Jurnal Sains Kesihatan Malaysia 20 (1) 2022: 83-95 DOI : http://dx.doi.org/10.17576/JSKM-2022-2001-08

Kertas Asli/Original Articles

PERSPECTIVES ON ANCESTRAL LINEAGES AND GENETIC MARKERS OF MALAY POPULATION IN PENINSULAR MALAYSIA (Perspektif Keturunan Dan Penanda Genetik Populasi Melayu Di Semenanjung Malaysia)

SHALINI PARTHIPAN & SERI MIRIANTI ISHAR*

ABSTRACT

The Malay people are the majority in Peninsular Malaysia, but their population structure and genetic profile remain poorly studied. The exposure to the origins of Malays and their sub-ethnic groups is vital prior to study about their genetic profiles as it can narrow down the haplogroups of their ancestral lineages. In this review, we have highlighted theories related to the origin of Malays from Yunnan, New Guinea, Taiwan, Sundaland, Nusantara and the theory of Bani Jawi. Nevertheless, these theories were established based on speculations without evidence. Despite the theories developed, the migration of Malay population is more prominent during the era of Malacca Sultanate. The trading activities and seafaring way of life had welcomed various ethnic groups in Peninsular Malaysia which formed a part of the Malay population today. Thus, the origin of major sub-ethnic groups of Malay population are discussed in this paper. The origin of Malay community has a key relationship with modern genomic field that was conducted through mitochondrial DNA analysis. Human identification in forensic application is tedious due to the need for sequencing whole DNA profile of Malay population. Therefore, identification of specific genetic markers for Malay population is vital to facilitate forensic investigation. We gathered data by systematically searched with Google Scholar, Pubmed, Science Direct with advanced search builder for papers titles with Malay population and genetic markers. This study shed some light on the mitochondrial DNA markers of indigenous people and Malay population in Peninsular Malaysia which can be used in future prospects.

Keywords: Malays; sub-ethnic; origin; migration; genetic markers

ABSTRAK

Sebahagian besar populasi di Malaysia terdiri daripada kaum Melayu, namun struktur populasi dan profil genetik mereka kurang ditakrifkan. Pendedahan ilmu mengenai asal usul orang Melayu dan setiap kumpulan etnik mereka adalah penting untuk mengkaji penanda genetik yang diwarisi secara turun-temurun. Oleh itu, kajian ini menjelaskan teori berkaitan asal usul orang Melayu dari Yunnan, New Guinea, Taiwan, tanah Sunda, Nusantara dan teori Bani Jawi. Meskipun, teori tersebut dikembangkan oleh para penyelidik berdasarkan spekulasi tanpa bahan bukti yang sebenar. Selain daripada perkembangan teori, penghijrahan penduduk Melayu lebih menonjol ketika era Kesultanan Melayu Melaka. Kegiatan perdagangan dan pelayaran di Selat Melaka telah menarik minat pelbagai etnik dari kepulauan Melayu berhijrah ke Semenanjung Malaysia dan membentuk populasi Melayu hari ini. Oleh yang demikian, makalah ini juga membincangkan sejarah keturunan setiap kumpulan etnik penduduk Melayu. Asal usul keturunan Melayu mempunyai hubungan utama dengan genetik Melayu moden yang dikenalpasti melalui kajian analisis DNA mitokondria. Namun, identifikasi manusia dalam bidang forensik merupakan kaedah yang rumit disebabkan penglibatan proses penjujukan DNA. Pencarian loci yang paling informatif dan spesifik amat diperlukan untuk identifikasi populasi Melayu. Data mengenai penanda genetik telah dikumpulkan dari artikel penyelidikan melalui pangkalan Google Scholar, Pubmed, Science Direct dengan carian khusus menggunakan kata kunci Melayu dan DNA mitokondria. Hasil daripada pencarian, penanda DNA mitokondria orang asli dan populasi Melayu telah diterangkan dalam penulisan ini untuk digunakan dalam kajian masa depan.

Kata Kunci: Melayu; kumpulan etnik; asal usul; penghijrahan; penanda genetik

INTRODUCTION

The Southeast Asian region is rich in a variety of ethnic cultures and traditions. The location of Malaysia at the crossroads of Southeast Asia (SEA) has been recognized as one of the hubs for early human migration. Southeast Asia (SEA) is shaped by two major migrations which are the ancient 'Out of Africa' migration ~50,000 years before present (YBP) and the recent 'Out of Taiwan' migration ~5,000YBP. Peninsular Malaysia is the primary home for natives including the Malays and indigenous populations (also known as Orang Asli). The indigenous population is defined as the notion of place-based human ethnic culture that has not migrated from its homeland. Although the government found nineteen subgroupings of Orang Asli, they are subdivided into three broad divisions consist of Negrito (Semang), Senoi and Proto-Malay (Aghakhanian et al. 2015).

