

RESEARCH ARTICLE

UPDATED KNOWLEDGE ON MALARIA VECTORS IN MALAYSIA: A SCOPING REVIEW

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ABSTRACT

Malaria is transmitted by the Anopheles mosquito. The list of human and zoonotic malaria vectors in Malaysia is being updated in this scoping review. Search were conducted at four electronic bases. Title, abstract, and full-text reviews were used to determine which studies were eligible for further assessment. A total of 631 papers were identified until June 2021, yielded to 30 studies were reviewed. Human malaria vectors in Malaysia are identified as *Anopheles maculatus*, *Anopheles sudaicus*, *Anopheles balabacensis*, *Anopheles donaldi*, *Anopheles campestris* and *Anopheles flavirostris*. Vector for zoonotic malaria are *Anopheles balabacensis*, *Anopheles introlatus*, *Anopheles cracens*, *Anopheles letifer*, *Anopheles donaldi*, *Anopheles hackeri*, *Anopheles latens*, *Anopheles collesi* and *Anopheles roperi*. On the other hand, *Anopheles aconitus*, *Anopheles kochi* and *Anopheles pujutensis* are recognized as the potential malaria vectors. In order to implement effective mosquito control measures, it is crucial to comprehend and be knowledgeable about malaria vector profile. This will help stakeholder to develop and establish holistic and efficient strategy framework for integrated vector management (IVM) and develop new strategies for the elimination of malaria based on available evidence.

KEYWORDS

Anopheles, potential vector, malaria vector, zoonotic malaria, Malaysia

1. INTRODUCTION

Anopheles mosquitoes is a responsible vector for transmitting malaria (WHO, 2007). 4,500 species of mosquitoes have been identified worldwide (WHO, 2007). It is consisting of 34 genera from family Culicidae, order Diptera, class Insecta and phylum Arthropoda. Among them, 70 Anopheles species are known to transmit malaria globally. In Southeast Asia, malaria vectors were identified as *Anopheles balabacensis*, *Anopheles dirus*, *Anopheles sudaicus*, *Anopheles campestris*, *Anopheles letifer* and *Anopheles latens* (Peyton, 1989). Sallum *et. al.*, (2005) also documented that *Anopheles balabacensis* as the vector for malaria at some parts of the Philippines, Brunei and Indonesia (Sallum *et. al.*, 2005). According to a previous study, Malaysia is host to different species of Anopheles, including *Anopheles balabacensis*, *Anopheles maculatus*, *Anopheles campestris*, *Anopheles sudaicus*, *Anopheles letifer*, *Anopheles donaldi*, *Anopheles dirus*, *Anopheles leucosphyrus* and *Anopheles flavirostris* *Anopheles latens*, *Anopheles introlatus* and *Anopheles cracens* which are known to transmit malaria (Rahman *et al.*, 1997 & Vythilingam I, Hii J., 2013). Malaria infection commonly reported at the rural areas and also areas that involved with opening new land that caused deforestation (Rahman *et al.*, 1997). Malaria is caused by *Plasmodium* species i.e., *Plasmodium malariae*, *Plasmodium ovale*, *Plasmodium vivax*, *Plasmodium falciparum* and *Plasmodium knowlesi* (Yek *et al.*, 2022).

Plasmodium knowlesi is a primate malaria parasite commonly found in Southeast Asia that causes malaria in long-tailed macaques that can also infect humans, naturally and artificially (Knowles & Gupta, 1932). Due to habitat degradation brought on by growing deforestation and

development activities in areas where macaques are found, a large number of primates are now coming into close and direct contact with people. (Vythilingam *et al.*, 2008). Hence more and more people who live or come close to these areas might be infected with knowlesi malaria. *Plasmodium knowlesi* is now considered the fifth species of *Plasmodium* causing malaria in humans (Cox-Singh & Singh, 2008).

Apparently, malaria posed a problem for public health in Malaysia. Malaysia is experiencing an upsurge in zoonotic malaria cases, as a result of *Plasmodium knowlesi* transmission, which went from 1960 cases to more over 4,000 cases between 2016 and 2018 (WHO, 2021). It was documented 23,214 cases of malaria, 87% of which were zoonotic cases, from 2015 to 2021 in Malaysia.

