocidura beccarii Sumatra	GAATTCTAGTAGCAGACCTAGCTACACTAACTTGAATTGGAGGCCAACCAGTTGAACATCCATTTGTAGTAATCGG
KX469629.1 Crocidura neglecta Sumatra	GAATCCTAGTAGCAGATCTACTTACACTAACTTGAATTGGAGGGCAACCAGTTGAACACCCATTTGTAGTAATTGG

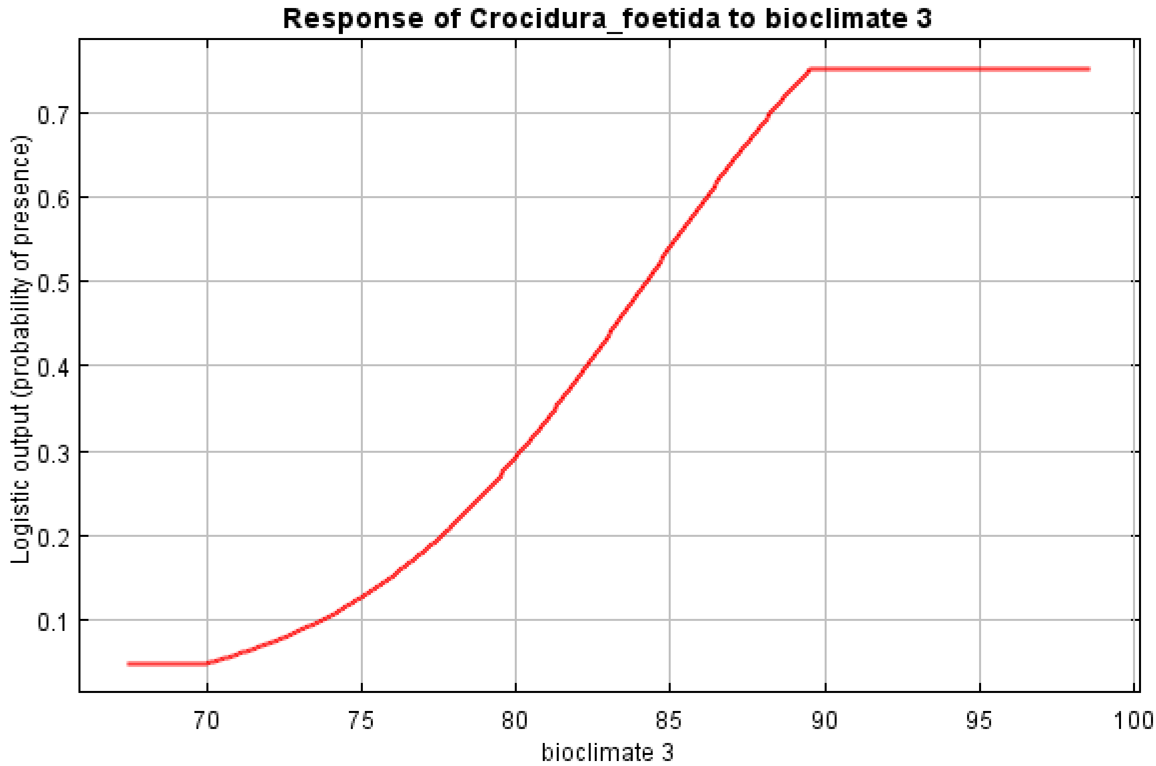
Appendix 6.0: The response curves for *Crocidura foetida* in MaxEnt analysis.



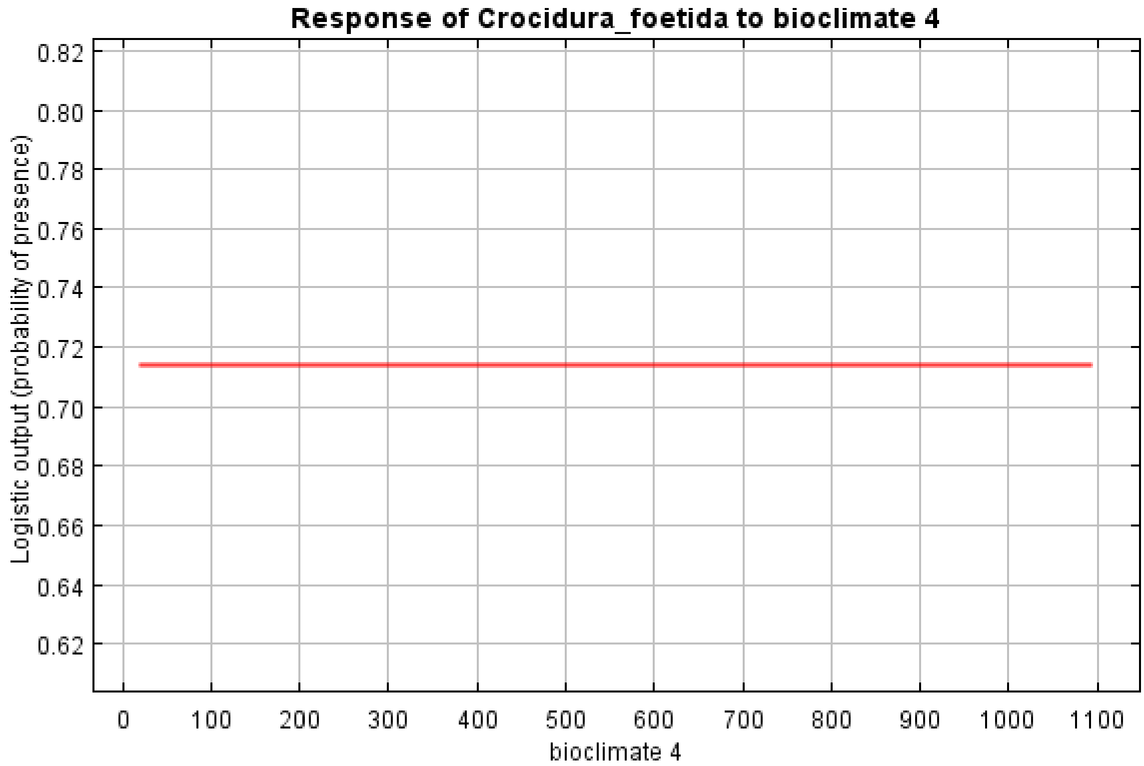


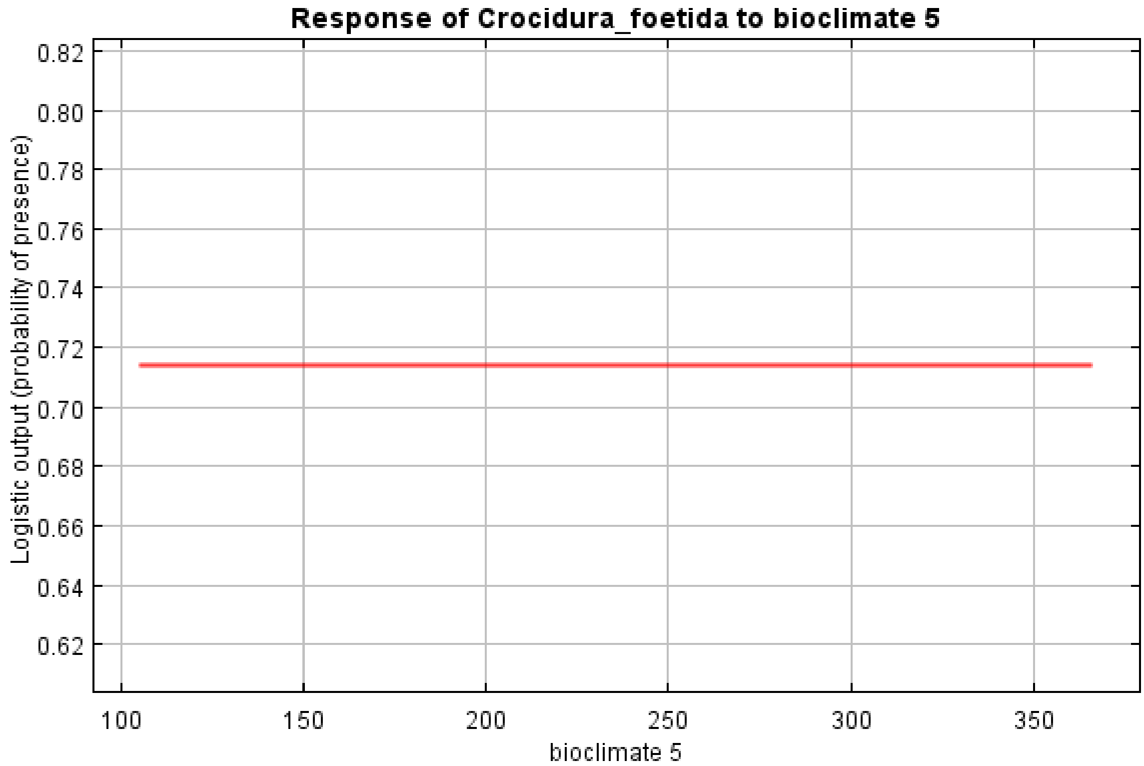


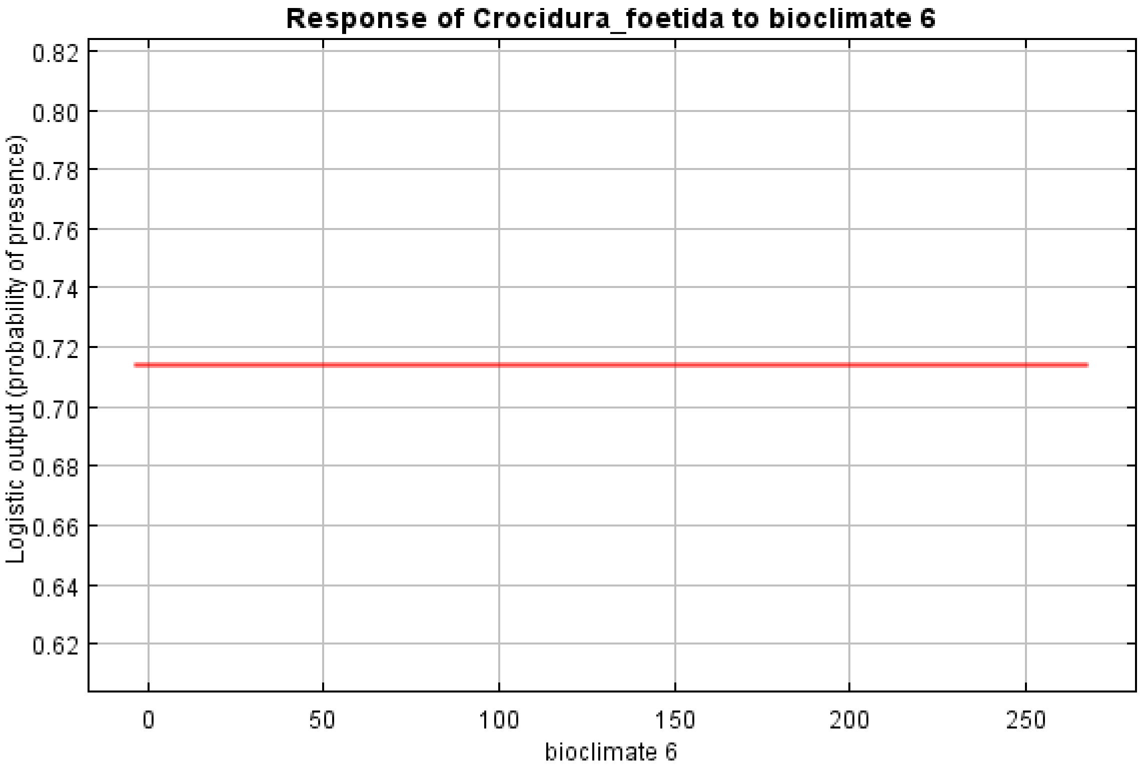
Response of Crocidura_foetida to bioclimate 2
Logistic output (probability of presence)
0.82
0.80
0.78
0.76
0.74
0.72
0.70
0.68
0.66
0.64
0.62
60
70
80
90
100
110
120
bioclimate 2

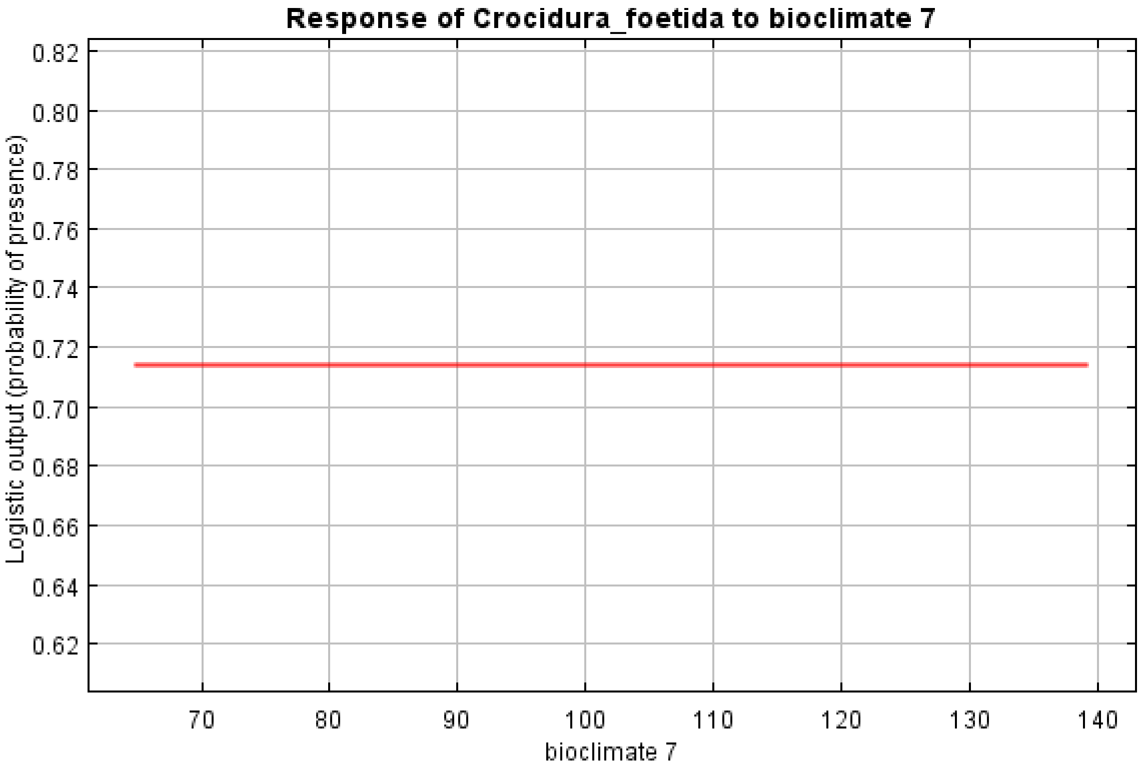


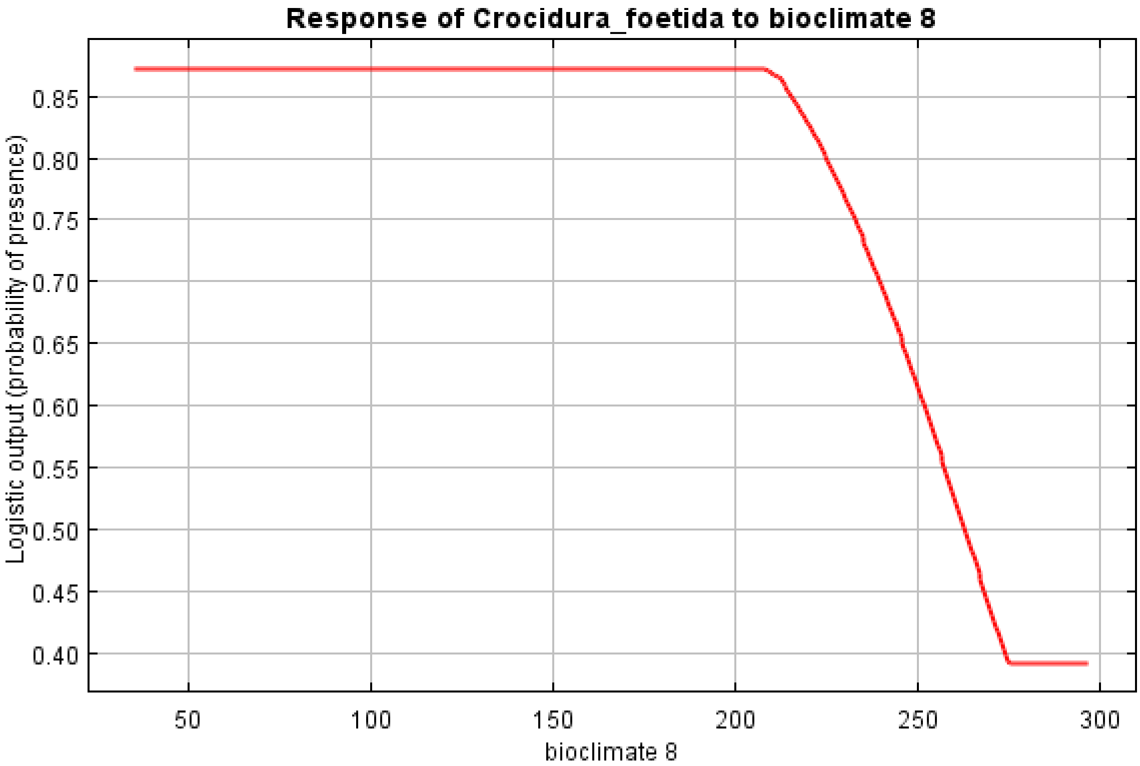
Response of Crocidura_foetida to bioclimate 3
Logistic output (probability of presence)
0.7
0.6
0.5
0.4
0.3
0.2
0.1
70
75
80
85
90
95
100
bioclimate 3

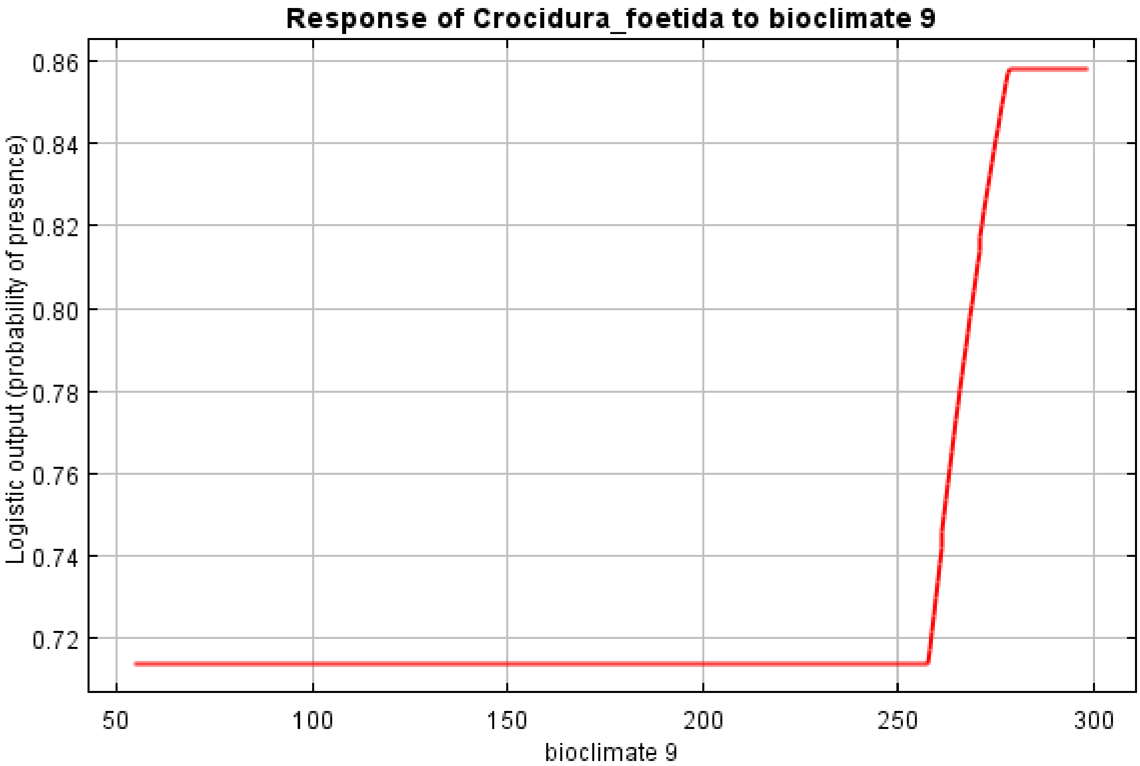

Response of Crocidura_foetida to bioclimate 4
Logistic output (probability of presence)
0.82
0.80
0.78
0.76
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0
100
200
300
400
500
600
700
800
900
1000
1100
bioclimate 4

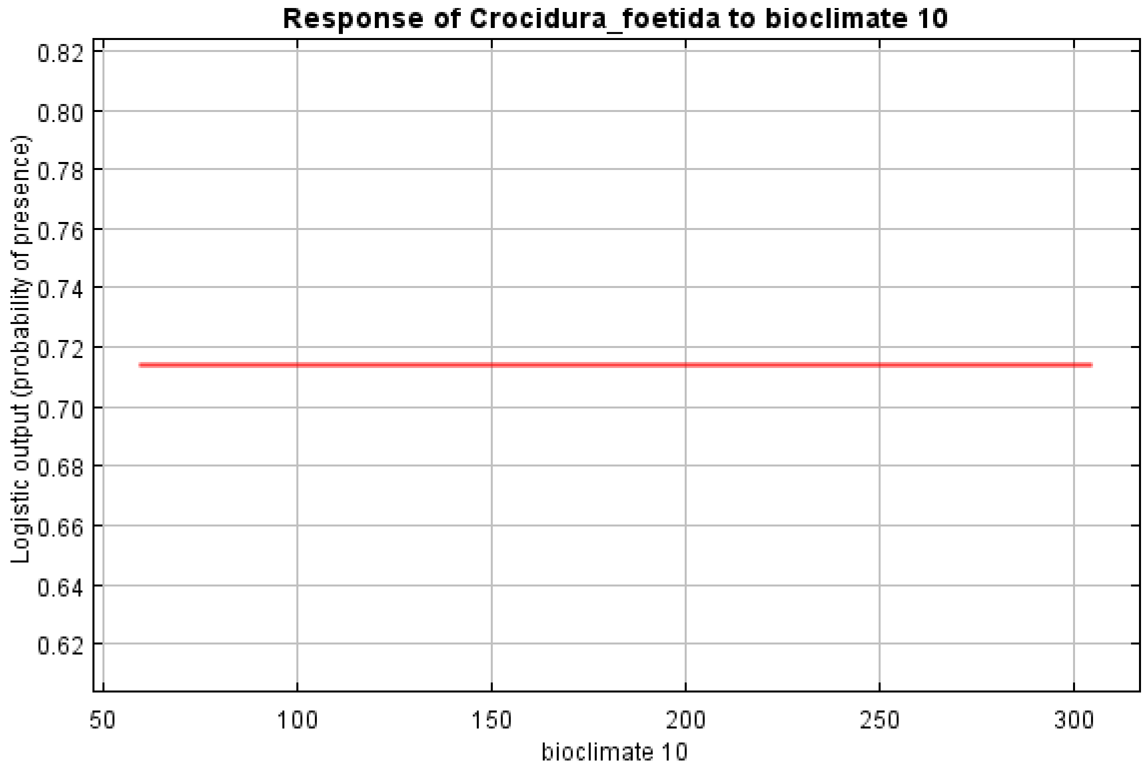

Response of Crocidura_foetida to bioclimate 5
Logistic output (probability of presence)
0.82
0.80
0.78
0.76
0.74
0.72
0.70
0.68
0.66
0.64
0.62
100
150
200
250
300
350
bioclimate 5

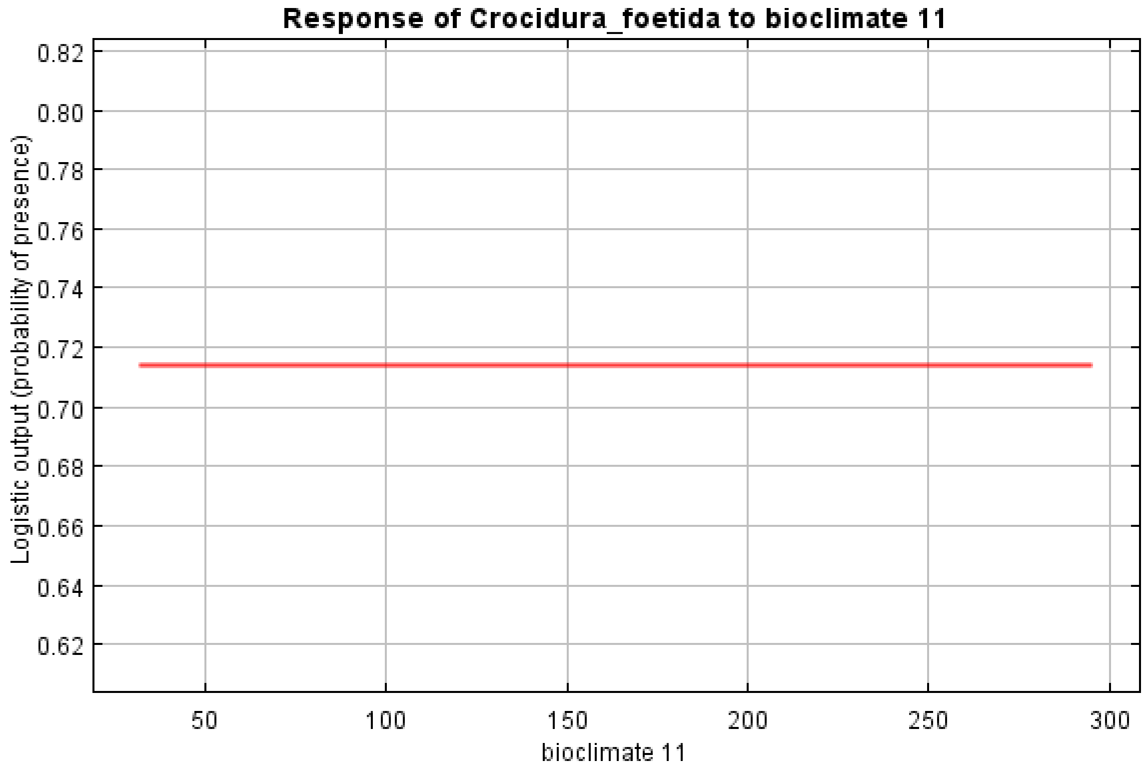

Response of Crocidura_foetida to bioclimate 6
Logistic output (probability of presence)
0.82
0.80
0.78
0.76
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0
50
100
150
200
250
bioclimate 6

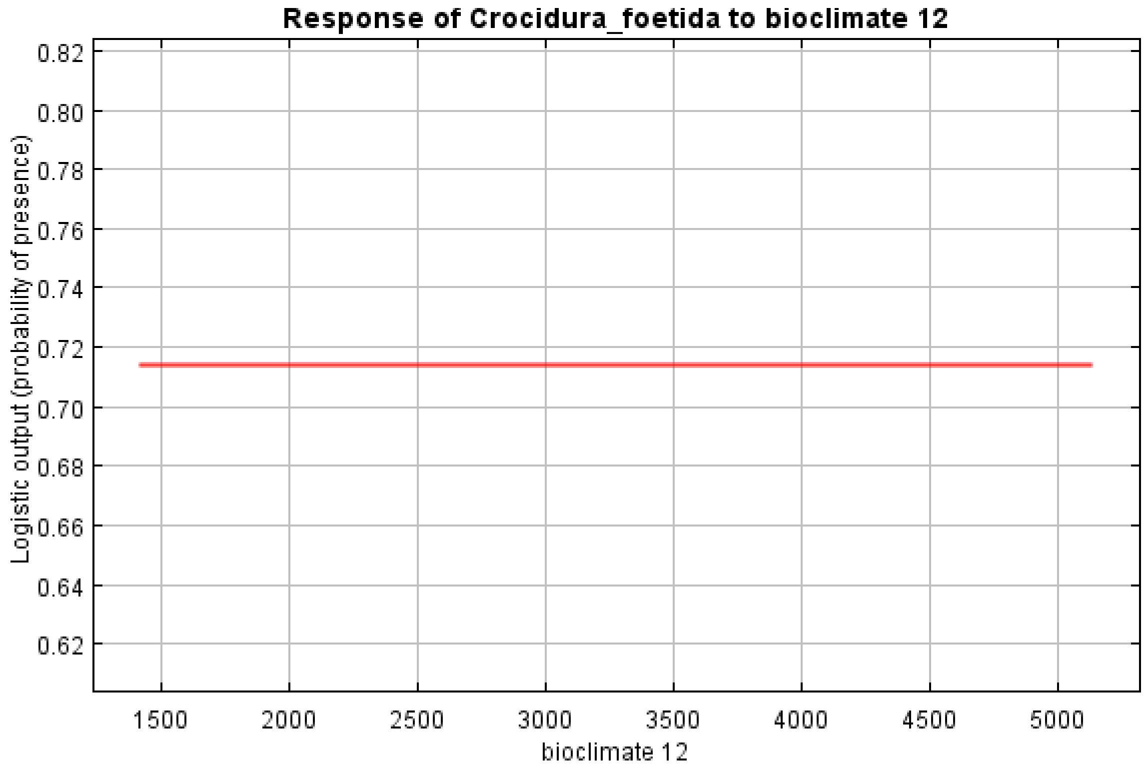

Response of Crocidura_foetida to bioclimate 7
Logistic output (probability of presence)
0.82
0.80
0.78
0.76
0.74
0.72
0.70
0.68
0.66
0.64
0.62
70
80
90
100
110
120
130
140
bioclimate 7


Response of Crocidura_foetida to bioclimate 8
Logistic output (probability of presence)
0.85
0.80
0.75
0.70
0.65
0.60
0.55
0.50
0.45
0.40
50
100
150
200
250
300
bioclimate 8

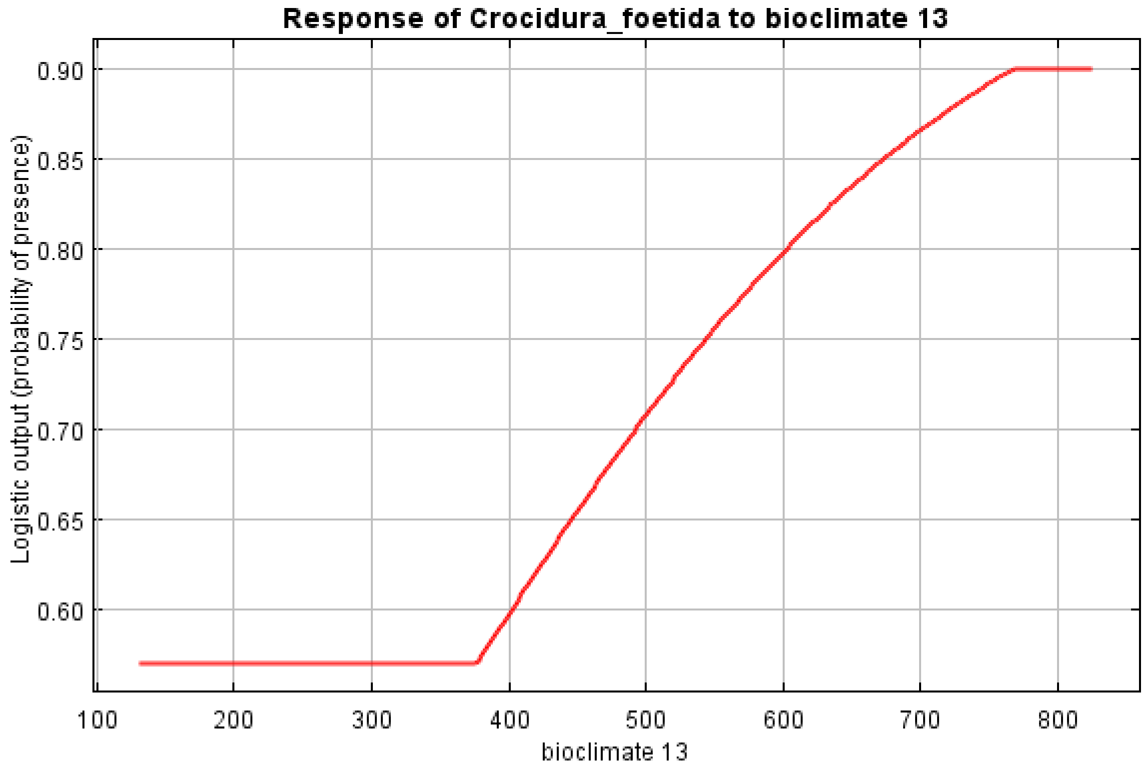

Response of Crocidura_foetida to bioclimate 9
Logistic output (probability of presence)
0.86
0.84
0.82
0.80
0.78
0.76
0.74
0.72
50
100
150
200
250
300
bioclimate 9


Response of Crocidura_foetida to bioclimate 10
Logistic output (probability of presence)
0.82
0.80
0.78
0.76
0.74
0.72
0.70
0.68
0.66
0.64
0.62
50
100
150
200
250
300
bioclimate 10

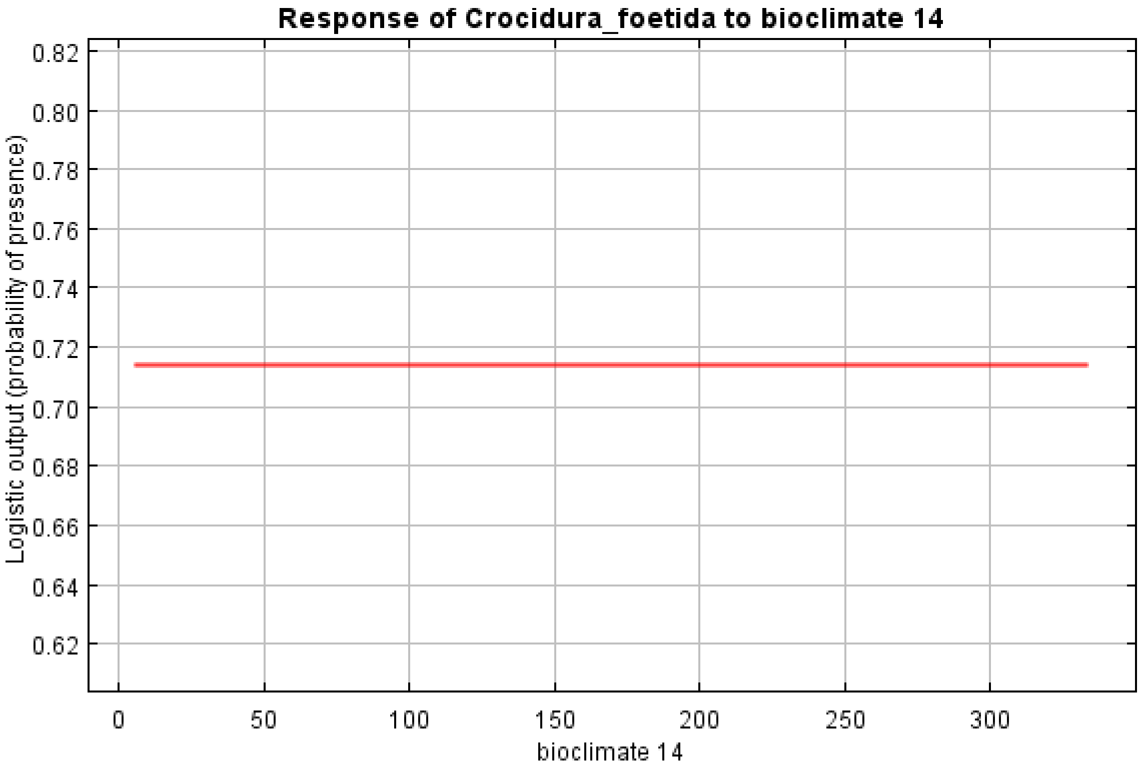

Response of Crocidura_foetida to bioclimate 11
Logistic output (probability of presence)
0.82
0.80
0.78
0.76
0.74
0.72
0.70
0.68
0.66
0.64
0.62
50
100
150
200
250
300
bioclimate 11



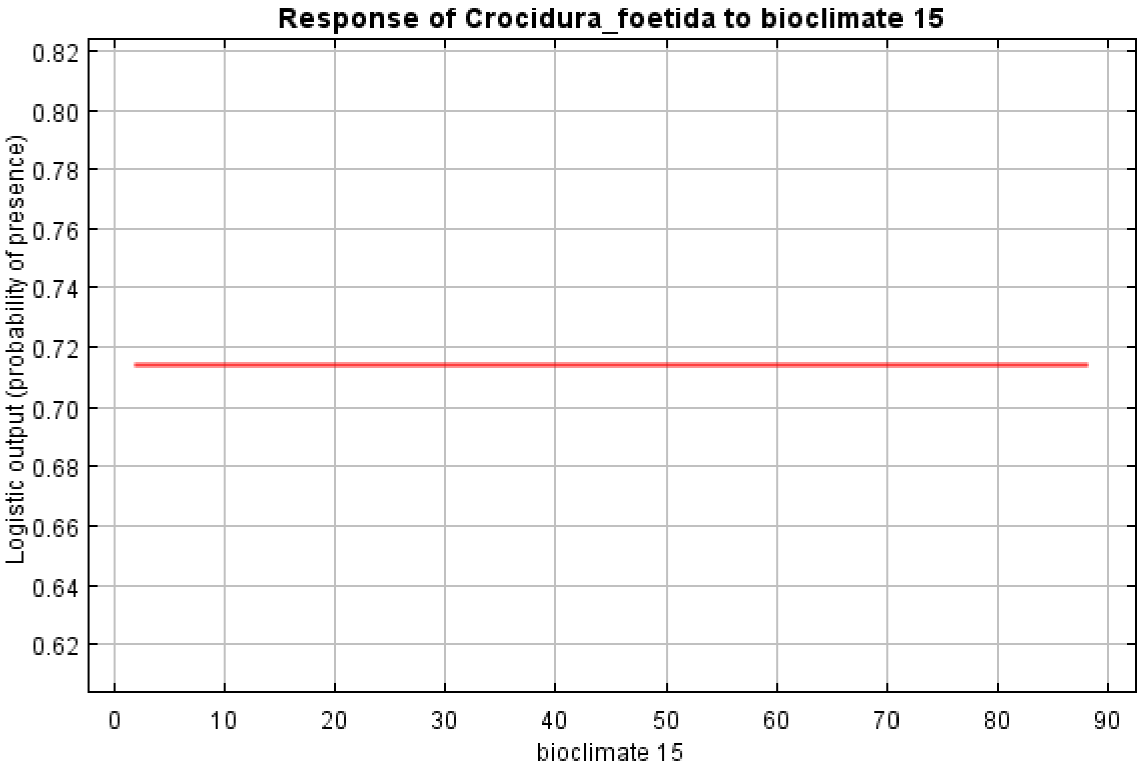
Response of Crocidura_foetida to bioclimate 12
Logistic output (probability of presence)
0.82
0.80
0.78
0.76
0.74
0.72
0.70
0.68
0.66
0.64
0.62
1500
2000
2500
3000
3500
4000
4500
5000
bioclimate 12



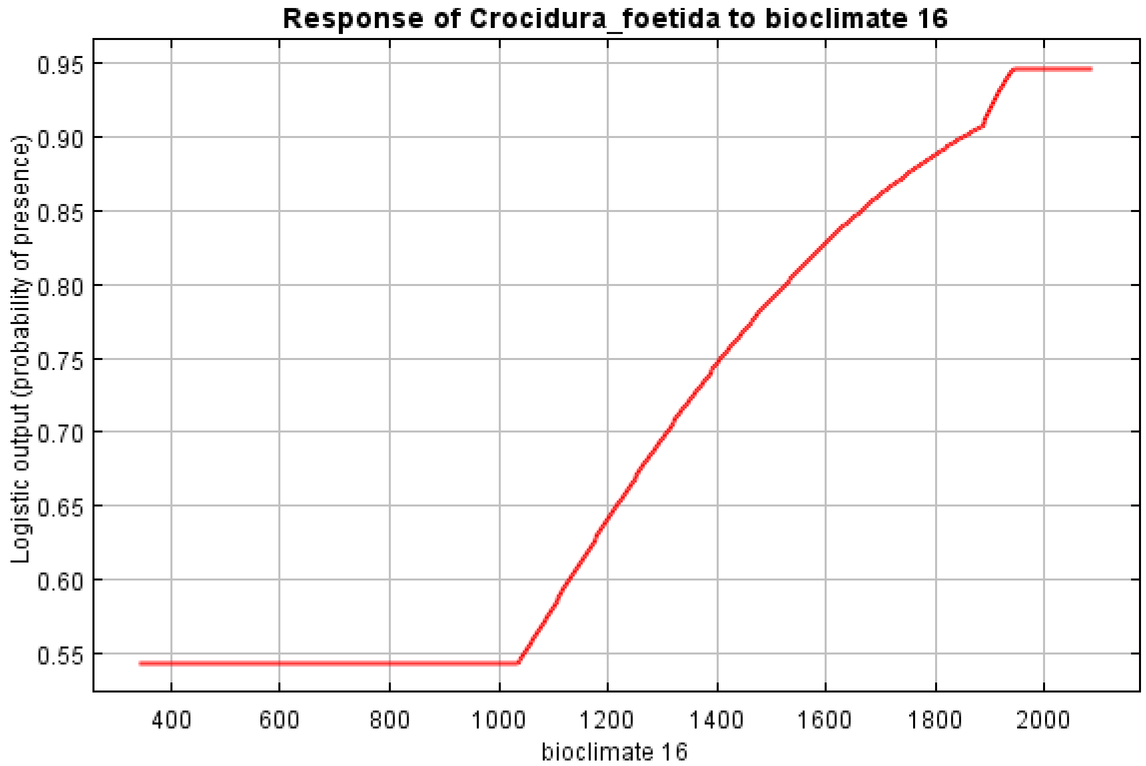
Response of Crocidura_foetida to bioclimate 13
Logistic output (probability of presence)
0.90
0.85
0.80
0.75
0.70
0.65
0.60
100
200
300
400
500
600
700
800
bioclimate 13

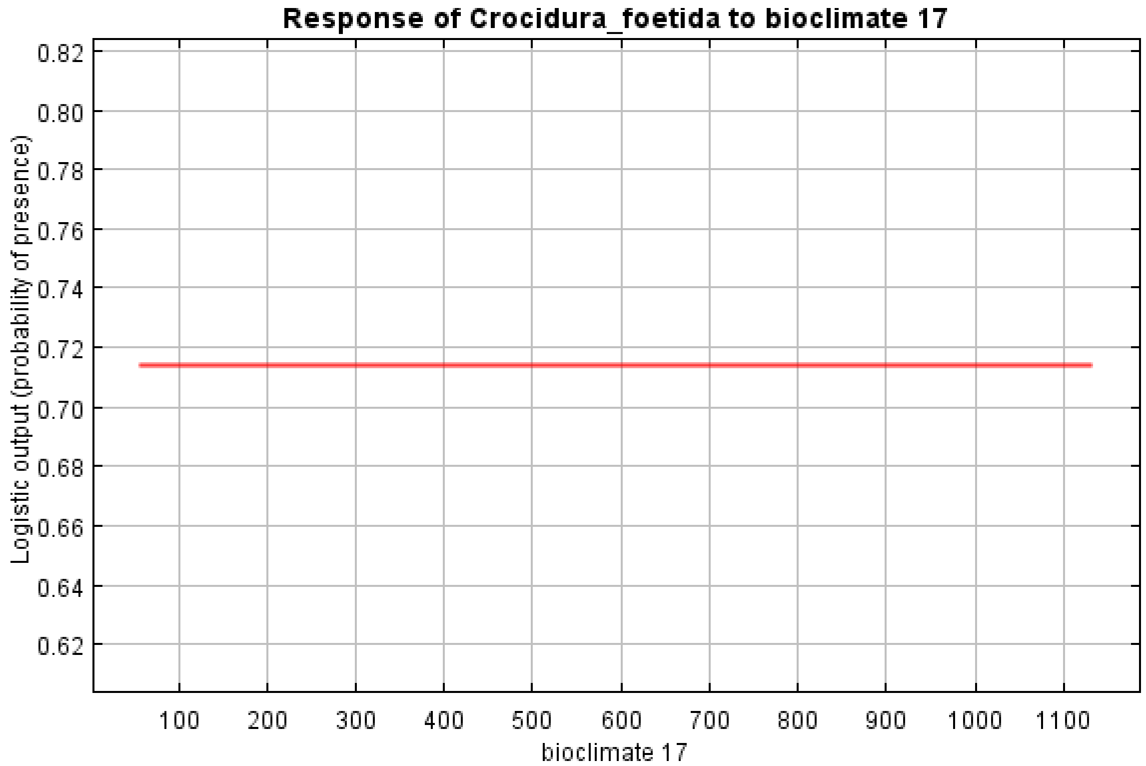


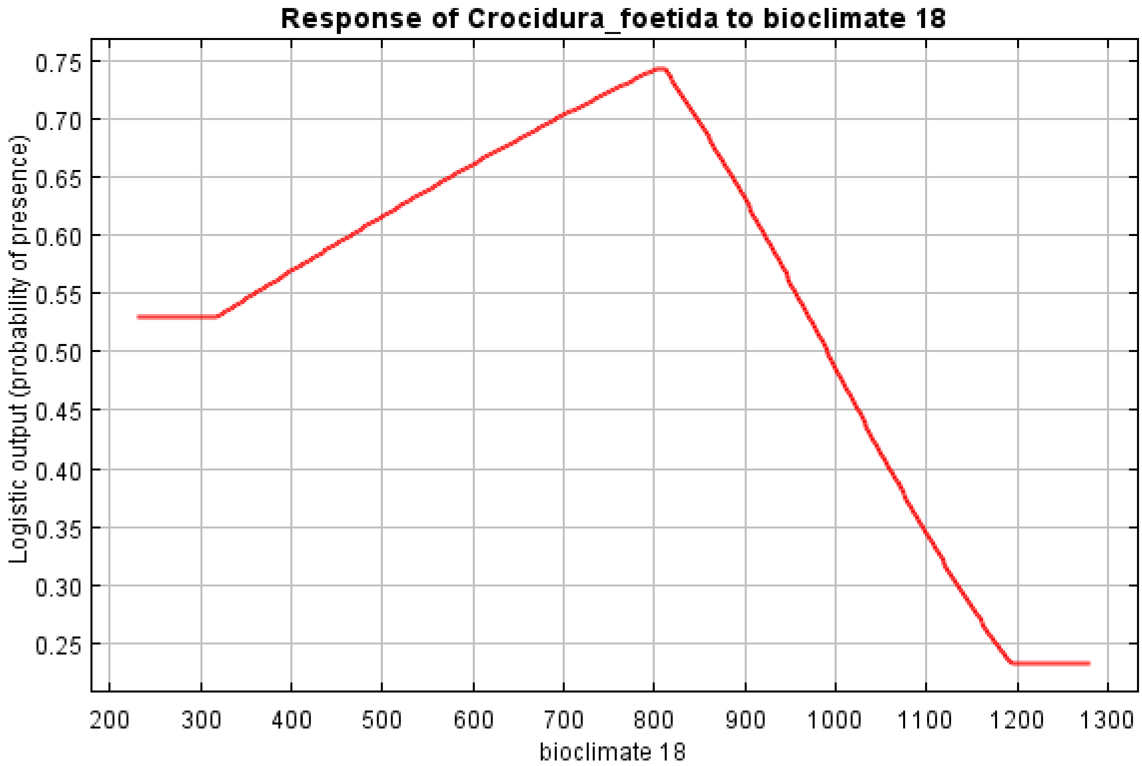
Response of Crocidura_foetida to bioclimate 14
Logistic output (probability of presence)
0.82
0.80
0.78
0.76
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0
50
100
150
200
250
300
bioclimate 14