With the purpose of fighting malaria, Malaysia has disembarked to a long journey of combating it since 1967 which was called Malaria Eradication Programme back then and later intensify to Malaria Elimination Program (Hussin *et al.*, 2020). In 2016, WHO initiated E-2020 plan which aims to accelerate elimination process to the potential countries to eliminate malaria such as Malaysia, South Korea, Timor Leste and few others (WHO, 2018). In order to attain the malaria elimination certification, few dossiers need to be prepared such as annual malaria surveillance reports, receptivity and intensity of transmission, entomological surveillance as well as reports of studies on malaria epidemiology and malaria vectors (WHO, 2017). Entomological expertise expedites the elimination of malaria by boosting the impact and effectiveness of critical actions (WHO, 2018), therefore this scoping review was designed to assist the stakeholder in document preparation.

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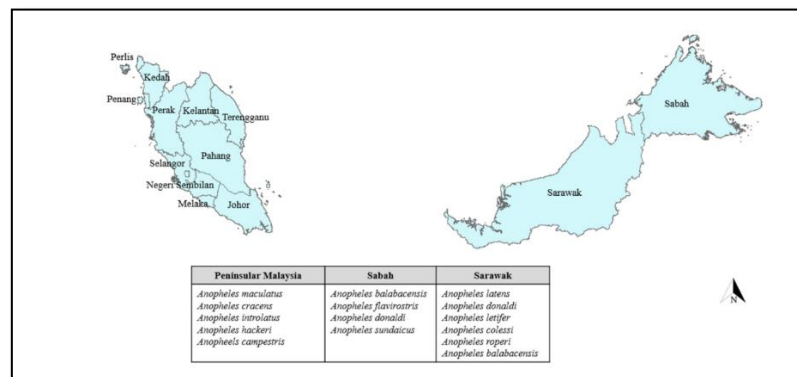


Figure 2: List of malaria vectors by region in Malaysia

Table 1: Key behavioral traits of human, zoonotic malaria vectors and potential malaria vectors in Peninsular Malaysia

Species (Complex or Group)	Location	Tropism	Trophic behavior	Habitat	Breeding sites	Peak biting times (hours)	Species identification method	Species of Plasmodium	Sporozoite rate (%)	Oocyst infection rate (%)	Parity rate (%)	Vectorial capacity	Entomological inoculation rate (EIR)	Human biting rate (HBR)	Life expectancy after plasmodium infection (days)	Refs
<i>Anopheles maculatus</i>	Peninsular Malaysia	Zoophilic	Exophagic	Forest		20:00-22:00 20:00-23:00 00:00-01:00 (indoor)	Phenotypic				41.6	nd		55.4		Ali <i>et al</i> (2011)
	Hulu Perak, Perak, Peninsular Malaysia			Cleared foothills			Phenotypic			10.8						Wahab <i>et al</i> (1993)
	Kuala Lipis, Pahang, Peninsular Malaysia			Forest	clear rock pool, clear water pocket, muddy water pocket, muddy rock pool		Phenotypic									Ahmad <i>et al</i> (2011)
	Kuala Lipis, Pahang, Peninsular Malaysia			Forest										0.42		Jiram <i>et al</i> (2012)
<i>Anopheles introlatus</i>	Hulu Gombak, Selangor, Peninsular Malaysia						Phenotypic	<i>Plasmodium c. bastianelli</i>	100							Eyles <i>et al</i> (1963)
	Hulu Selangor, Selangor, Peninsular Malaysia		Exophagic	Forest in lowland areas and hilly terrains		19:00-21:00	Phenotypic Molecular			1.82	65.5	1.94			7.2	Vythilingam <i>et al</i> (2014)
<i>Anopheles cracens</i>	Kuala Lipis, Pahang, Peninsular Malaysia	Simo-anthropophagic		Forest		19:00-21:00	Phenotypic Molecular	<i>Plasmodium knowlesi</i>	1.7							Vythilingam <i>et al</i> (2008)
	Kuala Lipis, Pahang, Peninsular Malaysia	Anthropophilic	Exophagic	Forest		20:00-21:00	Phenotypic	<i>Plasmodium knowlesi</i>	2.9		60%	1.09	0.08	1.24	8.6	Jiram <i>et al</i> (2012)
<i>Anopheles hackeri</i>	Klang, Selangor, Peninsular Malaysia	Zoophilic		Forest	Split bamboos, nipah palm leaves		Phenotypic	<i>Plasmodium knowlesi</i>	0.14							Wharton & Eyles (1961)
<i>Anopheles donaldi</i>	Perak, Peninsular Malaysia		Exophagic Endophagic	Forest with hilly areas		23:00-24:00 02:00-03:00	Phenotypic							44.6-64.4		Vythilingam <i>et al</i> (1996)
<i>Anopheles campestris</i>	Kuala Selangor, Peninsular Malaysia		Endophagic			23:00-24:00	Phenotypic									Thevasagayam ES, Khoon CC, Siong Y (1979) Moorhouse DE, Wharton RH. (1965)
<i>Anopheles aconitus</i>	Hulu Perak, Perak, Peninsular Malaysia	Zoophilic	Exophagic	Cleared foothills			Phenotypic									Rahman <i>et al</i> (1993)
	Hulu Perak, Perak, Peninsular Malaysia			Cleared foothills			Phenotypic			1.7						Wahab <i>et al</i> (1993)
<i>Anopheles kochi</i>	Hulu Perak, Perak, Peninsular Malaysia	Zoophilic	Exophagic	Secondary forest		19:00-21:00	Phenotypic									Rahman <i>et al</i> (1995)
<i>Anopheles balabacensis</i>	Perlis, Peninsular Malaysia						Phenotypic	<i>Plasmodium cynomolgi</i>	11.90							Cheong <i>et al</i> (1984)

Table 2: Key behavioral traits of primary and zoonotic malaria vectors in Borneo Malaysia