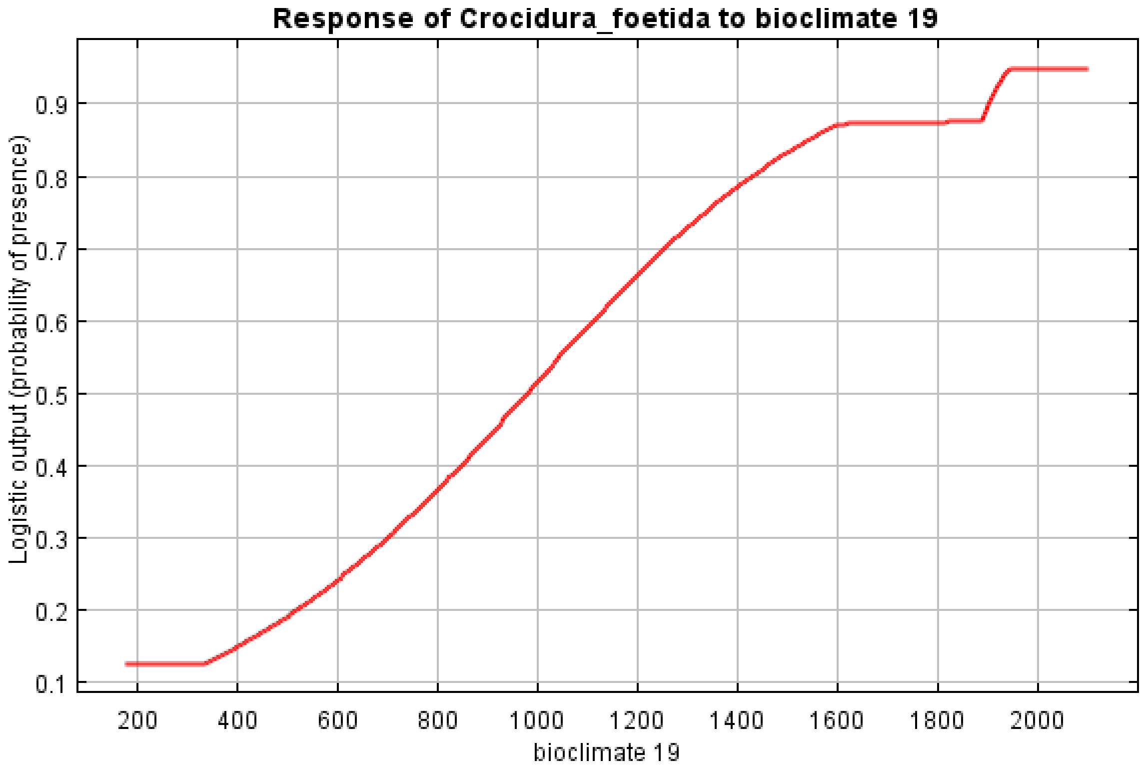
Response of Crocidura_foetida to bioclimate 15
Logistic output (probability of presence)
0.82
0.80
0.78
0.76
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0
10
20
30
40
50
60
70
80
90
bioclimate 15


Response of Crocidura_foetida to bioclimate 16
Logistic output (probability of presence)
0.95
0.90
0.85
0.80
0.75
0.70
0.65
0.60
0.55
400
600
800
1000
1200
1400
1600
1800
2000
bioclimate 16

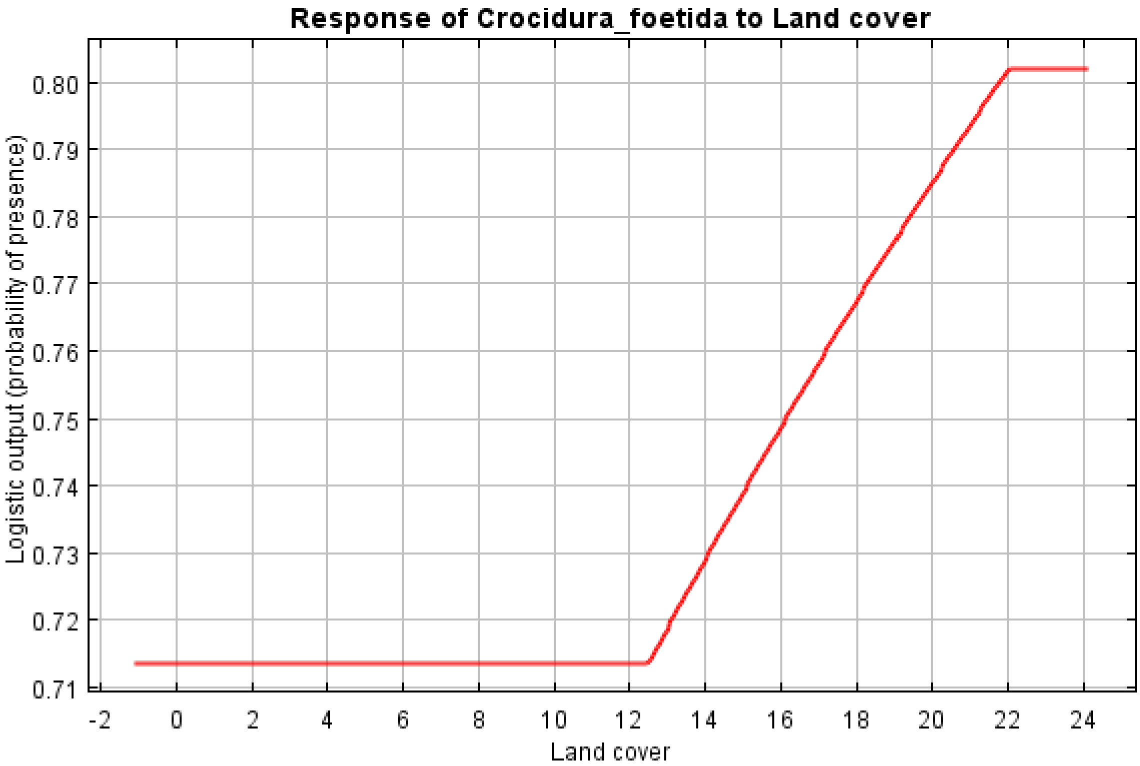

Response of Crocidura_foetida to bioclimate 17
Logistic output (probability of presence)
0.82
0.80
0.78
0.76
0.74
0.72
0.70
0.68
0.66
0.64
0.62
100
200
300
400
500
600
700
800
900
1000
1100
bioclimate 17



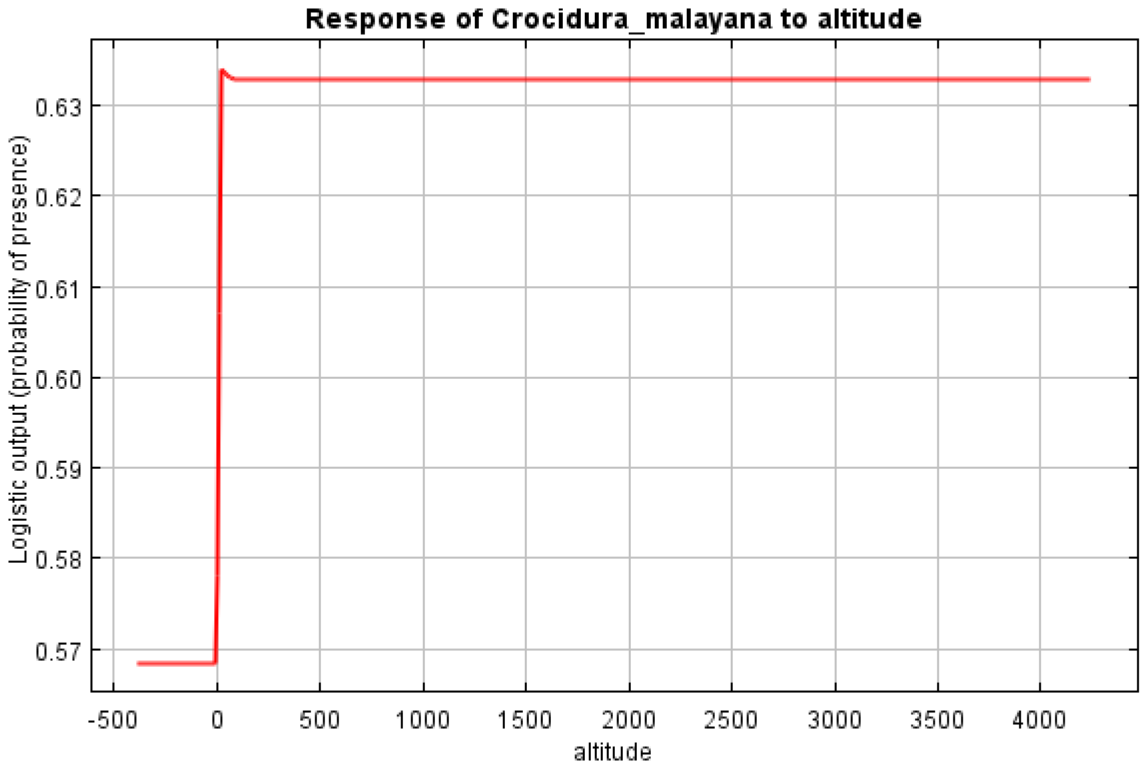
Response of Crocidura_foetida to bioclimate 18
Logistic output (probability of presence)
0.75
0.70
0.65
0.60
0.55
0.50
0.45
0.40
0.35
0.30
0.25
200
300
400
500
600
700
800
900
1000
1100
1200
1300
bioclimate 18

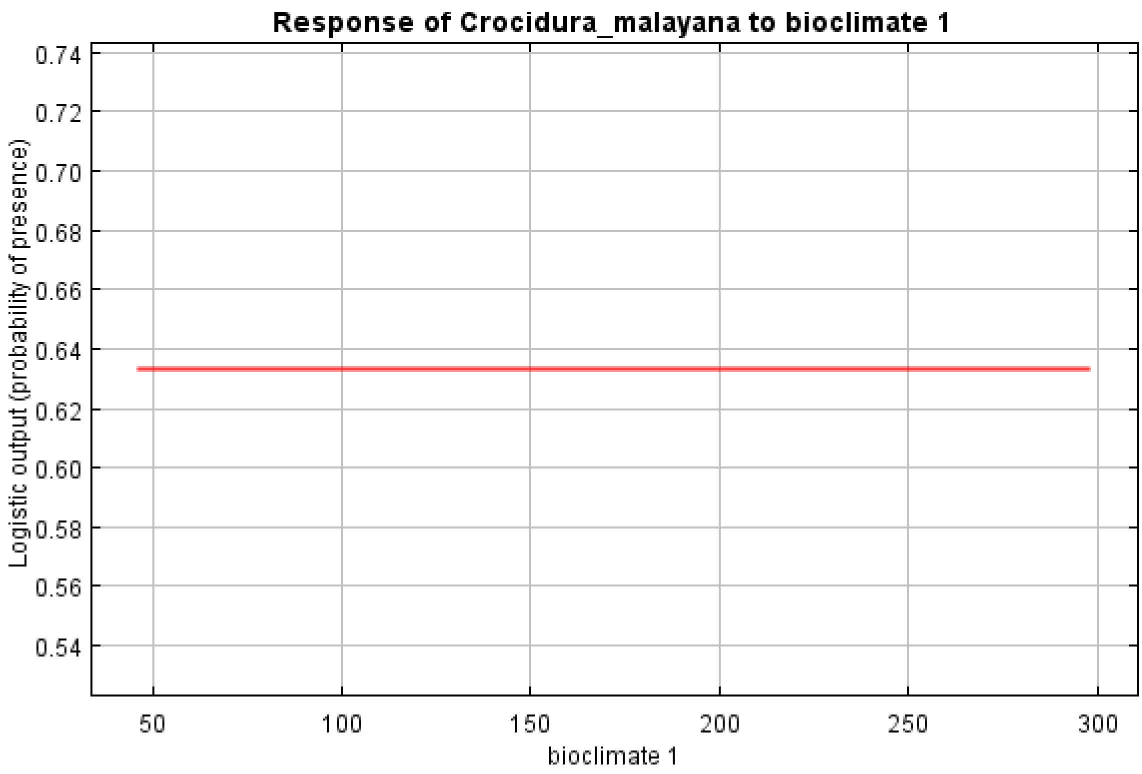


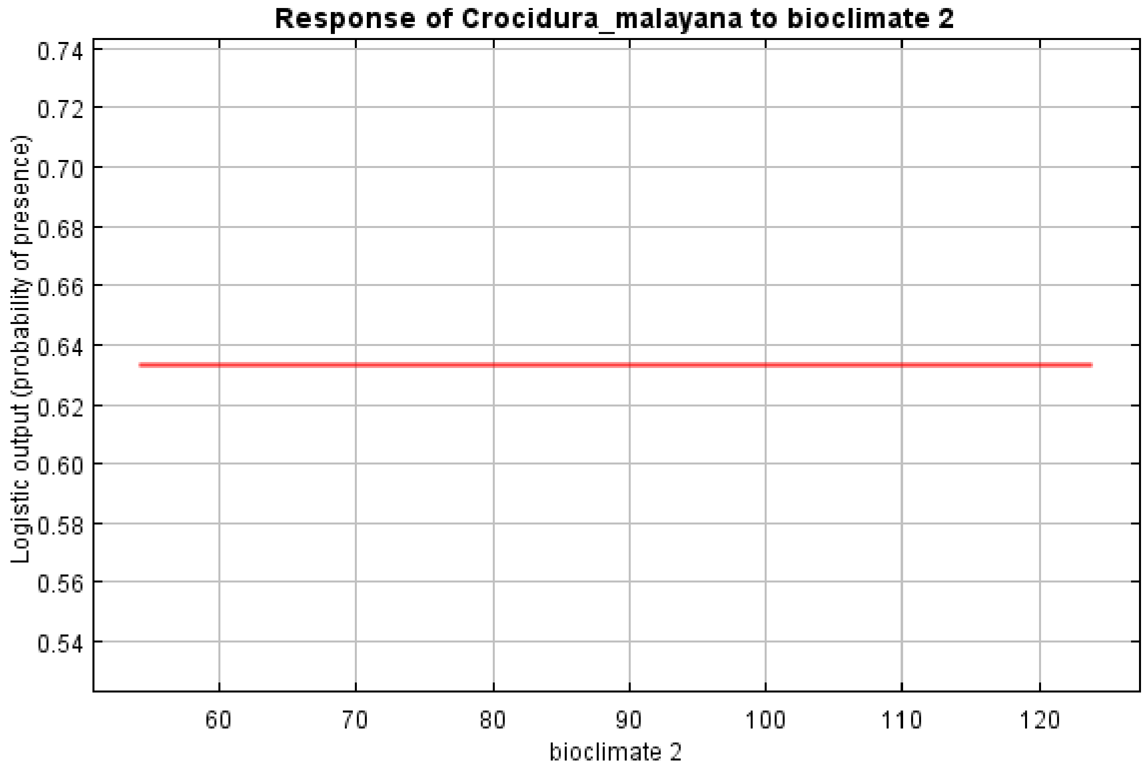
Response of Crocidura_foetida to bioclimate 19
Logistic output (probability of presence)
0.9
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
200
400
600
800
1000
1200
1400
1600
1800
2000
bioclimate 19


Response of Crocidura_foetida to Land cover
Logistic output (probability of presence)
0.80
0.79
0.78
0.77
0.76
0.75
0.74
0.73
0.72
0.71
-2
0
2
4
6
8
10
12
14
16
18
20
22
24
Land cover

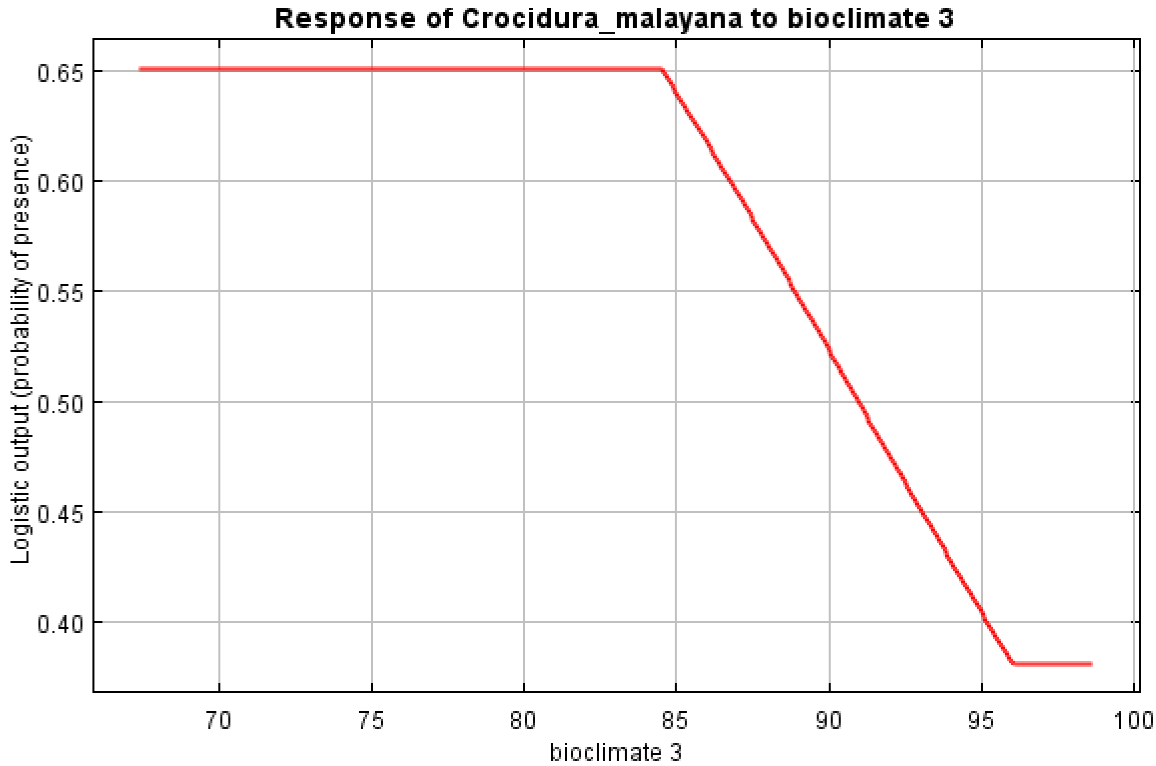
Appendix 6.0: The response curves for *Crocidura malayana* in MaxEnt analysis.



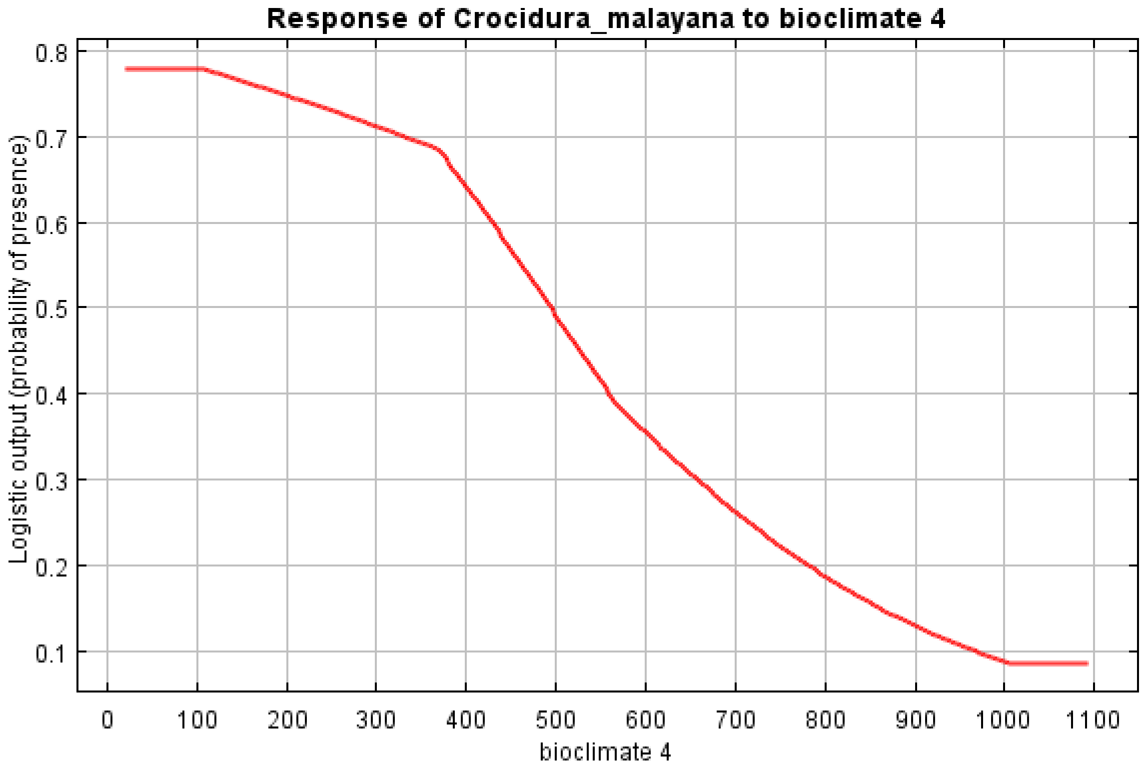


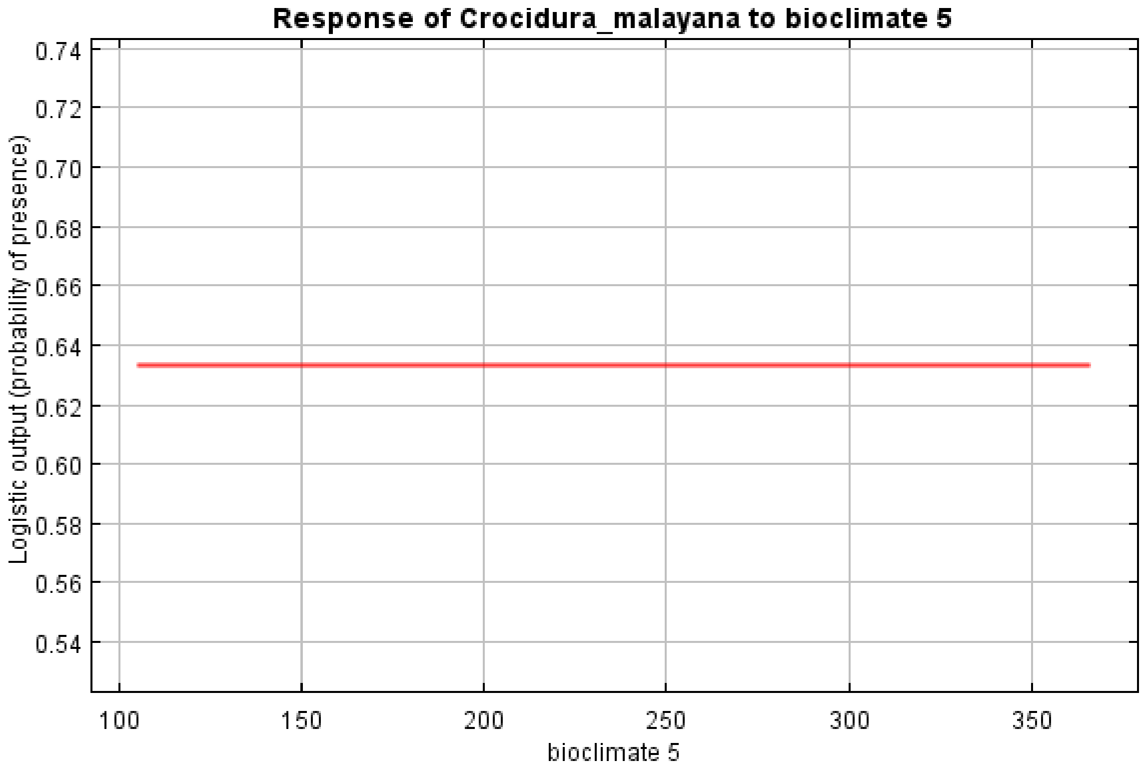


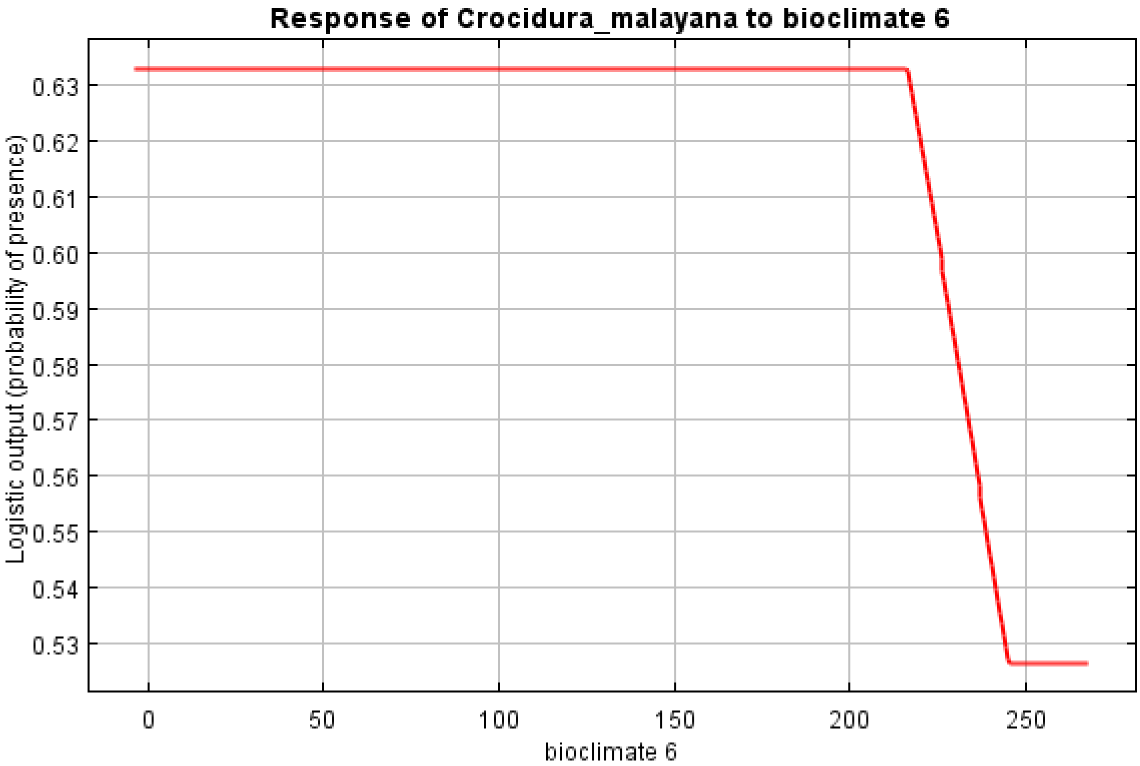
Response of Crocidura_malayana to bioclimate 2
Logistic output (probability of presence)
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0.60
0.58
0.56
0.54
60
70
80
90
100
110
120
bioclimate 2

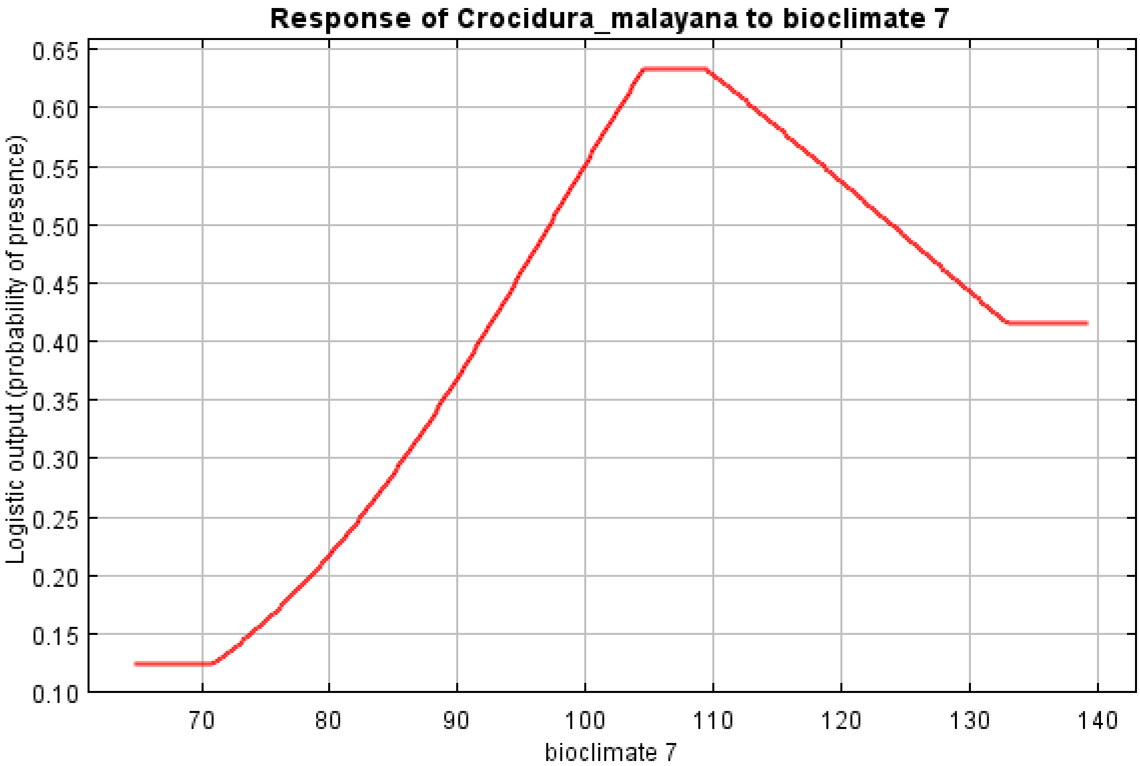


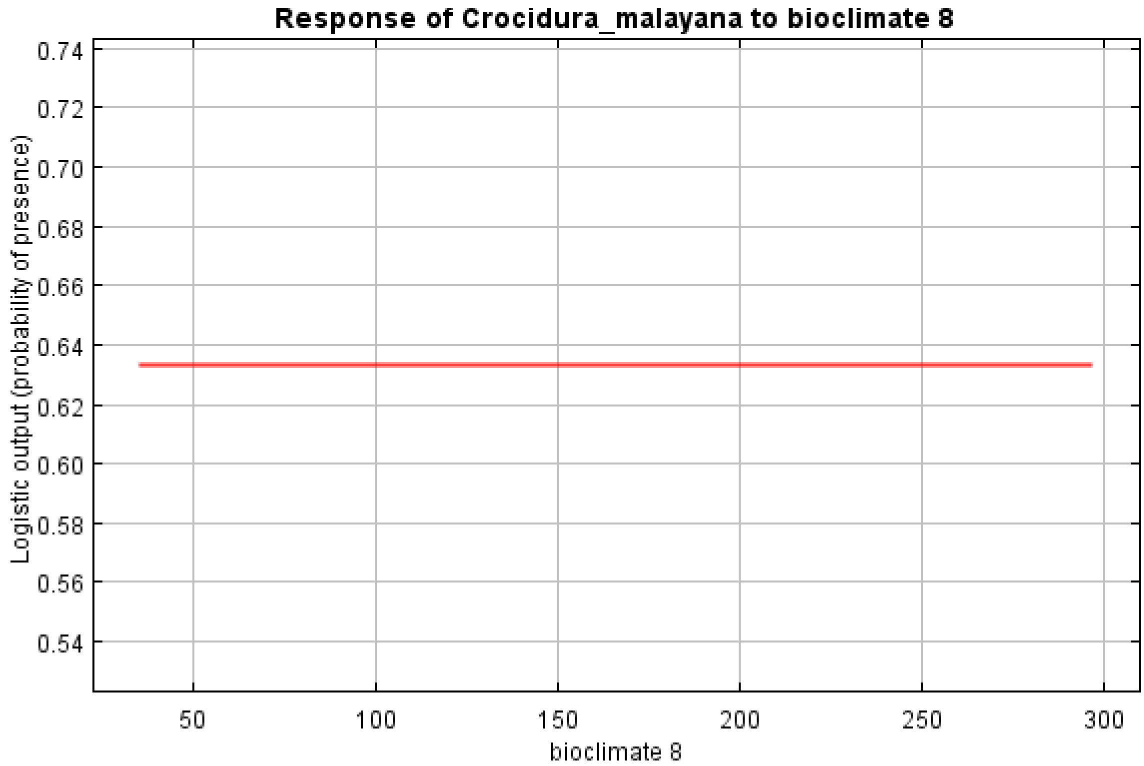
Response of Crocidura_malayana to bioclimate 3
Logistic output (probability of presence)
0.65
0.60
0.55
0.50
0.45
0.40
70
75
80
85
90
95
100
bioclimate 3

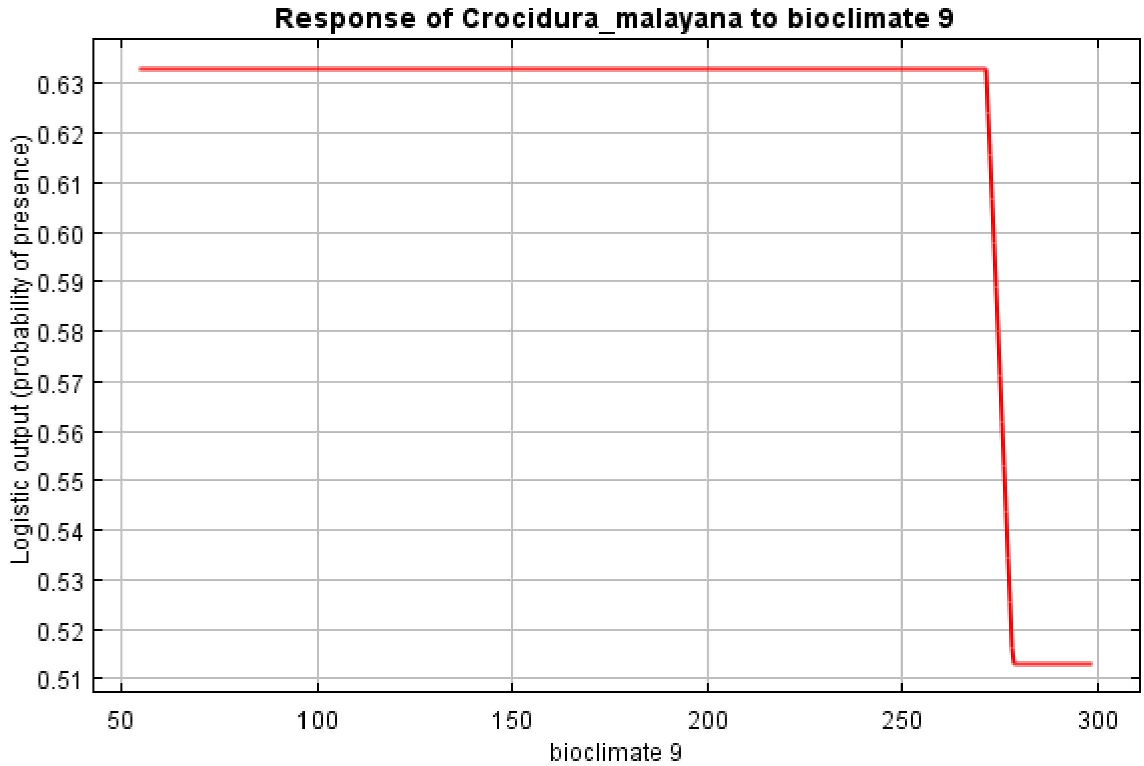

Response of Crocidura_malayana to bioclimate 4
Logistic output (probability of presence)
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
100
200
300
400
500
600
700
800
900
1000
1100
bioclimate 4

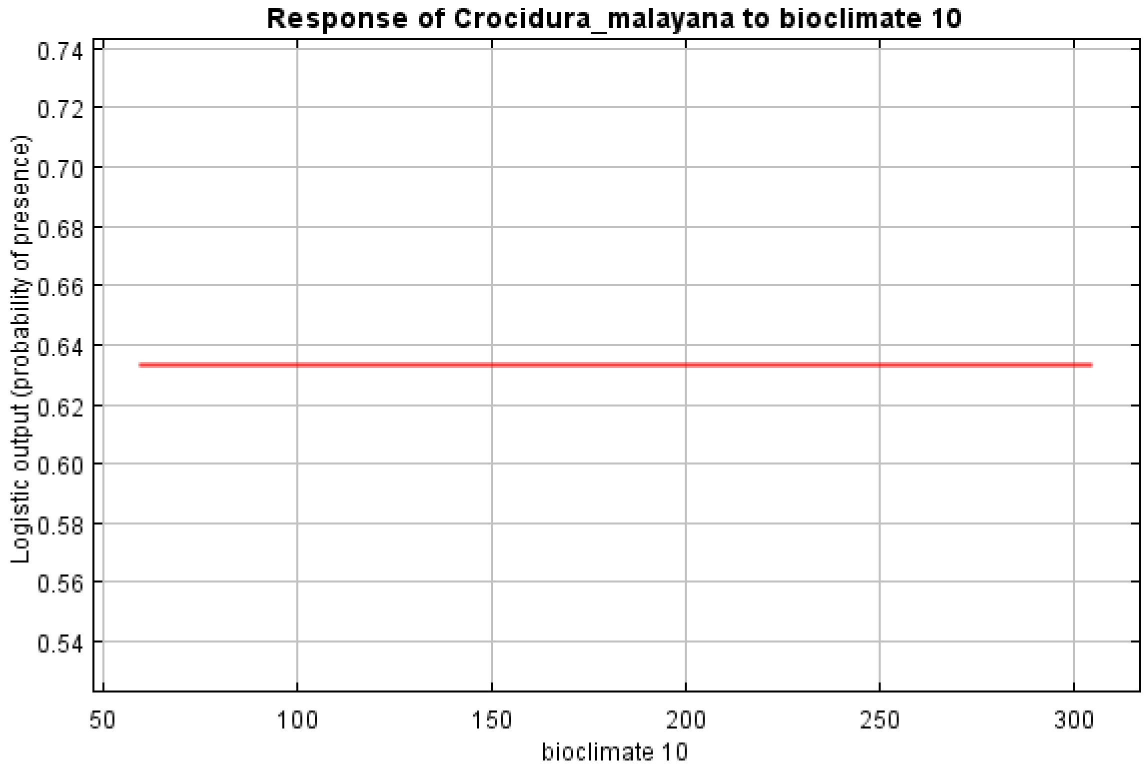

Response of Crocidura_malayana to bioclimate 5
Logistic output (probability of presence)
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0.60
0.58
0.56
0.54
100
150
200
250
300
350
bioclimate 5

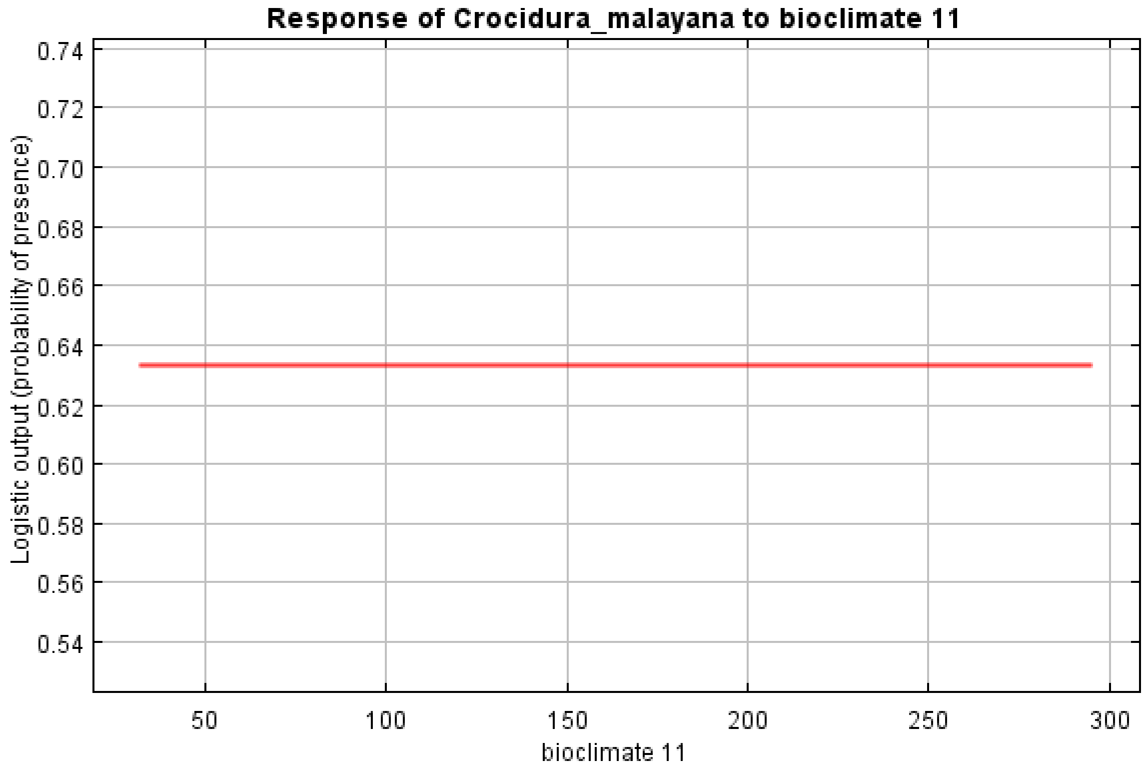

Response of Crocidura_malayana to bioclimate 6
Logistic output (probability of presence)
0.63
0.62
0.61
0.60
0.59
0.58
0.57
0.56
0.55
0.54
0.53
0
50
100
150
200
250
bioclimate 6