Species (Complex or Group)	Location	Tropism	Trophic behavior	Habitat	Breeding sites	Peak biting times (hours)	Species identification method	Species of Plasmodium	Sporozoite rate (%)	Oocyst infection rate (%)	Parity rate (%)	Vectorial capacity	Entomological inoculation rate (EIR)	Human biting rate (HBR)	Life expectancy after plasmodium infection (days)	Refs	
<i>Anopheles balabacensis</i>	Papar, Sabah		Exophagic			00:00-01:00 & 02:00-03:00 (outdoor) 00:00-01:00 & 03:00-04:00 (indoor)	Phenotypic									Tanrang <i>et al</i> (1999)	
	Kinabatangan, Sabah			Forested with hilly areas		19:00-20:00	Phenotypic	<i>Plasmodium falciparum</i>	0.00	0.55						Vythilingam <i>et al</i> (2005)	
	Kudat, Sabah			Secondary forest		18:00-20:00	Phenotypic Molecular	<i>Plasmodium knowlesi</i>	3.00			2.5-3.85	0.09-2.4		5.4-7.0	Wong <i>et al</i> (2015)	
	Ranau & Keningau, Sabah			Forest		19:00-20:00	Phenotypic Molecular	<i>Plasmodium knowlesi</i>	0.40							Hawkes <i>et al</i> (2019)	
	Perlis, Peninsular Malaysia							Phenotypic	<i>Plasmodium cynomolgi</i>	11.90							Cheong <i>et al</i> (1984)
	Banggi Island, Sabah		Anthropophilic		Forest			Phenotypic	<i>Plasmodium falciparum</i>	5.05		93.4	1.44-19.7		33.6		Hii <i>et al</i> (1988)
Lawas, Sarawak				Forest			Phenotypic Molecular	<i>Plasmodium knowlesi</i>	29.00							Ang <i>et al</i> (2020)	
<i>Anopheles latens</i>	Kapit, Sarawak		Simio-anthropagic Acrodrotophagic	Forested with hilly areas		19:00-20:00	Phenotypic	<i>Plasmodium knowlesi</i>	0.69-1.37	0.46-1.37	53.7-65.8	0.6-2.86	11.98-14.10		4.7-7.2	Tan <i>et al</i> (2008)	
	Kapit, Sarawak			Forest		23:00-00:00	Phenotypic Molecular	<i>Plasmodium knowlesi</i>	1.18	1.18			6.74 (Forest fridge) 1.85 (Forest) 0.28 (Longhouse)			Vythilingam <i>et al</i> (2006)	
<i>Anopheles donaldi</i>	Belaga, Sarawak			Forested with hilly areas			Phenotypic						0.035		2.3-4.07	Seng <i>et al</i> (1999)	
	Kapit, Sarawak						Phenotypic		0	0.16						Tan <i>et al</i> (2008)	
	Kinabatangan, Sabah			Forested with hilly areas		18:00-19:00	Phenotypic	<i>Plasmodium falciparum</i>	0.23							Vythilingam <i>et al</i> (2005)	
	Ranau & Keningau, Sabah					18:00-19:00	Phenotypic Molecular									Hawkes <i>et al</i> (2019)	
	Lawas, Sarawak			Forest			Phenotypic Molecular	<i>Plasmodium knowlesi</i>	27.8							Ang <i>et al</i> (2020)	
	Perak, Peninsular Malaysia			Exophagic Endophagic	Forest with hilly areas		23:00-24:00 02:00-03:00	Phenotypic				44.6-64.4					Vythilingam <i>et al</i> (1996)
<i>Anopheles flavirostris</i>	Banggi Island, Sabah			Forest			Phenotypic	<i>Plasmodium falciparum</i>	5.45			0.19-15.8				Hii <i>et al</i> (1988)	
	Banggi Island, Sabah		Anthropophilic	Forest		23:00-03:00 (indoor)	Phenotypic		0.9							Hii <i>et al</i> (1985)	
<i>Anopheles sudaicus</i>	Kuala Penyu, Sabah		Exophagic	Coastal area		21:00-22:00 (outdoor) 24:00-01:00 (indoor)	Phenotypic									Rahim <i>et al.</i> , (2019)	
	Landu, Sarawak			Coastal area	rock pools contained stagnant clear or coloured brackish water		Phenotypic Molecular									Linton <i>et al.</i> , (2001)	
<i>Anopheles letifer</i>	Miri, Sarawak			Forest	peat swamps, especially in jungle clearings and at forest edges		Phenotypic	<i>Plasmodium falciparum</i> / <i>Plasmodium vivax</i>	Forest (0.14) Clearing area(0.23)		Forest (71.1) Clearing area(74)	Forest (0.054±0.143) Clearing area(0.066±0.197)	Forest (38.5±9.9) Clearing area(28.7±11.5)			Chang <i>et al</i> (1997)	
	Balai Ringin, Serian, Sarawak		Anthropophilic	Exophagic	Peat swamp area	22:00-23:00	Phenotypic				Maintenance (0) Maintenance (63.6)	Maintenance (65.2)	Maintenance (7)	Maintenance (3.6±2.8)	Maintenance (2.6±2.8)	Thevasagayam & Fah (1980)	
<i>Anopheles colexi</i>	Betong, Sarawak		Simio-anthropagic	Exophagic	Secondary forest	1700-1800	Molecular	<i>Plasmodium knowlesi</i>								Ang <i>et al</i> (2021)	
<i>Anopheles roperi</i>	Betong, Sarawak		Simio-anthropagic	Exophagic	Secondary forest	1800-1900	Molecular	<i>Plasmodium knowlesi</i>								Ang <i>et al</i> (2021)	