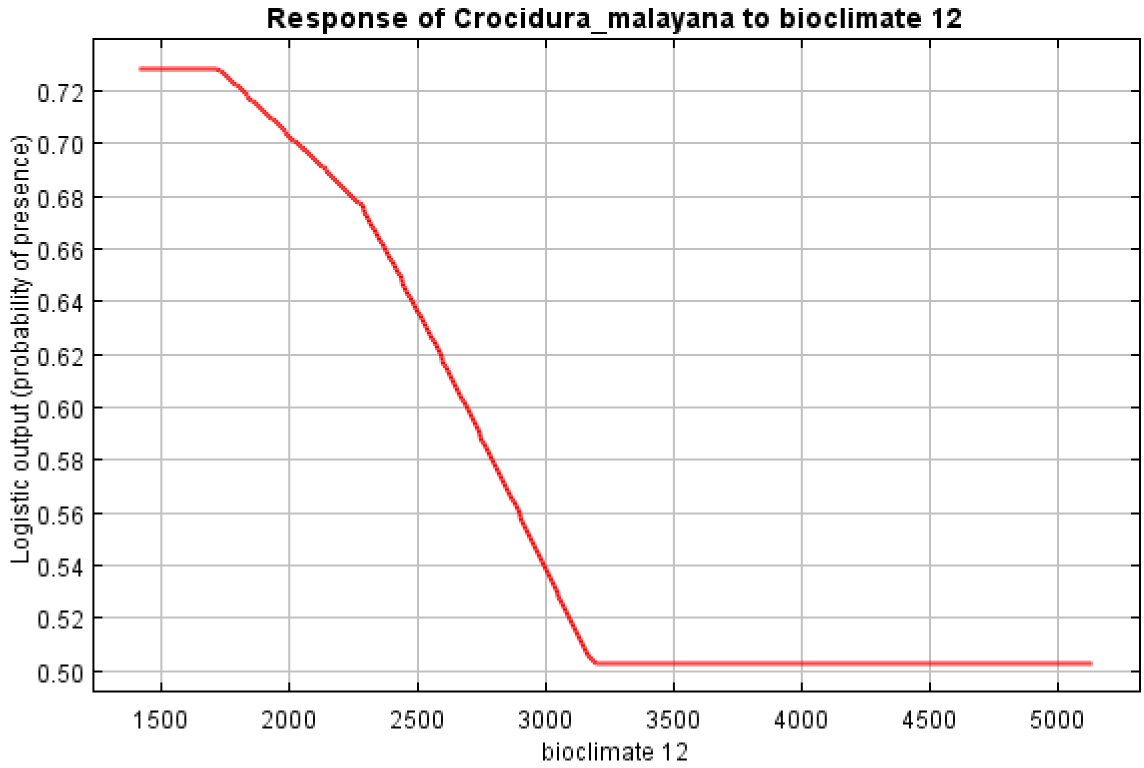

Response of Crocidura_malayana to bioclimate 7
Logistic output (probability of presence)
0.65
0.60
0.55
0.50
0.45
0.40
0.35
0.30
0.25
0.20
0.15
0.10
70
80
90
100
110
120
130
140
bioclimate 7

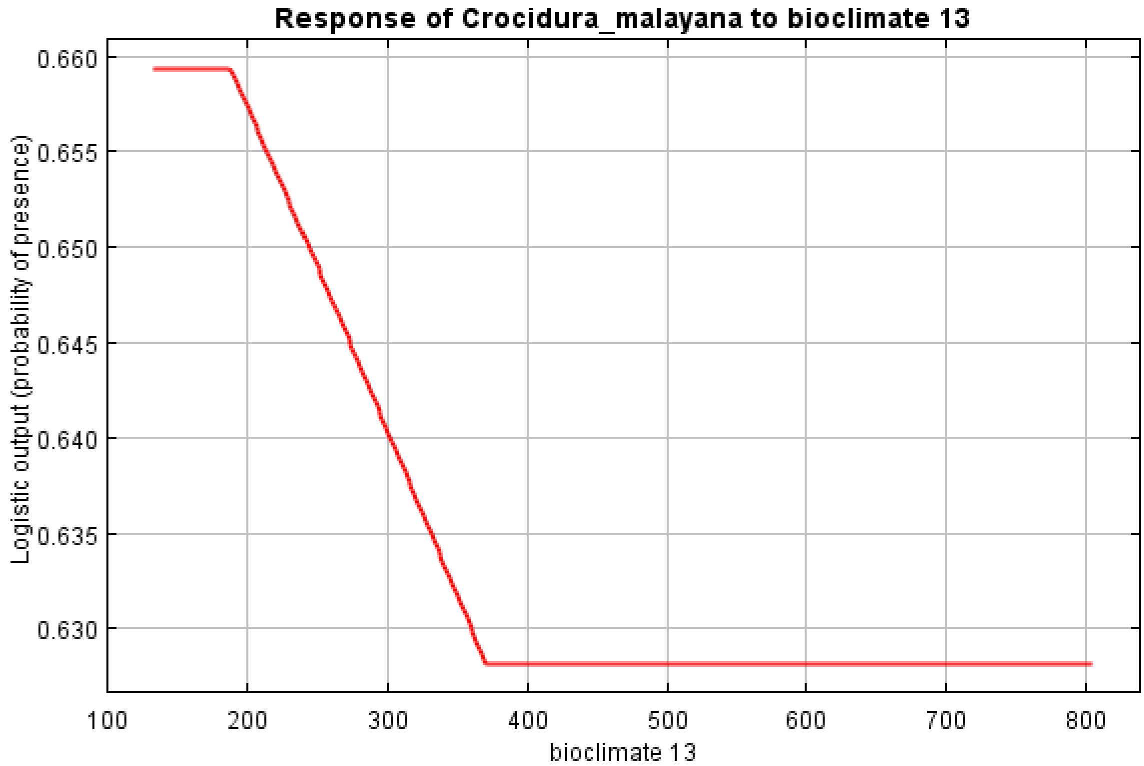

Response of Crocidura_malayana to bioclimate 8
Logistic output (probability of presence)
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0.60
0.58
0.56
0.54
50
100
150
200
250
300
bioclimate 8

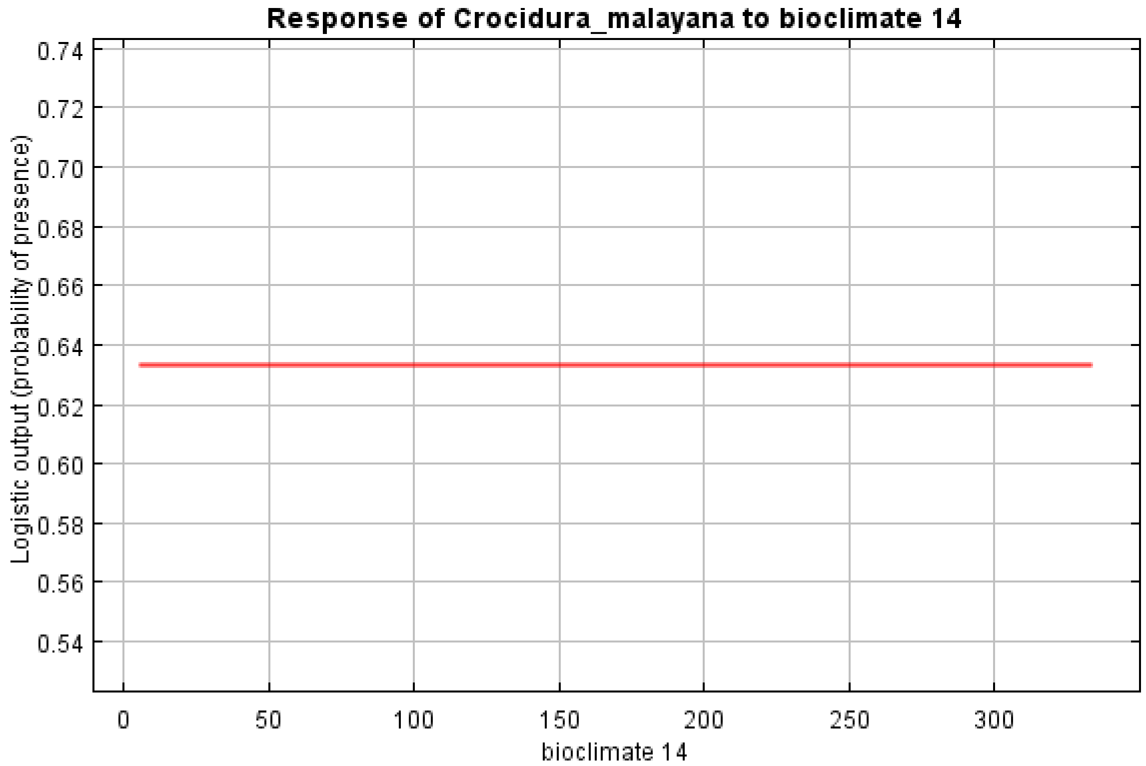

Response of Crocidura_malayana to bioclimate 9
Logistic output (probability of presence)
0.63
0.62
0.61
0.60
0.59
0.58
0.57
0.56
0.55
0.54
0.53
0.52
0.51
50
100
150
200
250
300
bioclimate 9

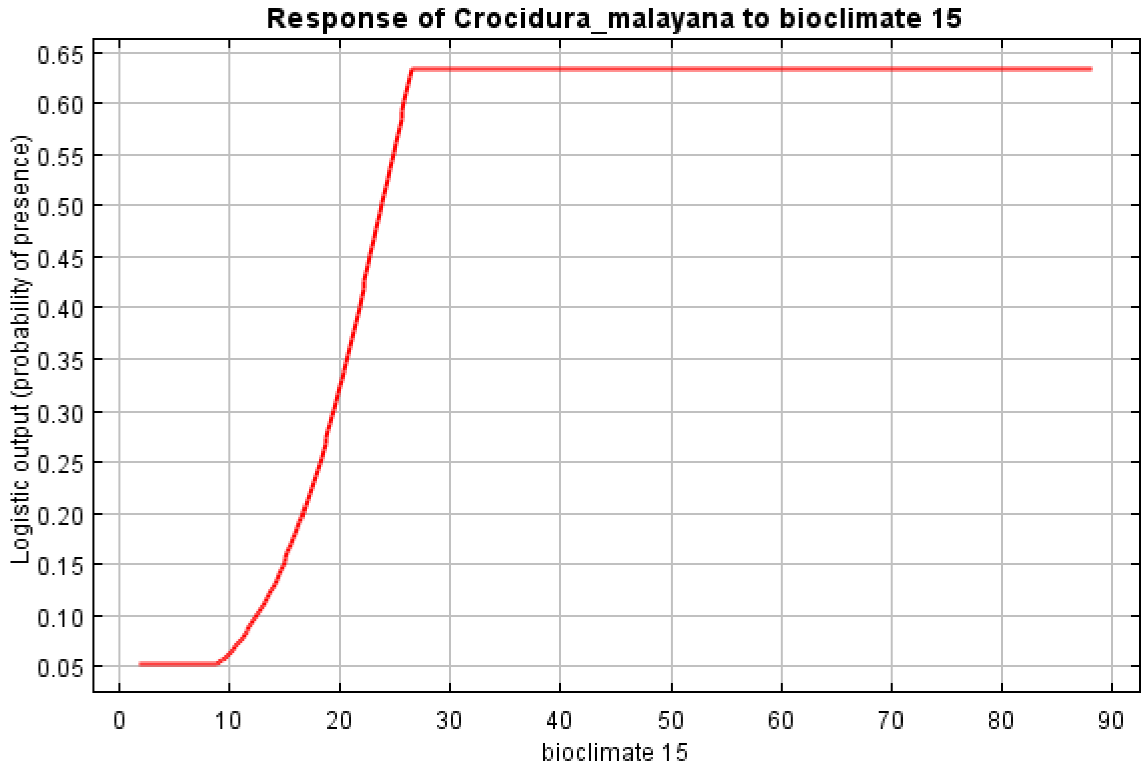

Response of Crocidura_malayana to bioclimate 10
Logistic output (probability of presence)
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0.60
0.58
0.56
0.54
50
100
150
200
250
300
bioclimate 10

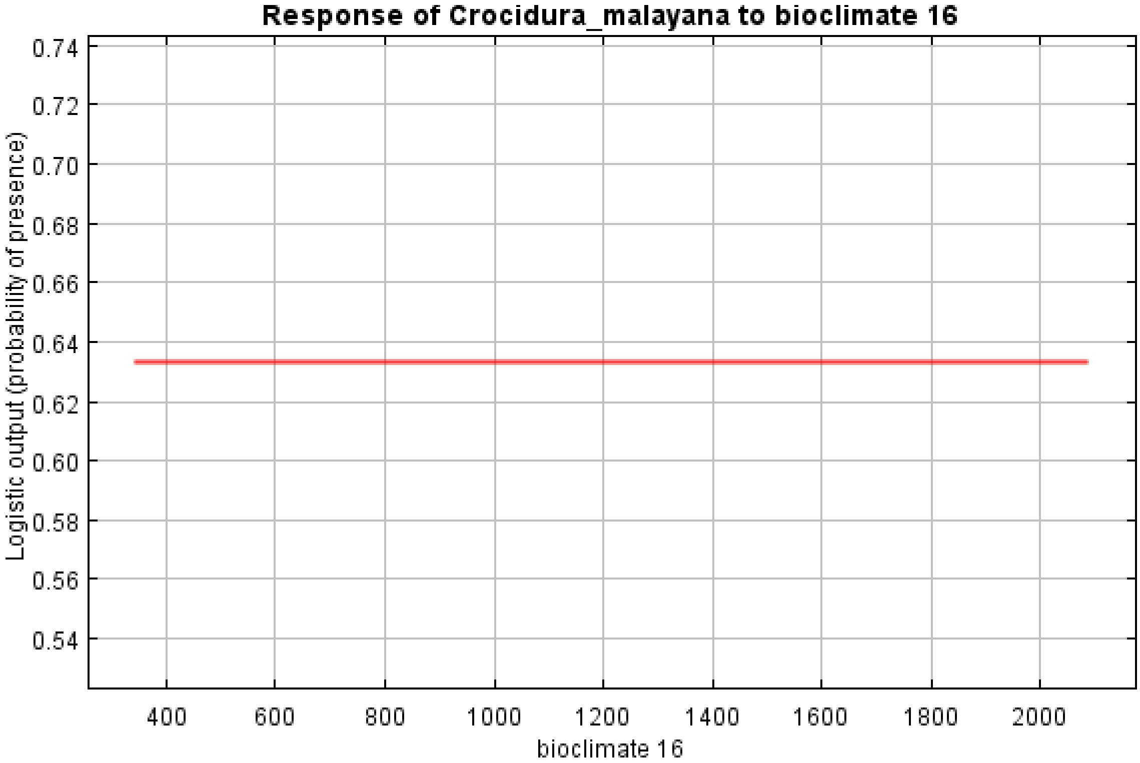

Response of Crocidura_malayana to bioclimate 11
Logistic output (probability of presence)
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0.60
0.58
0.56
0.54
50
100
150
200
250
300
bioclimate 11


Response of Crocidura_malayana to bioclimate 12
Logistic output (probability of presence)
0.72
0.70
0.68
0.66
0.64
0.62
0.60
0.58
0.56
0.54
0.52
0.50
1500
2000
2500
3000
3500
4000
4500
5000
bioclimate 12

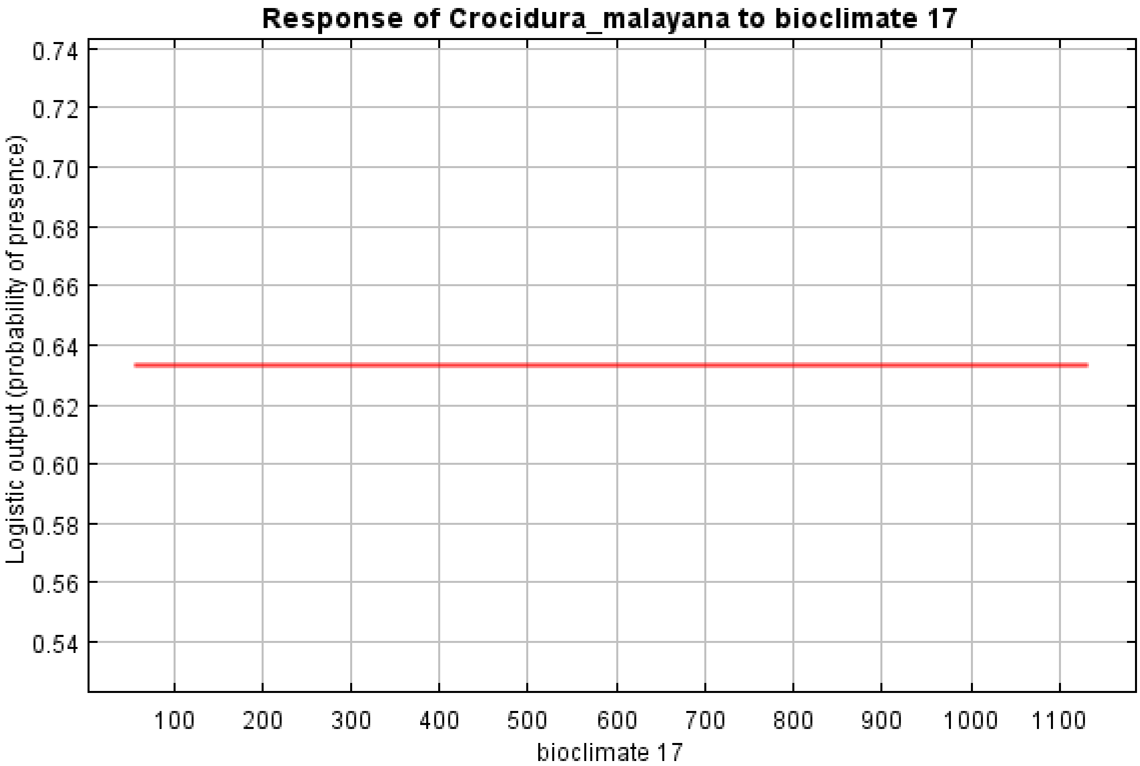

Response of Crocidura_malayana to bioclimate 13
Logistic output (probability of presence)
0.660
0.655
0.650
0.645
0.640
0.635
0.630
100
200
300
400
500
600
700
800
bioclimate 13


Response of Crocidura_malayana to bioclimate 14
Logistic output (probability of presence)
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0.60
0.58
0.56
0.54
0
50
100
150
200
250
300
bioclimate 14

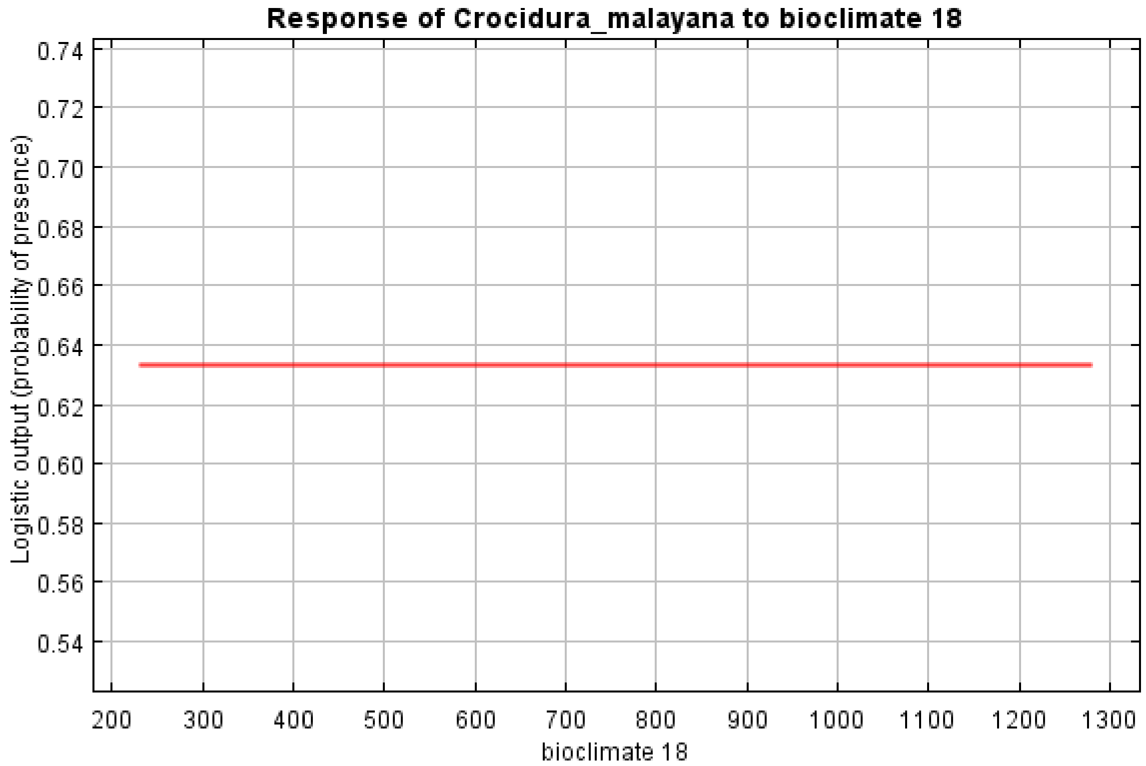

Response of Crocidura_malayana to bioclimate 15
Logistic output (probability of presence)
0.65
0.60
0.55
0.50
0.45
0.40
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0
10
20
30
40
50
60
70
80
90
bioclimate 15

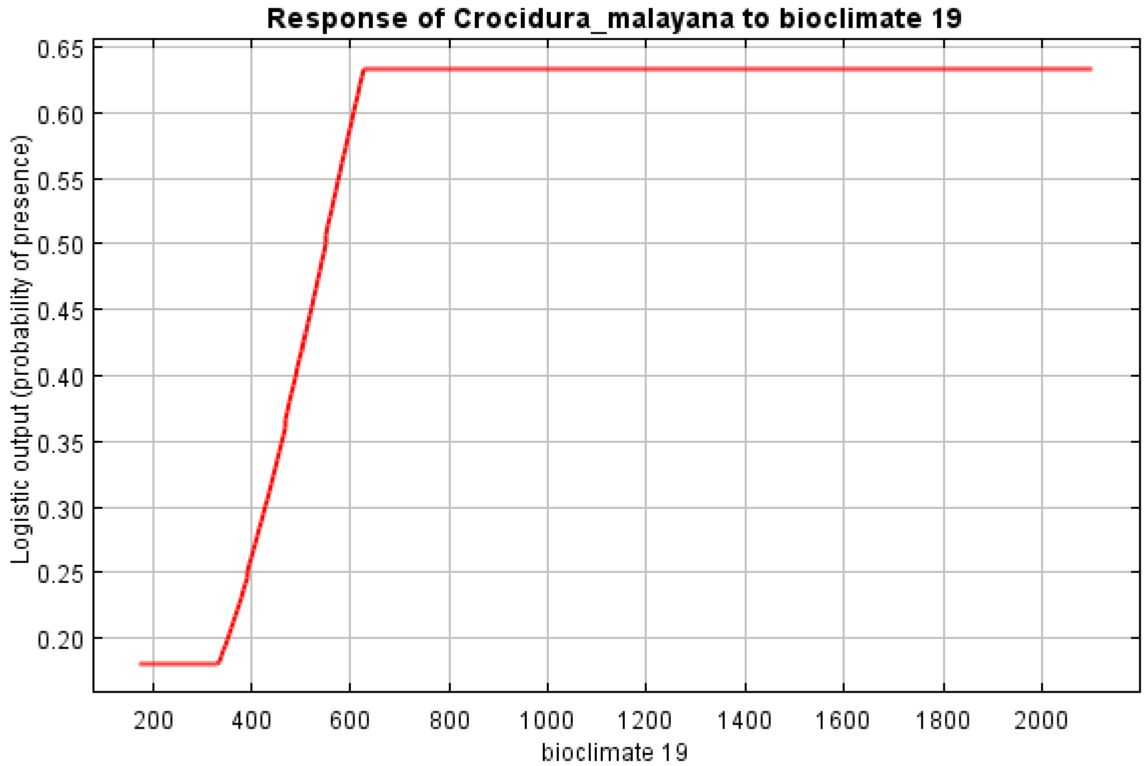


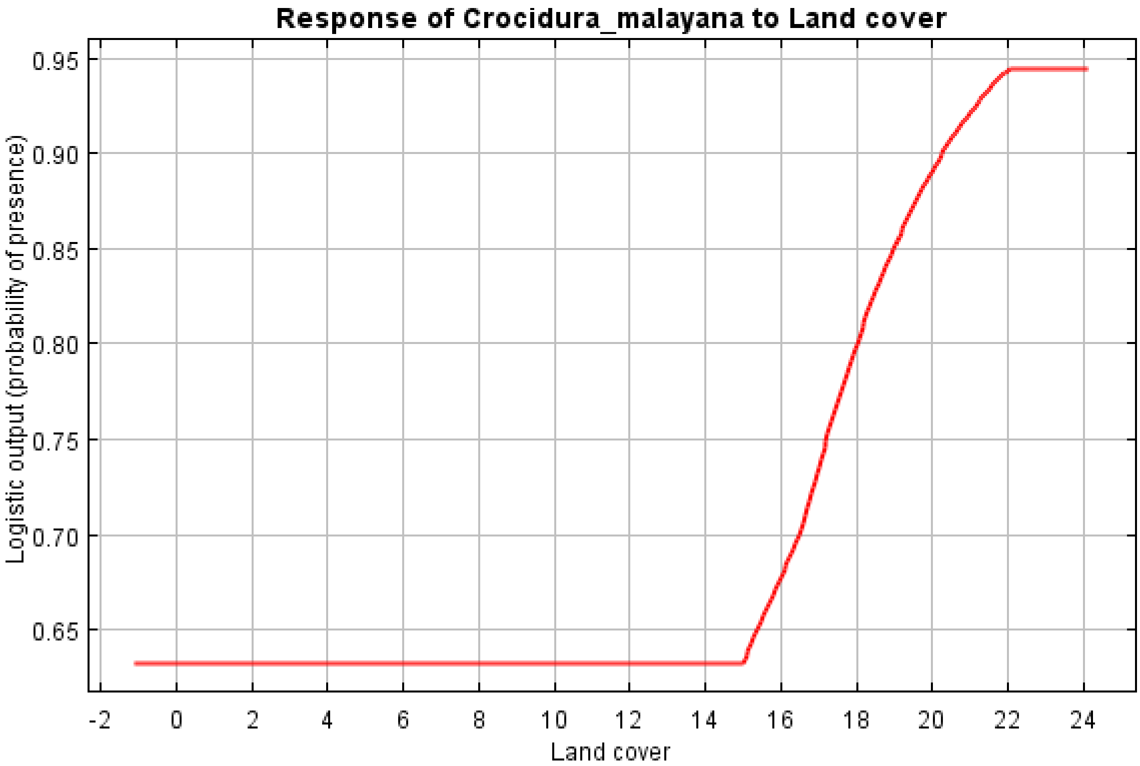
Response of Crocidura_malayana to bioclimate 16
Logistic output (probability of presence)
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0.60
0.58
0.56
0.54
400
600
800
1000
1200
1400
1600
1800
2000
bioclimate 16



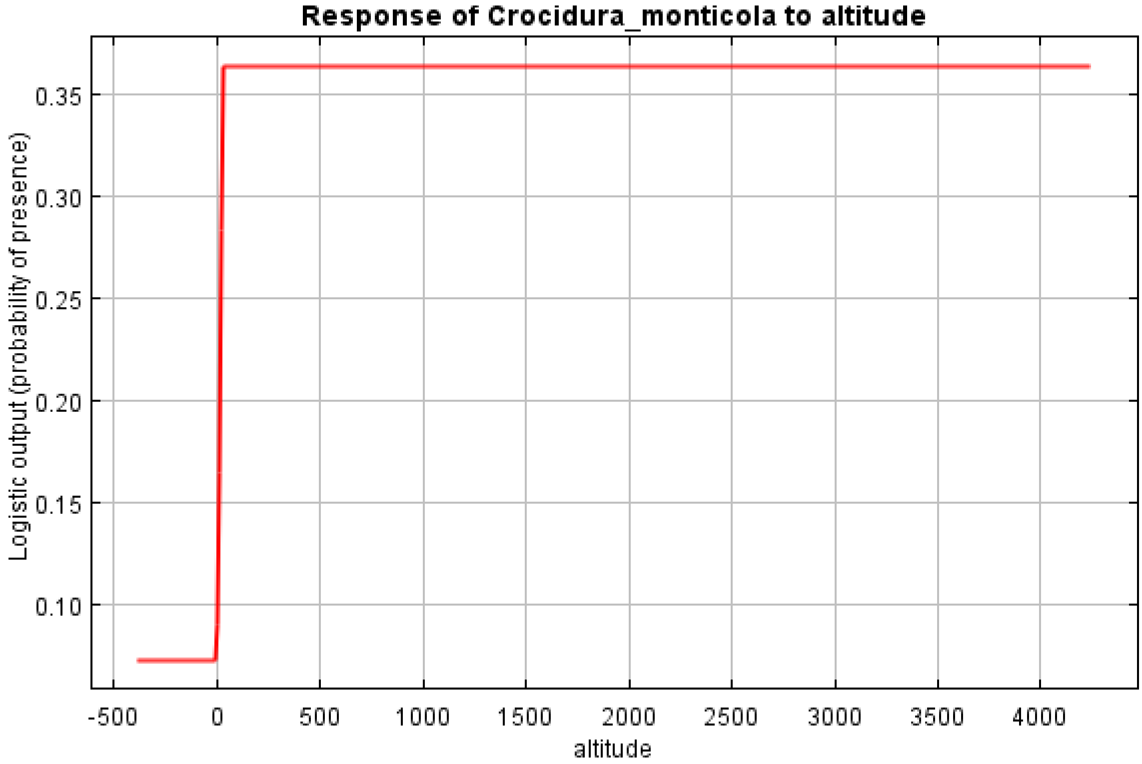
Response of Crocidura_malayana to bioclimate 17
Logistic output (probability of presence)
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0.60
0.58
0.56
0.54
100
200
300
400
500
600
700
800
900
1000
1100
bioclimate 17

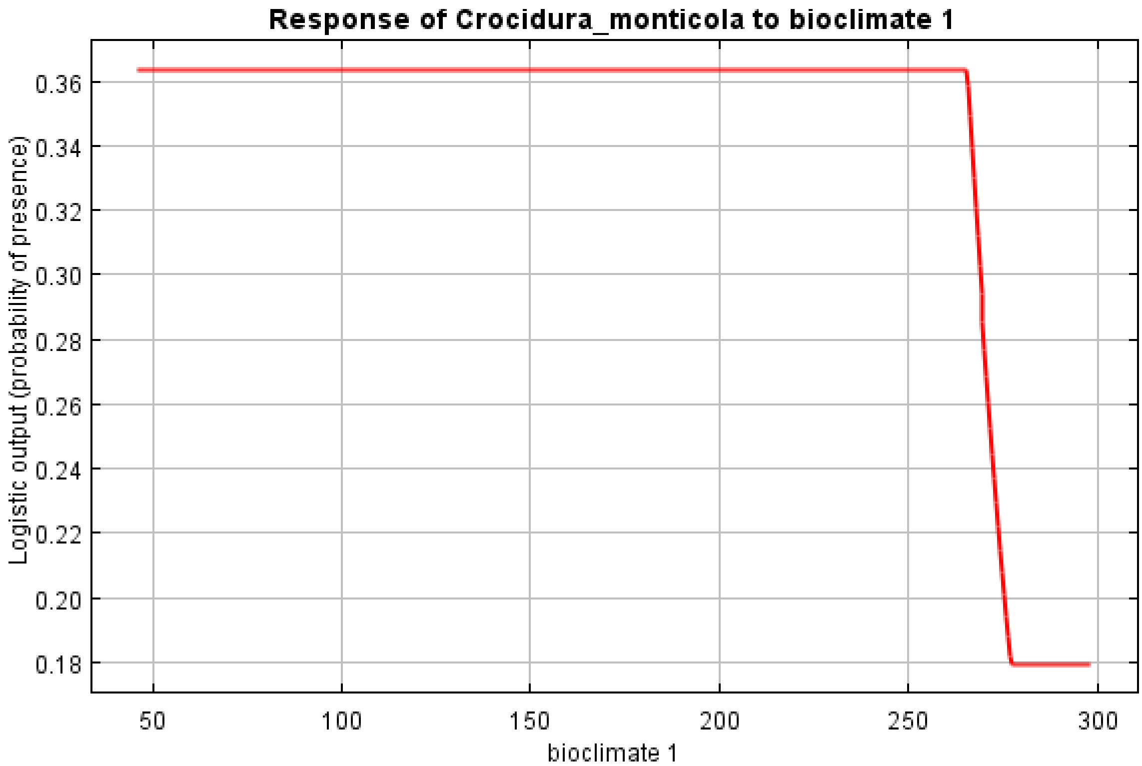

Response of Crocidura_malayana to bioclimate 18
Logistic output (probability of presence)
0.74
0.72
0.70
0.68
0.66
0.64
0.62
0.60
0.58
0.56
0.54
200
300
400
500
600
700
800
900
1000
1100
1200
1300
bioclimate 18

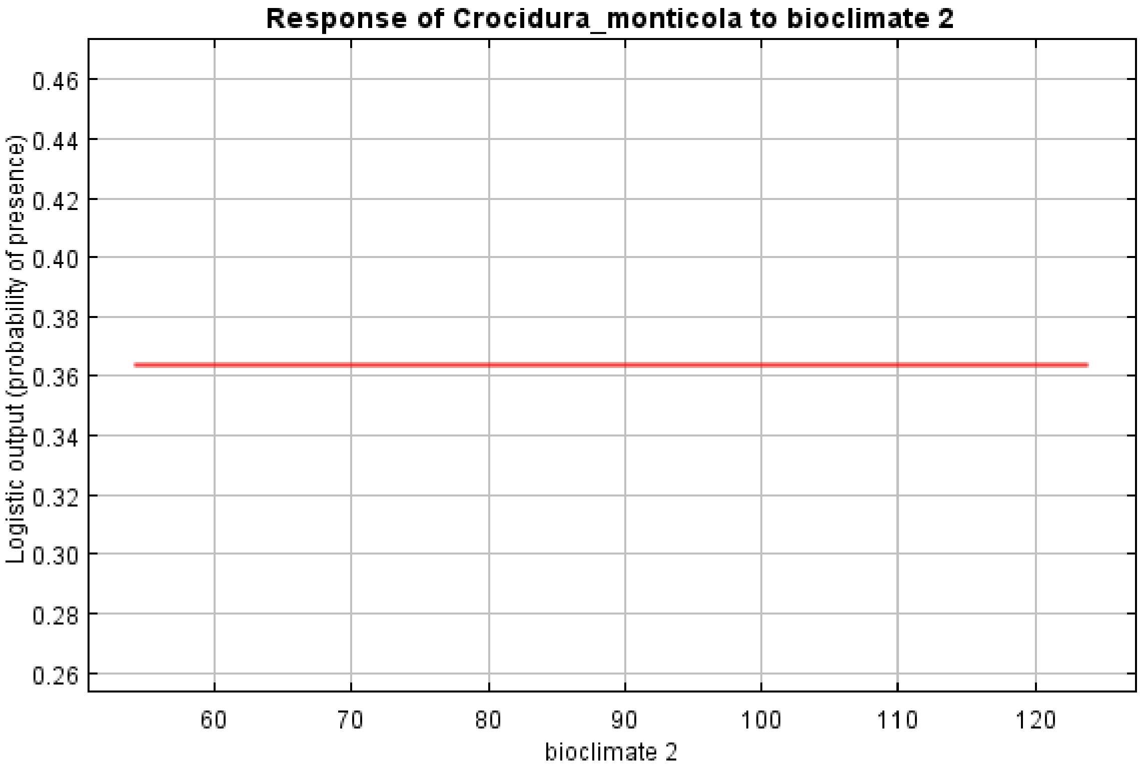

Response of Crocidura_malayana to bioclimate 19
Logistic output (probability of presence)
0.65
0.60
0.55
0.50
0.45
0.40
0.35
0.30
0.25
0.20
200
400
600
800
1000
1200
1400
1600
1800
2000
bioclimate 19


Response of Crocidura_malayana to Land cover
Logistic output (probability of presence)
0.95
0.90
0.85
0.80
0.75
0.70
0.65
-2
0
2
4
6
8
10
12
14
16
18
20
22
24
Land cover

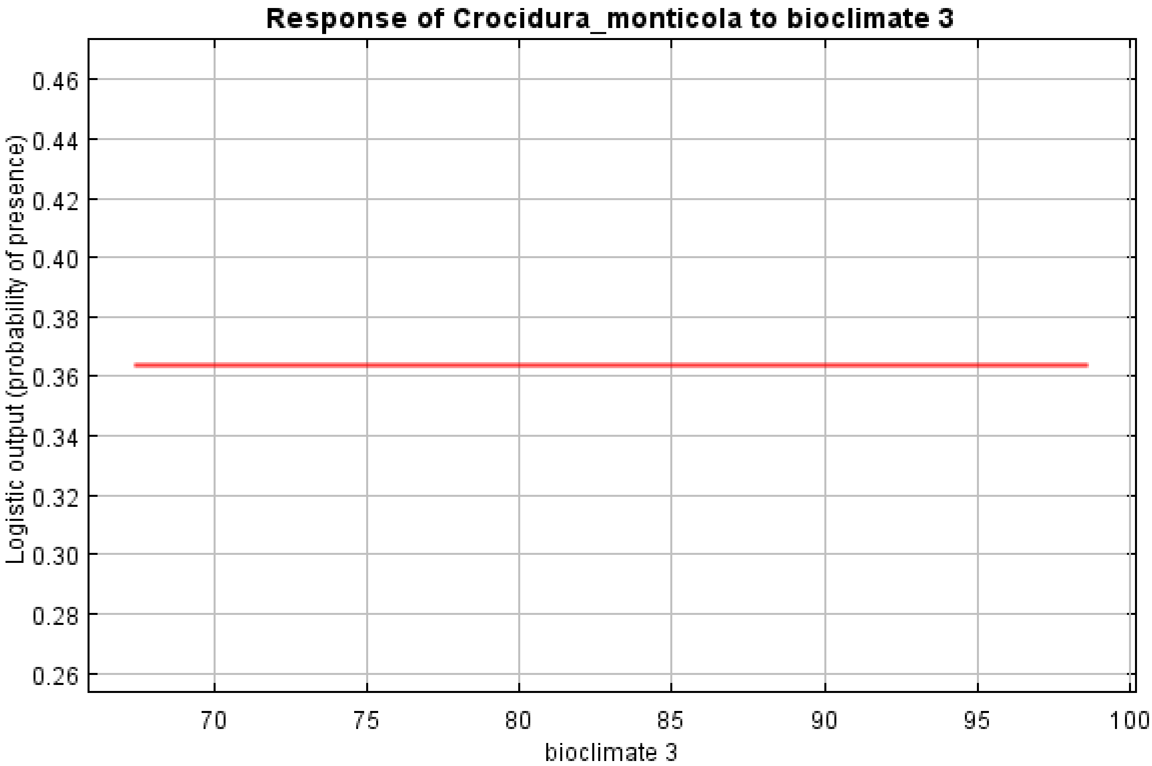
Appendix 7.0: The response curves for *Crocidura monticola* in MaxEnt analysis.



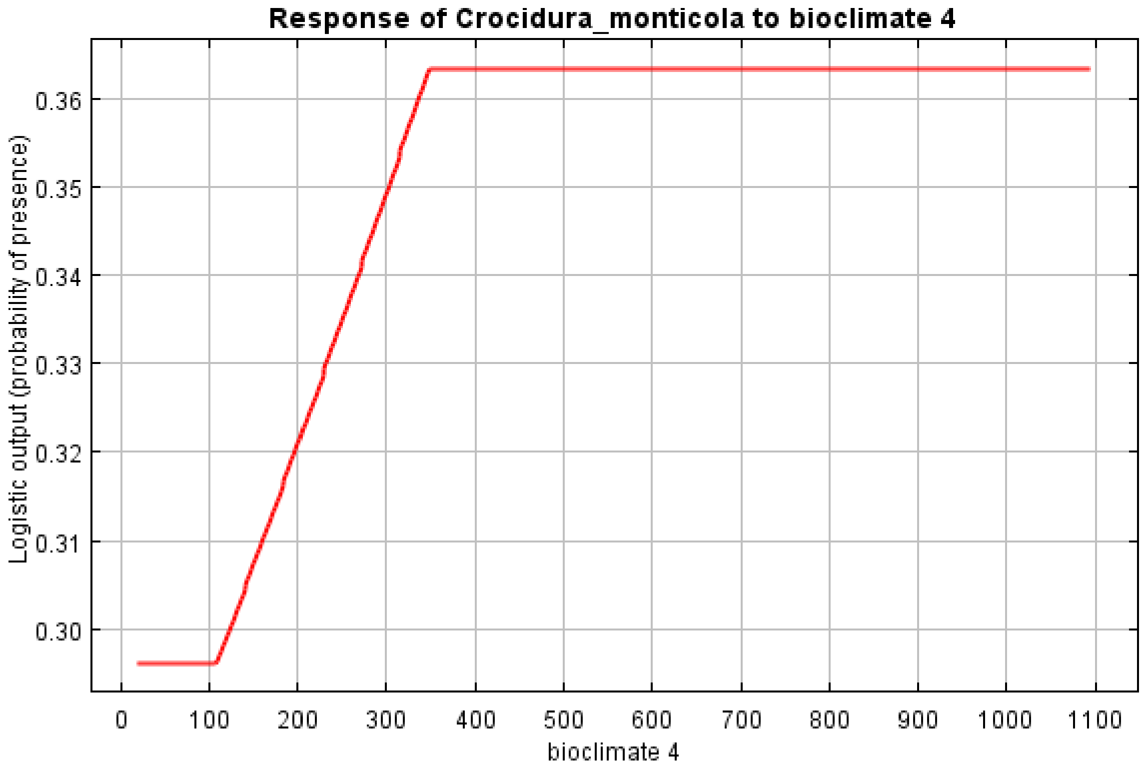


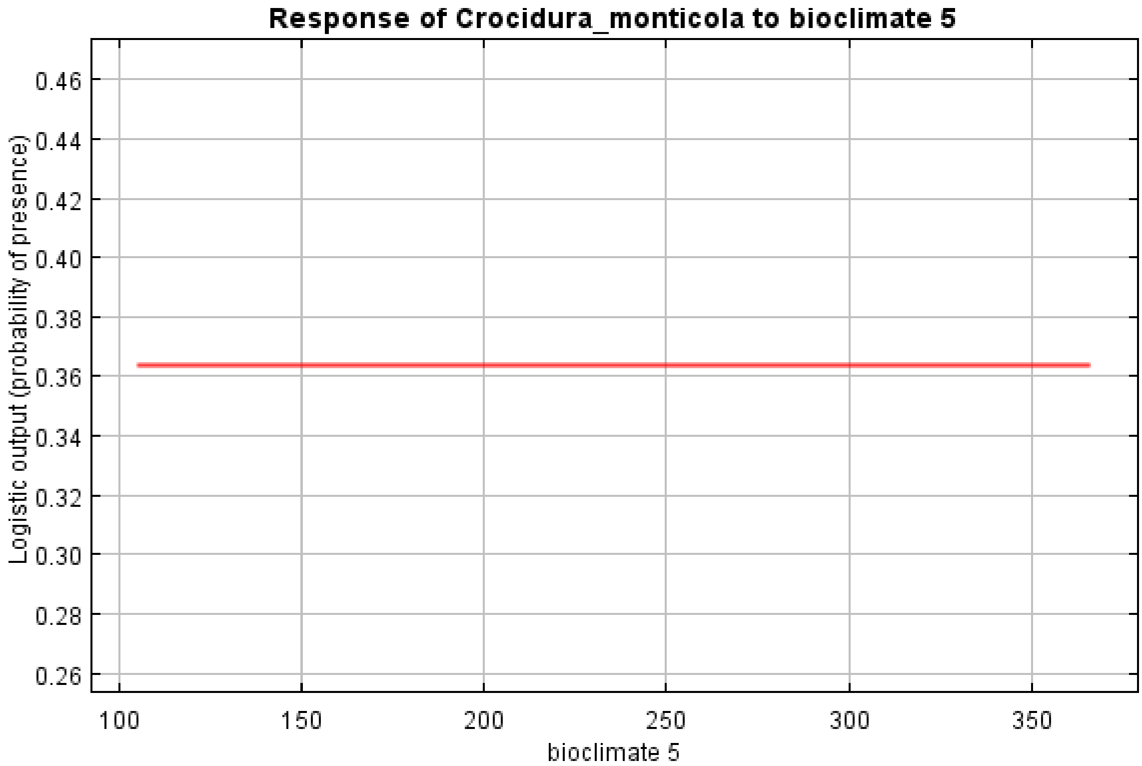


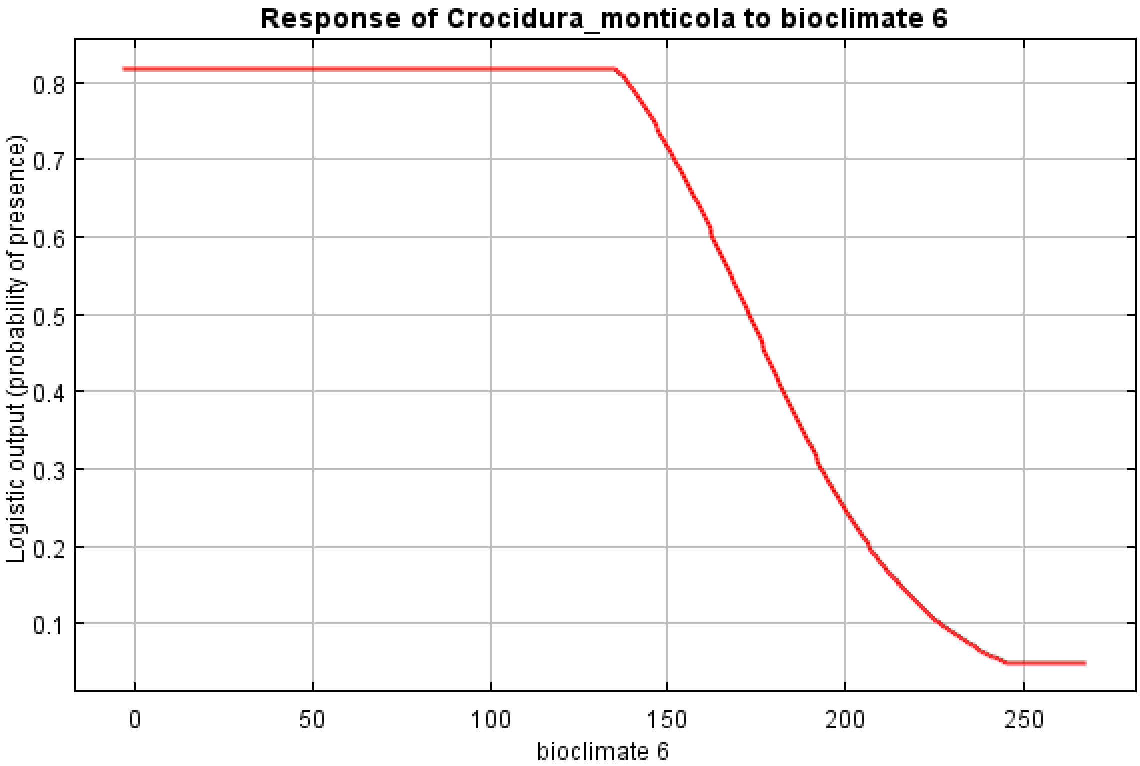
Response of Crocidura_monticola to bioclimate 2
Logistic output (probability of presence)
0.46
0.44
0.42
0.40
0.38
0.36
0.34
0.32
0.30
0.28
0.26
60
70
80
90
100
110
120
bioclimate 2