Table 3: Plasmodium infections in Anopheles species in Malaysia

Species (Complex or Group)	Location	Species identification method	Species of Plasmodium	Sporozoite rate (%)	Refs
<i>Anopheles cracens</i>	Kuala Lipis, Pahang, Peninsular Malaysia	Phenotypic Molecular	<i>P. knowlesi</i>	1.7	Vythilingam <i>et al.</i> , (2008)
	Kuala Lipis, Pahang, Peninsular Malaysia	Phenotypic	<i>P. knowlesi</i>	Forest = 2.9 Fruit orchard = 0.60	Jiram <i>et al.</i> , (2012)
<i>Anopheles letifer</i>	Miri, Sarawak	Phenotypic	<i>P. falciparum</i> / <i>P. vivax</i>	Forest (0.14) Clearing area(0.23)	Chang <i>et al.</i> , (1997)
<i>Anopheles hackeri</i>	Klang, Selangor	Phenotypic	<i>P. knowlesi</i>	0.14	Wharton & Eyles (1961)
<i>Anopheles balabacensis</i>	Kinabatangan, Sabah	Phenotypic	<i>P.falciparum</i>	0.00	Vythilingam <i>et al.</i> , (2005)
	Kudat, Sabah	Phenotypic Molecular	<i>P. knowlesi</i>	3.00	Wong <i>et al.</i> , (2015)
	Ranau & Keningau, Sabah	Phenotypic Molecular	<i>P. knowlesi</i>	0.14	Chua, T.H. <i>et al.</i> , (2017)
	Banggi Island, Sabah	Phenotypic	<i>P.falciparum</i>	5.05	Hii <i>et al.</i> , (1988)
	Lawas, Sarawak	Phenotypic Molecular	<i>P. knowlesi</i>	29.00	Ang <i>et al.</i> , (2020)
<i>Anopheles flavirostris</i>	Banggi Island, Sabah	Phenotypic	<i>P.falciparum</i>	5.05	Hii <i>et al.</i> , (1988)
	Banggi Island, Sabah	Phenotypic	<i>Plasmodium spp</i>	1.41	Hii <i>et al.</i> , (1988)
<i>Anopheles donaldi</i>	Kapit, Sarawak	Phenotypic	<i>P. knowlesi</i>	0	Tan <i>et al.</i> , (2008)
	Kinabatangan, Sabah	Phenotypic	<i>P.falciparum</i>	0.23	Vythilingam <i>et al.</i> , (2005)
	Lawas, Sarawak	Phenotypic Molecular	<i>P. knowlesi</i>	27.8	Ang <i>et al.</i> , (2020)
<i>Anopheles latens</i>	Kapit, Sarawak	Phenotypic	<i>P. knowlesi</i>	Farm = 0.69 Forest = 1.37	Tan <i>et al.</i> , (2008)
	Kapit, Sarawak	Phenotypic Molecular	<i>P. knowlesi</i>	1.18	Vythilingam <i>et al.</i> , (2006)
<i>Anopheles donaldi</i>	Kinabatangan, Sabah	Phenotypic	<i>P.falciparum</i>	0.23	Vythilingam <i>et al.</i> , (2005)

3.2 Potential Malaria Vectors

The potential human malaria vectors are identified as *Anopheles aconitus* from Minimus Group in this review. *Anopheles kochi* (Kochi Group) and *Anopheles pujutensis* from Leucopshyrus Group were categorized as potential zoonotic malaria vectors in Peninsular Malaysia.

Summary of this study finding were showed in Table 4, which identifies human and zoonotic malaria vector as well as potential malaria vectors in Malaysia. Vectorial status for each Anopheles species were describe with the intention to acquaintance and thus understand the intensity of malaria transmission.

4. DISCUSSION

In 1988, nine species were established as a malaria vector in Malaysia namely *Anopheles balabacensis*, *Anopheles maculatus*, *Anopheles campestris*, *Anopheles sunaicus*, *Anopheles letifer*, *Anopheles donaldi*, *Anopheles dirus*, *Anopheles leucosphyrus* and *Anopheles flavirostris* (MOH Malaysia, 1988). However, our finding showed 16 Anopheles species vectors were incriminated as a malaria vector with three potential vectors for zoonotic malaria (Table 1). This finding was coherent with review made by Vythilingam & Hii (2013), where they conclude the *Anopheles latens*, *Anopheles introlatus*, *Anopheles balabacensis*, *Anopheles cracens* as malaria vectors and *Anopheles pujutensis* (as probable vector).