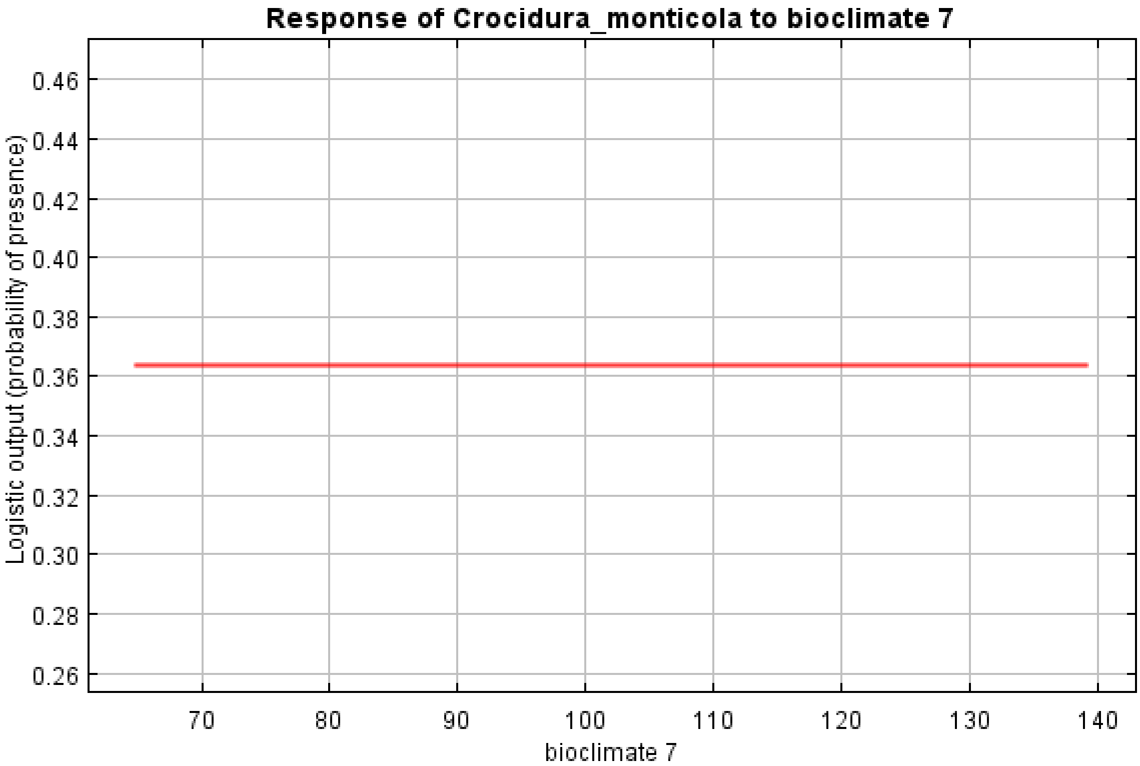


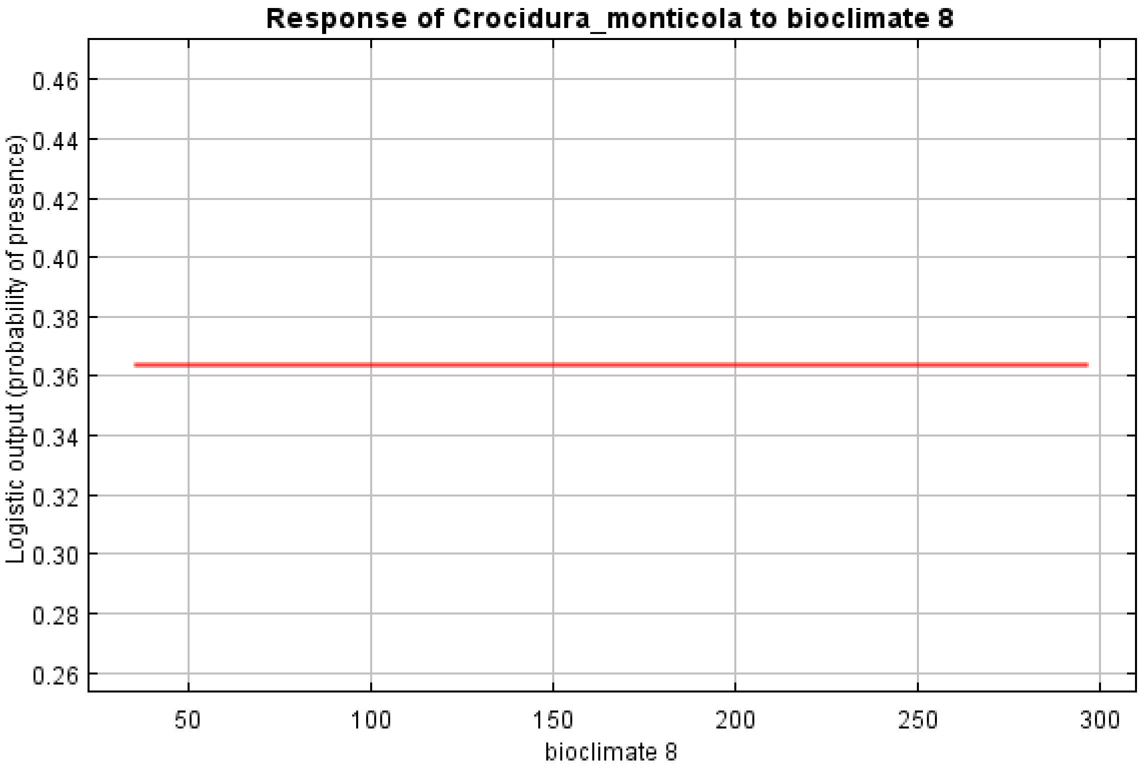
Response of Crocidura_monticola to bioclimate 3
Logistic output (probability of presence)
0.46
0.44
0.42
0.40
0.38
0.36
0.34
0.32
0.30
0.28
0.26
70
75
80
85
90
95
100
bioclimate 3

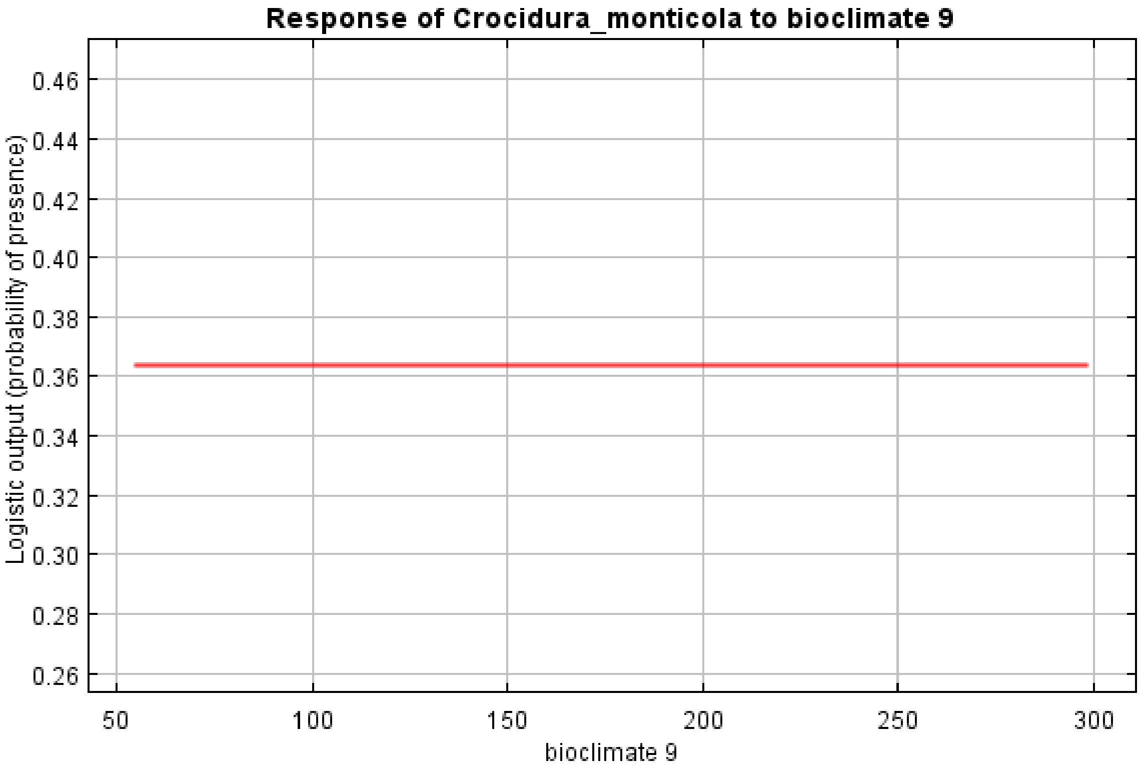

Response of Crocidura_monticola to bioclimate 4
Logistic output (probability of presence)
0.30
0.31
0.32
0.33
0.34
0.35
0.36
0
100
200
300
400
500
600
700
800
900
1000
1100
bioclimate 4

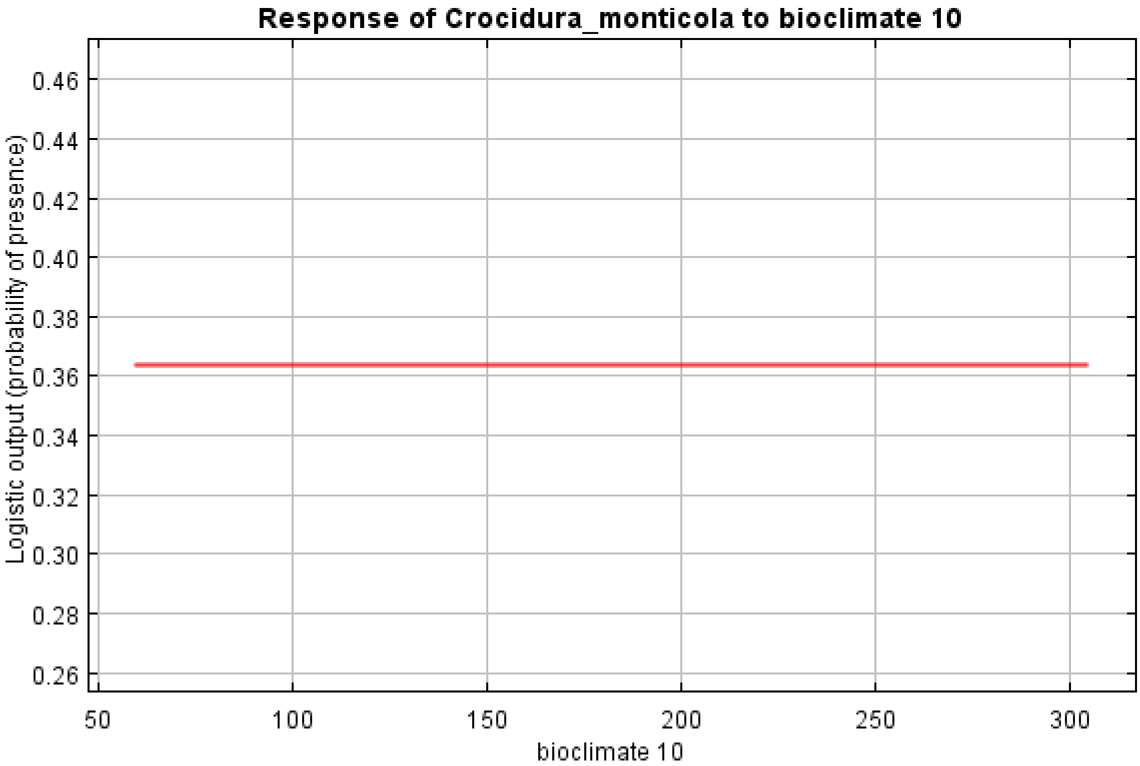

Response of Crocidura_monticola to bioclimate 5
Logistic output (probability of presence)
0.26
0.28
0.30
0.32
0.34
0.36
0.38
0.40
0.42
0.44
0.46
100
150
200
250
300
350
bioclimate 5

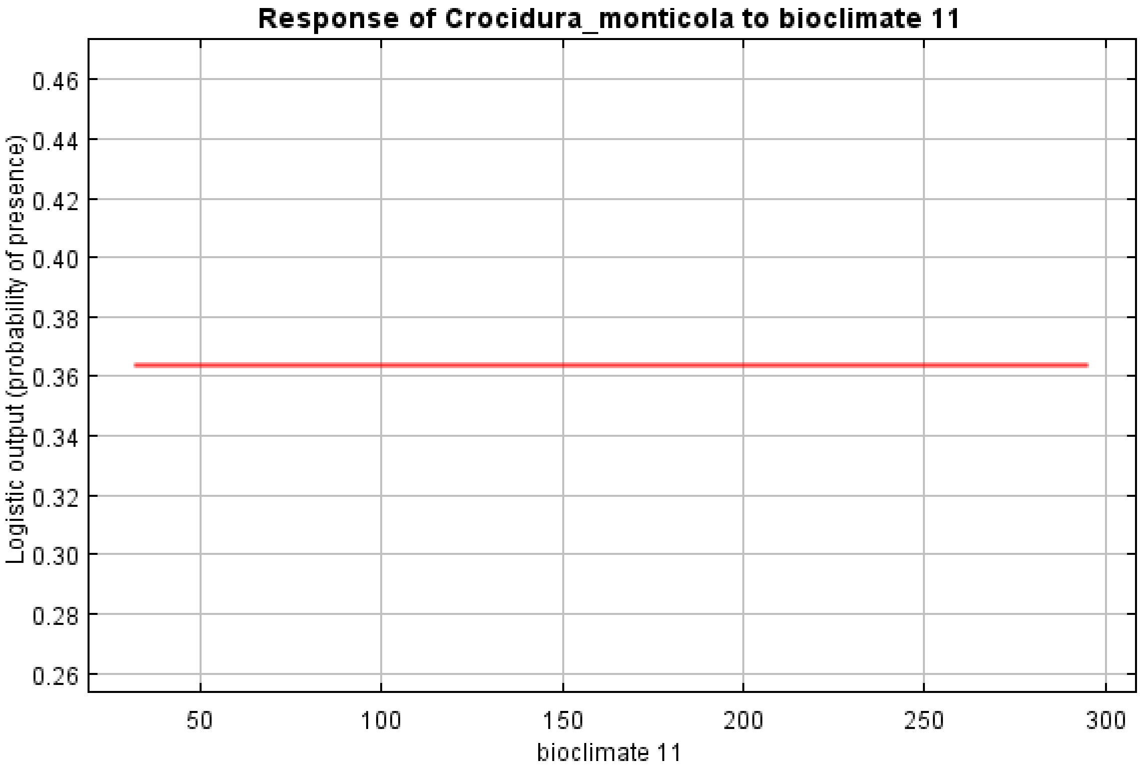

Response of Crocidura_monticola to bioclimate 6
Logistic output (probability of presence)
0.8
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0
50
100
150
200
250
bioclimate 6

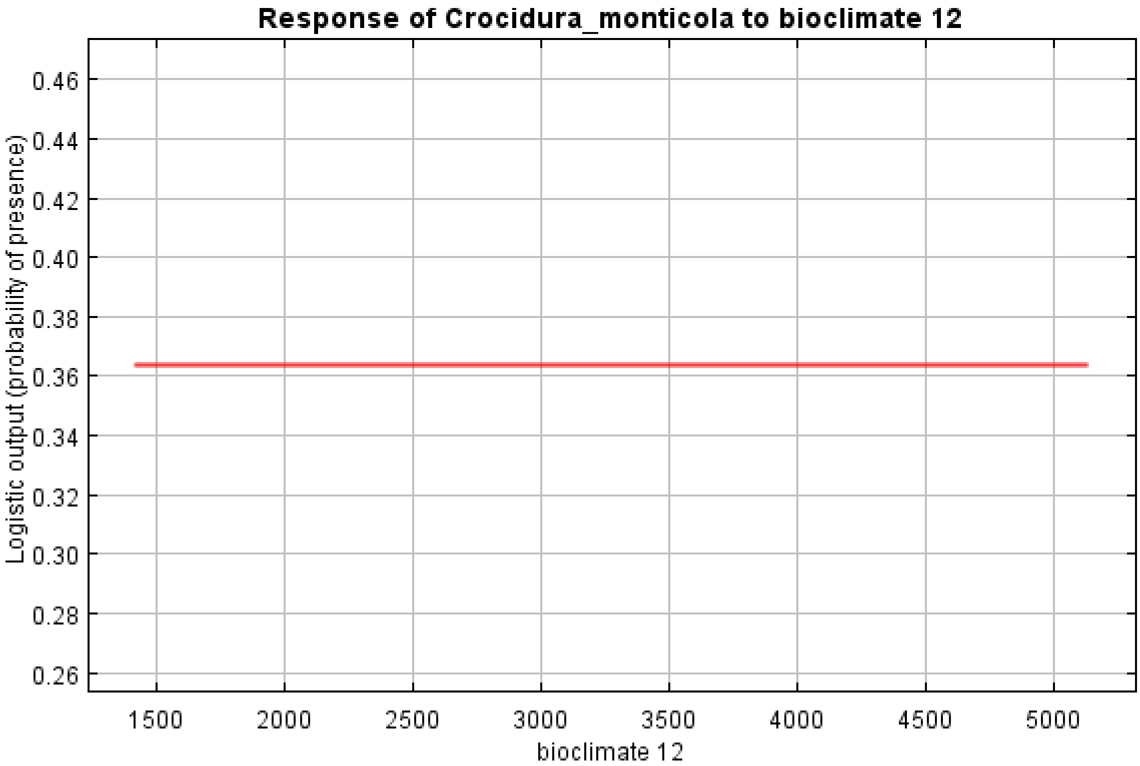

Response of Crocidura_monticola to bioclimate 7
Logistic output (probability of presence)
0.46
0.44
0.42
0.40
0.38
0.36
0.34
0.32
0.30
0.28
0.26
70
80
90
100
110
120
130
140
bioclimate 7

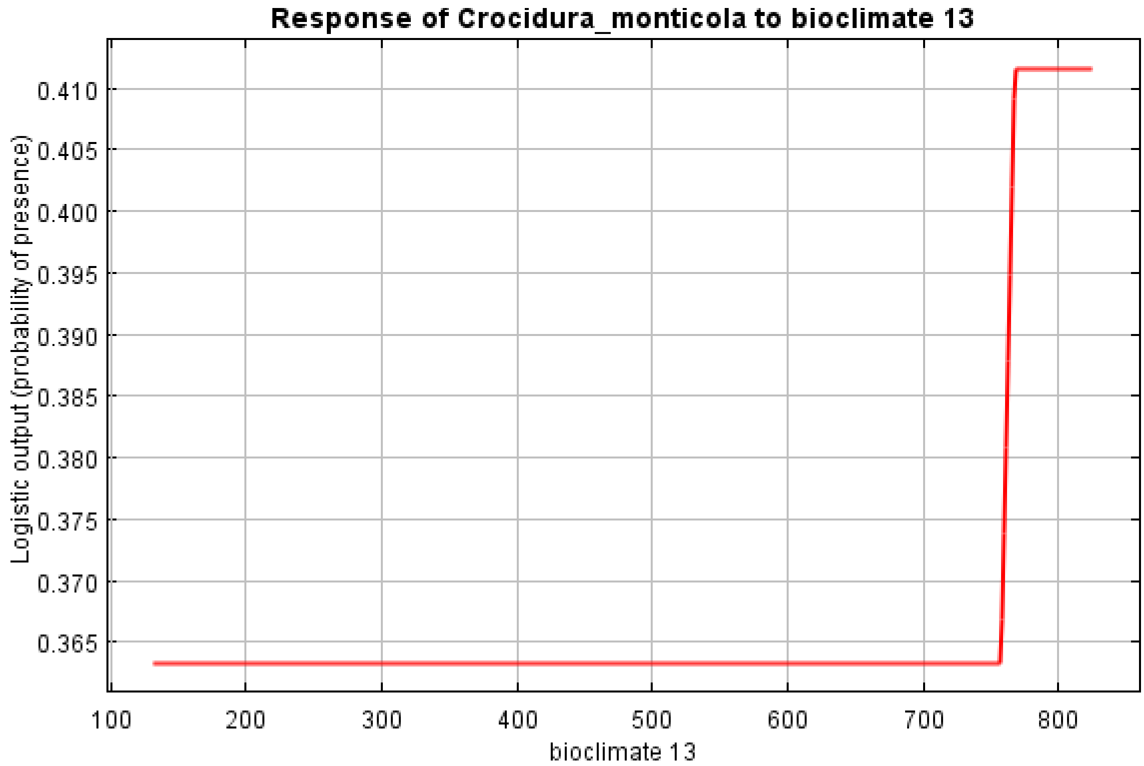

Response of Crocidura_monticola to bioclimate 8
Logistic output (probability of presence)
0.46
0.44
0.42
0.40
0.38
0.36
0.34
0.32
0.30
0.28
0.26
50
100
150
200
250
300
bioclimate 8


Response of Crocidura_monticola to bioclimate 9
Logistic output (probability of presence)
0.46
0.44
0.42
0.40
0.38
0.36
0.34
0.32
0.30
0.28
0.26
50
100
150
200
250
300
bioclimate 9

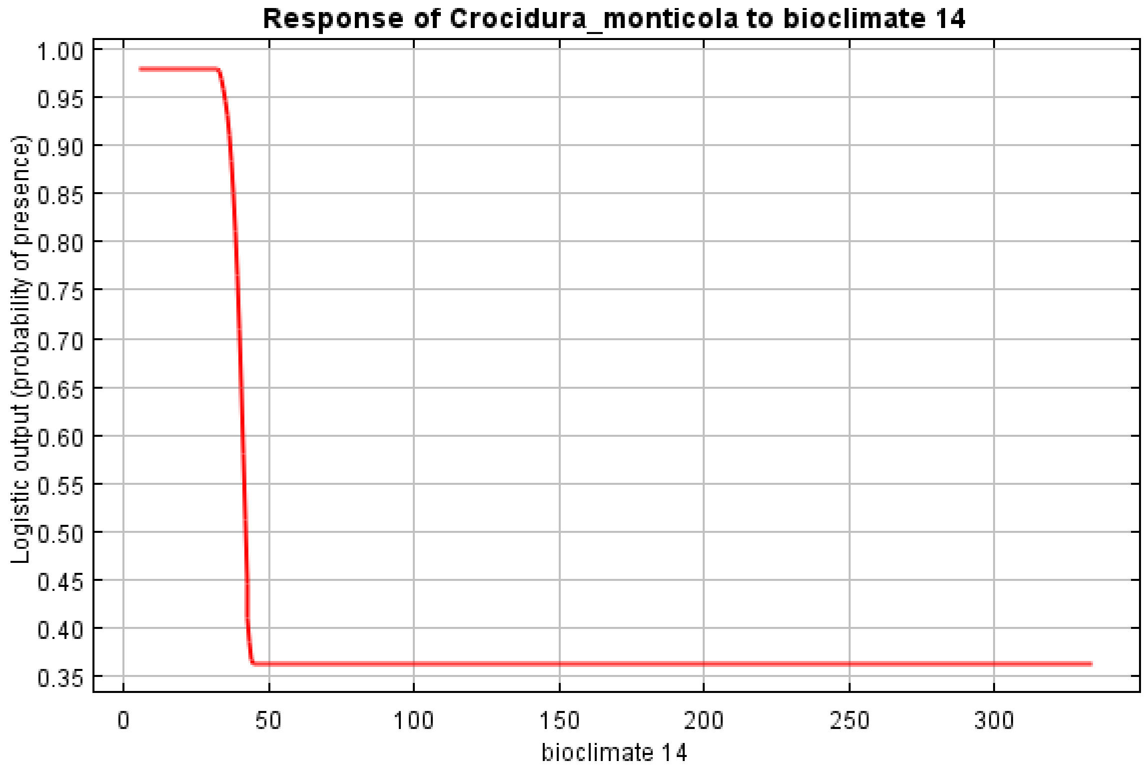

Response of Crocidura_monticola to bioclimate 10
Logistic output (probability of presence)
0.46
0.44
0.42
0.40
0.38
0.36
0.34
0.32
0.30
0.28
0.26
50
100
150
200
250
300
bioclimate 10


Response of Crocidura_monticola to bioclimate 11
Logistic output (probability of presence)
0.46
0.44
0.42
0.40
0.38
0.36
0.34
0.32
0.30
0.28
0.26
50
100
150
200
250
300
bioclimate 11

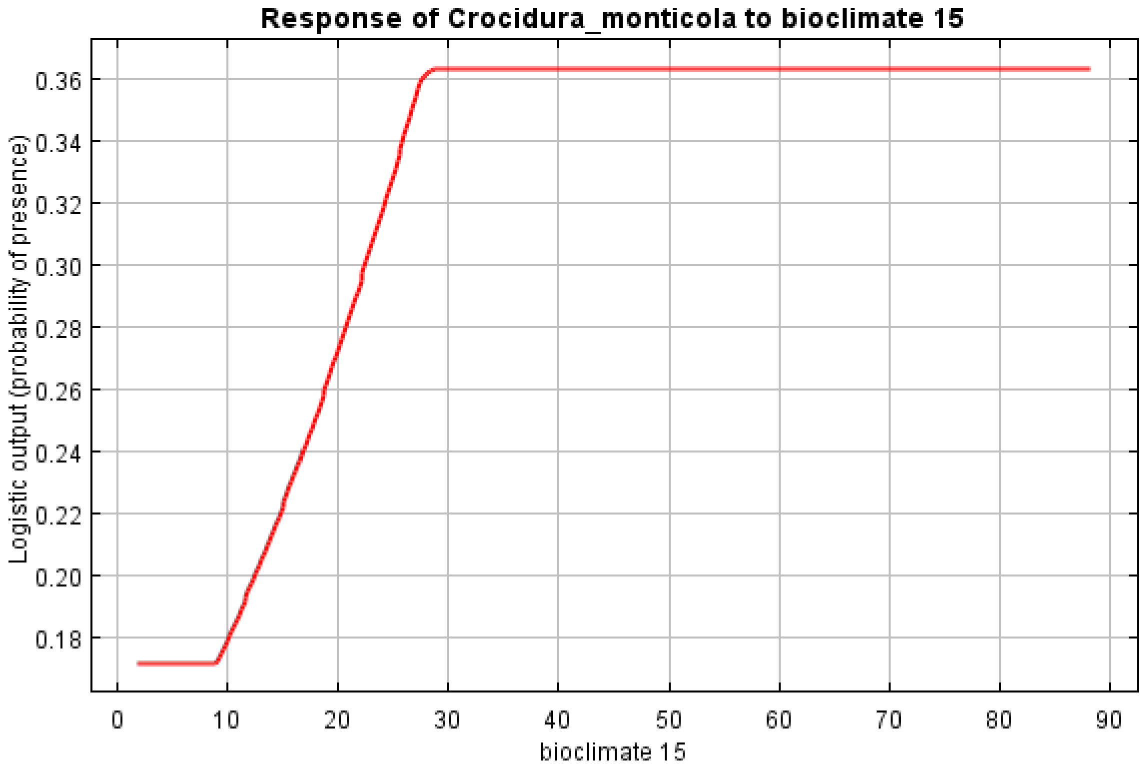

Response of Crocidura_monticola to bioclimate 12
Logistic output (probability of presence)
0.46
0.44
0.42
0.40
0.38
0.36
0.34
0.32
0.30
0.28
0.26
1500
2000
2500
3000
3500
4000
4500
5000
bioclimate 12

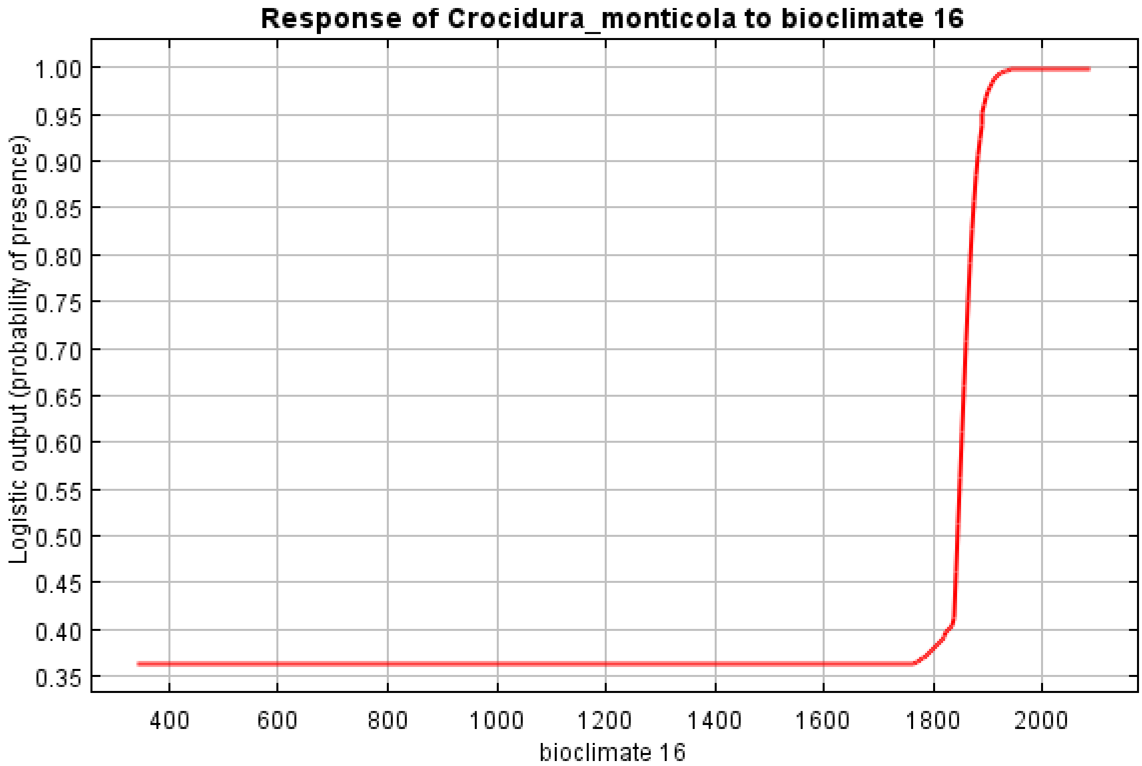


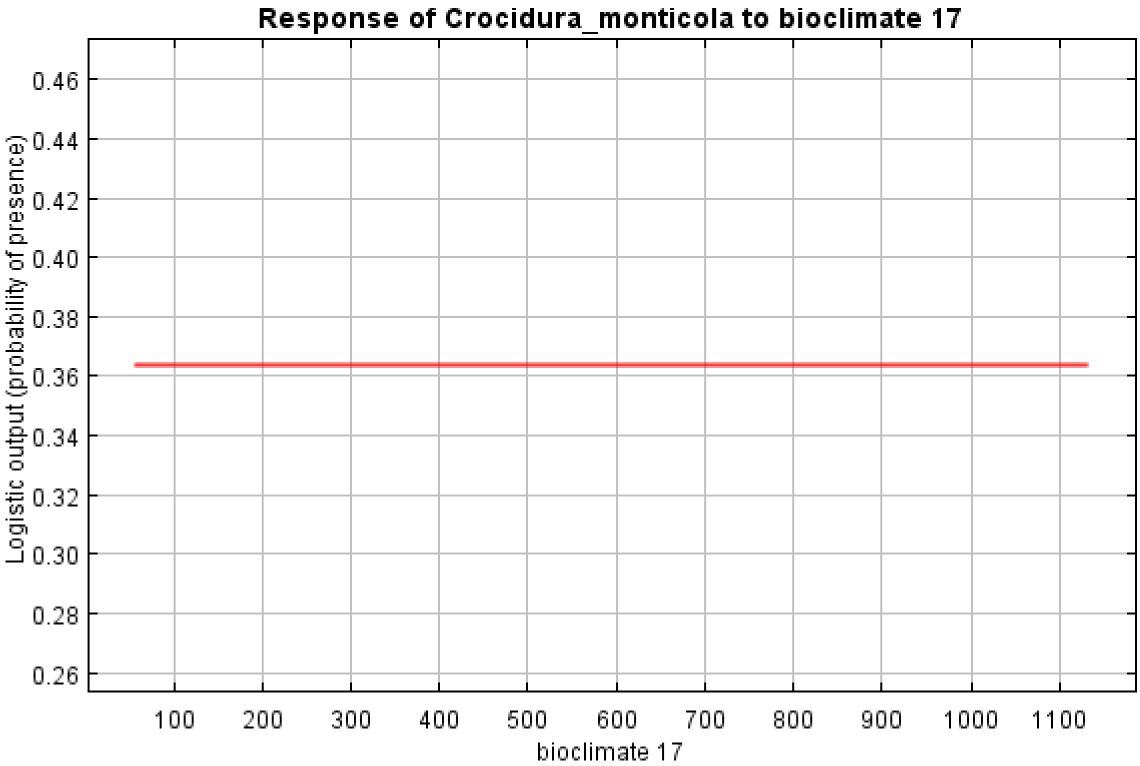
Response of Crocidura_monticola to bioclimate 13
Logistic output (probability of presence)
0.410
0.405
0.400
0.395
0.390
0.385
0.380
0.375
0.370
0.365
100
200
300
400
500
600
700
800
bioclimate 13

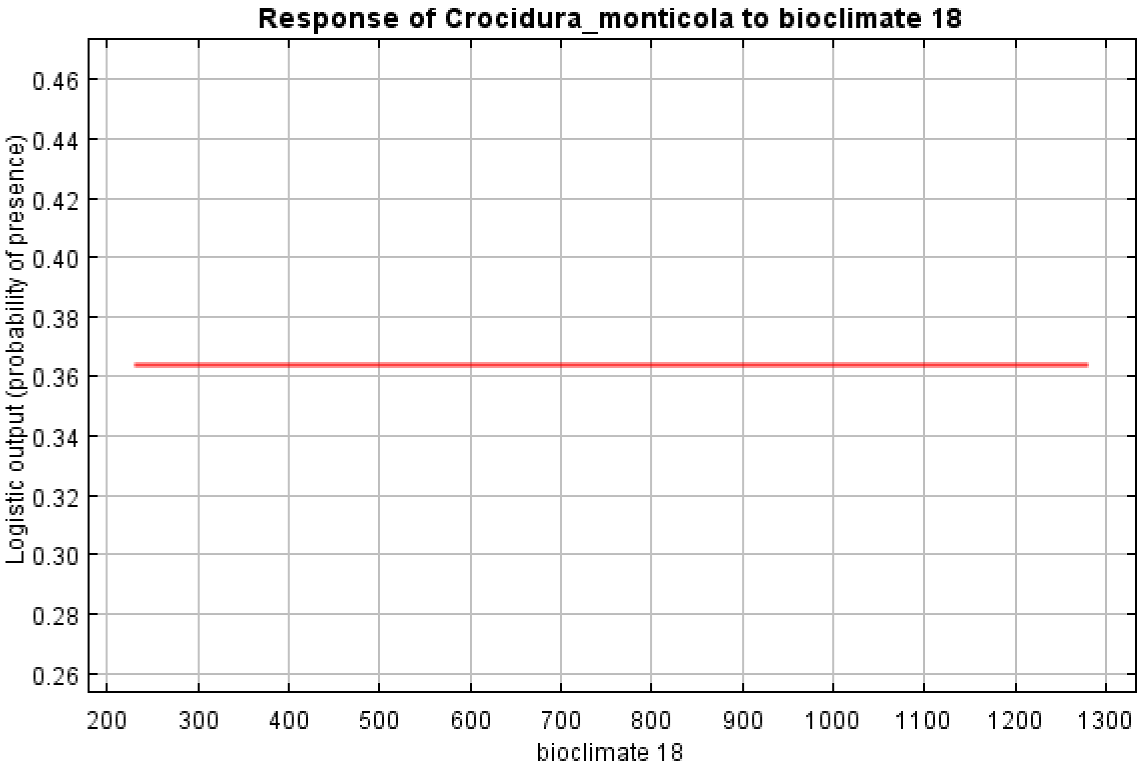


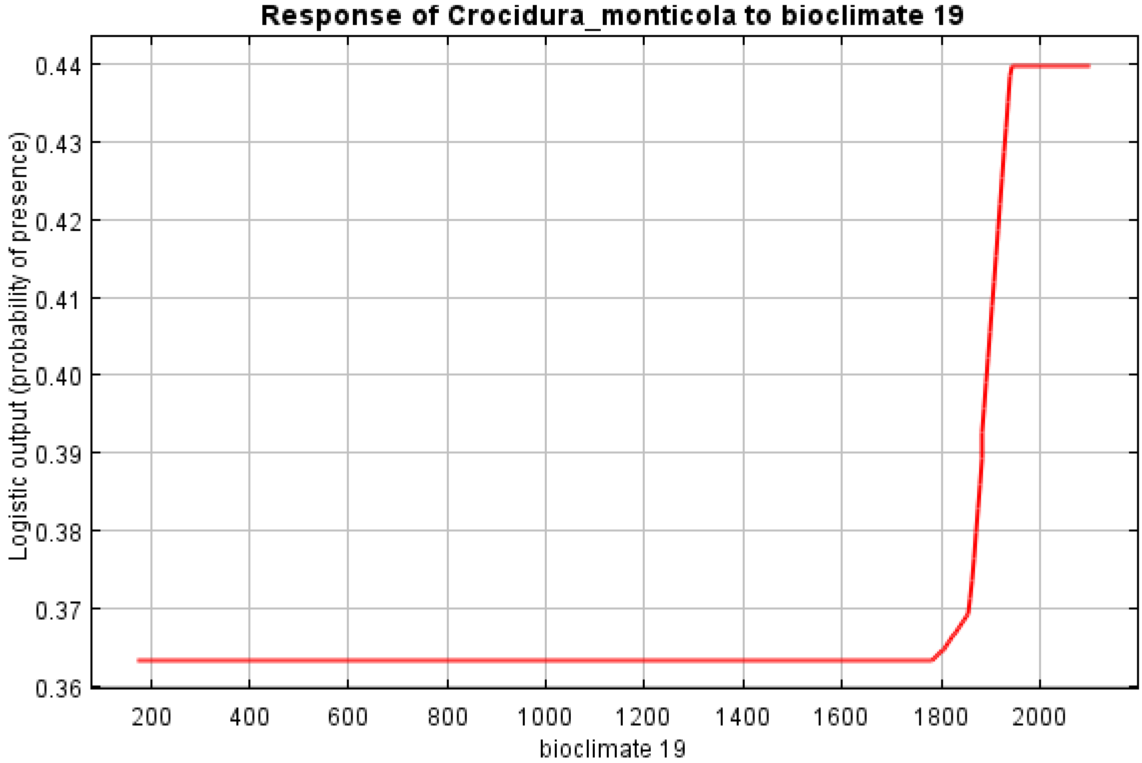
Response of Crocidura_monticola to bioclimate 14
Logistic output (probability of presence)
1.00
0.95
0.90
0.85
0.80
0.75
0.70
0.65
0.60
0.55
0.50
0.45
0.40
0.35
0
50
100
150
200
250
300
bioclimate 14

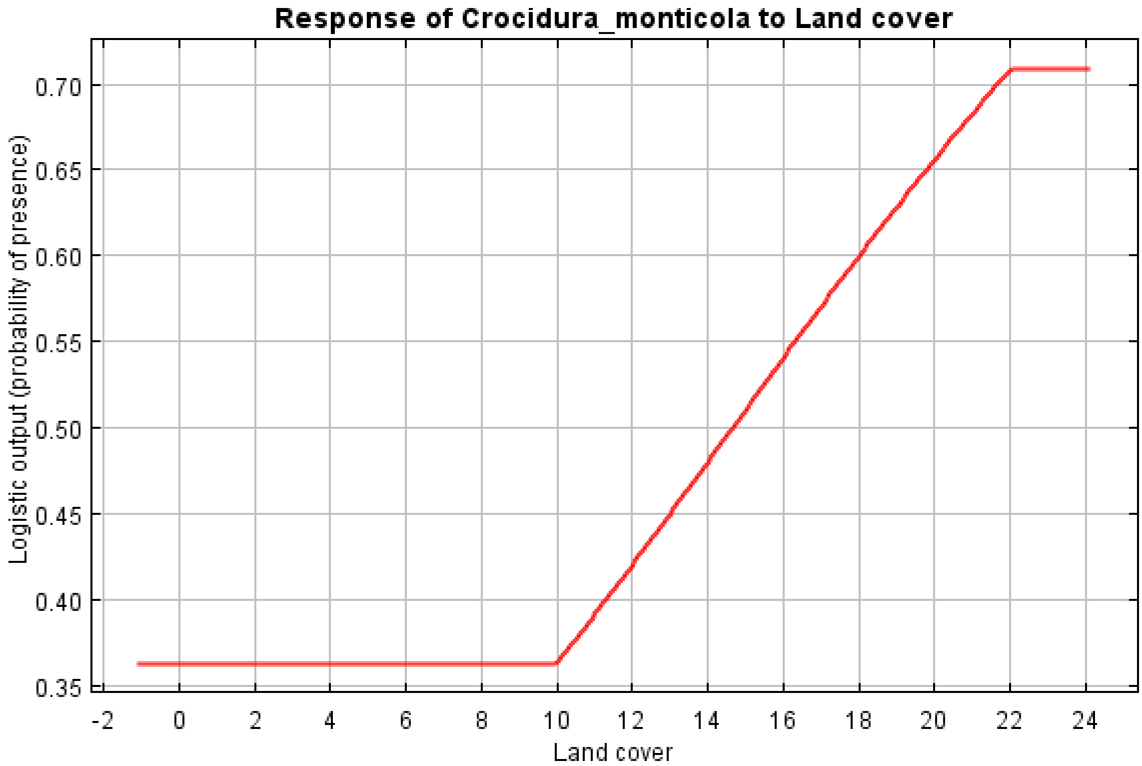

Response of Crocidura_monticola to bioclimate 15
Logistic output (probability of presence)
0.36
0.34
0.32
0.30
0.28
0.26
0.24
0.22
0.20
0.18
0
10
20
30
40
50
60
70
80
90
bioclimate 15


Response of Crocidura_monticola to bioclimate 16
Logistic output (probability of presence)
1.00
0.95
0.90
0.85
0.80
0.75
0.70
0.65
0.60
0.55
0.50
0.45
0.40
0.35
400
600
800
1000
1200
1400
1600
1800
2000
bioclimate 16


Response of Crocidura_monticola to bioclimate 17
Logistic output (probability of presence)
0.46
0.44
0.42
0.40
0.38
0.36
0.34
0.32
0.30
0.28
0.26
100
200
300
400
500
600
700
800
900
1000
1100
bioclimate 17


Response of Crocidura_monticola to bioclimate 18
Logistic output (probability of presence)
0.46
0.44
0.42
0.40
0.38
0.36
0.34
0.32
0.30
0.28
0.26
200
300
400
500
600
700
800
900
1000
1100
1200
1300
bioclimate 18


Response of Crocidura_monticola to bioclimate 19
Logistic output (probability of presence)
0.44
0.43
0.42
0.41
0.40
0.39
0.38
0.37
0.36
200
400
600
800
1000
1200
1400
1600
1800
2000
bioclimate 19


Response of Crocidura_monticola to Land cover
Logistic output (probability of presence)
0.70
0.65
0.60
0.55
0.50
0.45
0.40
0.35
-2
0
2
4
6
8
10
12
14
16
18
20
22
24
Land cover