Based on this review, the majority of vectors bite early in the evening, with peak biting occurring between 7 and 8 pm. This similar trend was observed for *Anopheles cracens* in Thailand (Baimai *et al.*, 1988), *Anopheles maculatus* in Thailand (Tainchum *et al.*, 2014) and *Anopheles sudaicus* in Nicobar Island, where peak biting activity was recorded as early as 7pm (Dusfour *et al.*, 2004; Phan, 1998).

Most of the malaria vectors are forest inhabitants, as indicated by this study. *Anopheles latens*, *Anopheles balabacensis* and *Anopheles flavirostris* can be found at forest and forest fridges in West Sumba and Kalimantan, Indonesia, Philippine Islands (Balabac, Culion, Palawan), Brunei and Thailand, (Barbara *et al.*, 2011; Sallum *et al.*, 2005; Maekawa *et al.*, 2009; Stoops *et al.*, 2007; Peyton *et al.*, 1979; Harbach *et al.*, 1987a).

Sporozoite infection rate in malaria vectors were recorded with various percentage indicating the intensity of malaria transmission (Gu, 1995). This scoping review revealed that sporozoite rate in *Anopheles balabacensis* were recorded between 1.6% to 29% whilst in Palawan, Philippines it was recorded at 29.4% (Schultz, 1992), 8.7% in Thailand (Scanlon *et al.*, 1967) and less than 1.3% in Indonesia (Harbach *et al.*, 1987b). Thus, it demonstrates that sporozoite rate were lower in South East Asia countries. However, factors such as site of mosquito collection play a role as study sites in forest will record higher sporozoite rate compared to forest fridges and long house (Dalla Bona & Silva, 2010).

According to Manquin *et al.* (2008), vector status is much dependable to the environmental or seasonal changes as a species can play a role as primary or secondary in one area or at in a different place (Manquin *et al.*, 2008). In order a species to become a primary vector, it needs to be i) extensive distribution, ii) highly abundance, iii) significant dispersal, iv) adaptive towards environment for breeding, v) preferences of biting human as source of food (anthropophilia) and vi) susceptible to Plasmodium (Donnelly *et al.*, 2002). Another criterion to become a primary vector is to have a longer life span (Dalla Bona & Silva, 2010) thus, concludes that longevity of primary is longer than secondary vector.

The vectorial capacity of vector population to transmit malaria are the factors that classified mosquito as a potential vector (Oaks *et al.*, 1991). The importance of knowing the potential malaria vector because it's a partly from the early warning system before the malaria transmission occur, probably at the free malarious area, and low receptive localities. This will be a leverage to the Vector Control Programme as preventive measures can be initiated. A good epidemiology and entomological surveillance would benefit this information as it will prevent the re-introduction of malaria cases (MOH, 2016).

This review, however suggested status *Anopheles aconitus* as a malaria vector needs to be confirmed again. A study unable to utilized establish methods in order to proven *Anopheles aconitus* as a malaria vector (Rahman *et al.*, 1993). This concurs with other researchers' decisions, *Anopheles aconitus* were not recognize as a human malaria vector since there was insufficient supporting data (Vythilingam & Hii, 2013). The study sites were located near Malaysia-Thailand border; thus, we came to the conclusion that *Anopheles aconitus* should not be considered as a malaria vector, but as potential malaria vector in our review.

Anopheles aconitus is a secondary malaria vector in Thailand (Chen *et al.*, 2012). Our review would like to emphasize that any study conducted close to the Malaysia-Thailand border, particularly in Perak, Malaysia, should not be taken lightly because *Anopheles aconitus* can be a vector for the transmission of malaria. More research is required to incriminated *Anopheles aconitus* as a malaria vector in Malaysia.

Further research was also conducted on potential malaria vectors like *Anopheles pujutensis* and *Anopheles kochi*. However, information on behavioral on these species were scarce as it was not a malaria vector, thus less attention was given (Tan *et al.*, 2008). Nevertheless, *Anopheles pujutensis* and *Anopheles kochi* were suspected as vector because its display a simiophagic behavior and susceptibility of *Plasmodium knowlesi* (Pramasivan *et al.*, 2022; Imwong *et al.*, 2019; Jeslyn *et al.*, 2011; Vythilingam *et al.*, 2008; Eyles *et al.*, 1963; Warren & Wharton *et al.*, 1963). It might be a challenge to the researchers, suggested incriminating secondary vectors difficult as they are also harboring sporozoites, displayed an opportunistic behavior by biting humans and species were uncommon (Tanachai *et al.*, (2019).

This study was conducted without specific time frame; therefore, no specific coordinate was found in some of the studies conducted before the utilization of geographical integrated system (GIS) in public health. GIS is a powerful entomological surveillance tool as it detected and predicted seasonal hotspots of malaria cases in Zimbabwe based on the habitat

suitability of the mosquito *Anopheles arabiensis* (Gwitira *et al.*, 2018). In addition to that, in Rio de Janeiro it also successfully helps in initiating effective vector control activities by developing territory receptivity model based on potential larval habitats (Albuquerque *et al.*, 2018).

On the other hand, this study also observed a lacking of some entomological indices reported by researchers. This probably because, it depends on the objectives of the study. However, relevant information was still extracted from the context.

The exploitation of molecular technique, polymerase chain reaction (PCR) in species identification is important, especially in identifying sibling species. All these differences may indicate the presence of isomorphic species within a taxonomic species (defined morphologically), but these differences cannot confer species status on populations. Hence, genetic techniques that can demonstrate reproductive isolation within a morphologically similar taxonomic species are needed (Rafidah *et al.*, 2018).

Emerging new malaria vector were made thanks to the technology used in order to determine sister species between species complex as well as detection of parasites in salivary gland. It's interesting to note that the majority of malaria vectors can spread the disease to humans and animals. Therefore, the vector management technique for malaria caused by zoonosis can equally be applied to the human malaria vector.

5. CONCLUSION

This review collected available scientific evidence on malaria vectors, regards human malaria vectors, zoonotic malaria vectors and potential malaria vectors as it was intended to give the updated list of malaria vectors in Malaysia. It identified *Anopheles maculatus*, *Anopheles sudaicus*, *Anopheles balabacensis*, *Anopheles donaldi*, *Anopheles campestris* and *Anopheles flavirostris* as human malaria vectors. Nevertheless, *Anopheles balabacensis*, *Anopheles sudaicus*, *Anopheles flavirostris*, *Anopheles donaldi* and *Anopheles letifer* are the human malaria vectors in West Malaysia (Sabah and Sarawak).

The findings from this research successfully discovered *Anopheles collesi* and *Anopheles roperi* as two novel zoonotic malaria vectors in Sarawak. As a result, the currently recognized list of zoonotic malaria vectors was updated to *Anopheles cracens*, *Anopheles introlatus*, *Anopheles hacker*, *Anopheles donaldi*, *Anopheles balabacensis*, *Anopheles letifer*, *Anopheles donaldi*, *Anopheles latens*, *Anopheles collesi* and *Anopheles roperi*.

In the current study, *Anopheles kochi* and *Anopheles pujutensis* were identified as possible zoonotic malaria vectors in addition to *Anopheles aconitus*, which has been acknowledged as a possible human malaria vector. Gaps in knowledge of behavioural and larval site characteristic of each human malaria vectors and zoonotic malaria vectors were acknowledged and discussed in this review.

There is a need for research to incriminate the probable malaria vectors and exploration on the bionomics and breeding grounds for secondary vectors. The key to developing a successful malaria intervention is having a thorough understanding of Anopheles' role as a malaria vector and the knowledge obtained from their behavioral traits (Ijumba *et al.*, 2001). It will assist stakeholder to design a global strategic framework for integrated vector management (IVM) and forming new policies for malaria elimination (WHO, 2004; Sinka *et al.*, 2010; Moonen *et al.*, 2010; Montoya-Lerma *et al.*, 2011) based on evidence decision making.

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