Genetic studies found that ancestors from Negrito were the earliest settlers in Peninsular Malaysia and they are believed to have originated from the ancient migrations (Yew et al. 2018). They speak Austro-Asiatic language, practice nomadic lifestyle and carry out hunting gatherings. Negritos were phenotypically differentiated from other populations by black wooly hair morphology, darker skin pigmentation, rounded face, wide nose and short average stature (Ismail et al. 2013). They were found to be occupied in the coastal foothills and inland river valleys of Perak, Pahang and Ulu Kelantan. Genomic studies conducted on ancient hair and skeletal remains of Negritos show that they are mainly descendants of Paleolithic and Mesolithic populations (Benjamin 2013; Ricaut et al. 2006). This statement is also supported by archaeological assembles found in Hoabinhian sites dated between 16,000 to 8,000 years ago, which shows Hoabinhians were ancestral to Negritos (Leonard Y.Andaya 2014).

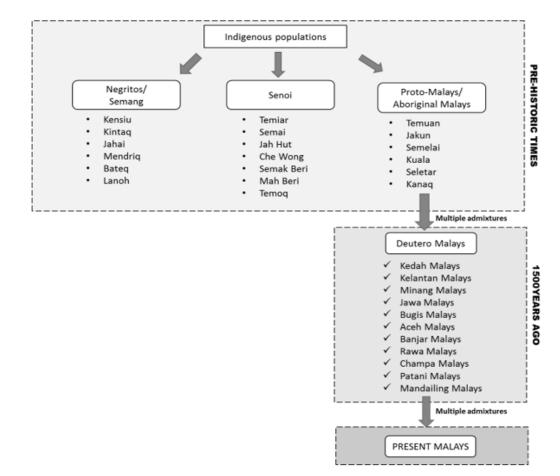


Figure 1. Nineteen(19) sub tribes of indigenous populations/Orang Asli and ten(10) major subethnic groups of Deutero Malay population. Deutero Malays are ancestors of present day Malays in Peninsular Malaysia

Furthermore, Senoi is the largest subpopulation among Orang Asli communities. They migrated from the mainland of Southeast Asia to Peninsular Malaysia between 8,000 to 6,000 B.C. (Hill et al. 2006). Studies found that half of the Senoi maternal lineages tracing back to the ancestors of Semang and another half migrations from Indochina (Jeffrey Hays 2015). Nevertheless, the differences of Aslian languages between northern Aslian-speaking Semang and central Aslian-speaking Senoi have separated them into two major branches eventhough they originated from common ancestors (Benjamin 2018). In the prehistoric era, they were agriculturalists which have been proved by archaelogists based on excavation of cord-marked pottery which linked to the Senoi way of life in Southern China (Khoo & Lubis 2005).

In addition, Proto-Malays (also known as aboriginal Malays) have a more diverse origin and various theories had been developed by researchers regarding the origin of Malays in prehistoric times as early as the 1800s (Isa & Zen 2014). These theories were developed based on archaeological evidence and linguistic culture of Malayo-Polynesian language spoken among aboriginal Malay population (Donohue & Denham 2011; Jeffrey Hays 2015). Thereafter, the historic influx and multiples admixture of events over centuries had introduced Deutero Malays. Deutero Malays are described as ancestors of present day Malays and descendants of Proto-Malays. The rise of Deutero Malays caused the aboriginal Malays to be pushed to inland areas of the further upriver. Their migration and assimilation of historical tribes during Malayization had drifted the genetic pool of Deutero Malays into modern Malays today as summarized in Figure 1. Besides that, the emergence of various sub-ethnic groups among Malay population was more prominent during the rise of Malacca Sultanate. Intermarriages that occurred between locals and traders had caused various genetic admixtures among the local Malay population (Wey & Harun 2018).

Knowledge regarding group of inherited alleles known as haplotypes is important in forensic studies of human identification. A combination of similar haplotypes will be grouped into haplogroups. Haplogroups strongly correlate to geographic origin, thus screening of haplogroup markers might narrow down the scope of investigation in cases that involved unclassified populations. Researches regarding Malay haplogroups and essential markers had bloomed following the HUGO Pan-Asian SNP consortium which aimed to map human genetic diversity in Asia (Yahya et al. 2017). Malay population has become an interest in Malaysia because they are present in majority compared to other populations. Zainuddin & Goodwin 2004 showed that 48% of Malays belong to macrohaplogroup N and 52% of them are categorized into macrohaplogroup M. Nevertheless, studies regarding the specific branches of Malay haplogroups are still not widespread. Therefore, learning about the origin of Malays is vital before researching about Malay haplogroups in Peninsular Malaysia to narrow down the branches of specific haplogroups present among them. Hence, this review aims to highlight:

- 1. Theories about the origin of Malays,
- 2. Genetic admixtures of each Malay sub-ethnic groups in Peninsular Malaysia
- 3. Haplogroup diversity and genetic markers useful in human identification

THEORIES ABOUT ORIGIN OF MALAYS

The development of Malay language and divergence of various Malay sub-ethnic groups were more prominent during the rise of Malacca Sultanate following the religious conversion of King of Parameswara to Islam, later then known as Sultan Iskandar Shah (Wain 2012). During the 14th century, the Straits of Malacca was a major international trading center from India, China and South East Asia. Traders and seafarers had settled in Peninsular Malaysia and entered the realm of the Malays (Leonard Y.Andaya 2008). Besides that, these traders built their temporary home while waiting for the end of Monsoon season before beginning their sail again. Intermarriages that occurred between the traders and locals during this time had caused genetic admixtures and arise of various sub-ethnic groups in Peninsular Malaysia (Wain 2012; Wey & Harun 2018).

Nevertheless, the Niah Caves archaeological evidence of the oldest human remains shows modern human inhabitation in Peninsular Malaysia dates back as early as 40,000 years ago (Jeffrey Hays 2015). The aboriginal Malays were thought to be the early inhabitants before the rise of Malacca Sultanate (Embong et al. 2016). There are three main theories featured by researchers related to the origin of Malays which are the Yunnan, New Guinea and Taiwan theories as explained:

1. The Yunnan theory (1889)

Malays are believed to have originated from Yunnan, China approximately 4000 to 6000 years ago. This theory was supported by an Austrian scientist, R.H Geldern and his team who mentioned that Proto-Malays migrated from the Mekong river to Malay Peninsula (Van Nguyen et al. 2000). Then, the migration was followed by an early Holocene dispersal through the Peninsular Malaysia into Malay Archipelago. The migration pattern is outline in Figure 2. There is other evidence that uprights this theory which includes stone tools found at Malay Archipelago are analogous to Central Asian looks where show similarity of Malay and Assamese (from northeastern India) customs (Kossak & Watts 2001).

Besides that, Malay and Cambodian languages are related since Cambodian ancestors originated from the Mekong river (Breurec et al. 2011). However, many researchers pointed out that there is no direct evidence to prove the relationship between Peninsular Malaysia and Yunnan, thus they believed this theory was speculated based on general historical facts connected from many studies (Nik Hassan Shuhaimi Nik Abd Rahman 2016). The presence of stone tools (shouldered axe and rectangular axe) at north of Malay Peninsula and Mekong as well as throughout Indonesia is evident to link between Yunnan and the Malay Peninsula (Wan Fahmi 2004; M.W.F.Tweedie 1953). Mathew Spriggs (2011) suggested the spread of Austro-Asiatic language based on the evidence of the stone tools found by archaeologists Nevertheless, the spread of languages can also occur through waves of migrations. Therefore, Van Heekerens advised that it is inaccurate to measure the origins of people based on the spread of language which can generate false-positive results.

Multi Dimensional Scale (MDS) analysis using Fixation Index Statistics (Fst) (Hatin et al. 2014) suggested that phylogenetic affinities of Proto-Malays especially Temuan population shows genetic relationship with Yunnan Chinese as they are grouped under Cluster II of a common ancestor in neighbour joining tree among analyzed fifteen populations. However, few local researchers vehemently disagreed with the origins of Malays from Yunnan. After all, studies show that migration to Peninsular Malaysia is more probable to happen from south to north because most of the Malay subethnic groups arrived in historical times are mainly from Sulawesi, Java and Sumatra (Lipson et al. 2014; Norhalifah et al. 2016; Yew et al. 2018). Thus, the absence of direct evidence and speculations developed by many researchers show the hypothesis of Malays originated from the north, Yunnan was ambiguous.

2. The New Guinea/Seafarers theory (1965)

Historically, early human migration from one place to other different countries occurred due to many factors such as extending their empire, colonialism and business trades (Wan Fahmi 2004). Similarly, Proto Malays/Orang Asli are believed to have migrated to Peninsular Malaysia as seafarers whose knowledge is diverse in oceanography and extends their agricultural skills. They worked as crews and labours in the ships of Indian, Arab, Persian and Chinese traders for nearly 2,000 years then traveled from one island to another island between New Zealand and Madagascar (Md-Zain et al. 2017). Their morphology features look similar to Negroids from Africa (Jinam et al. 2017). During their migration, they settled at various places temporarily or permanently and expanded their cultures (Jinam et al. 2012). Besides that, Negritos in Peninsular Malaysia are believed to be the descendants of aboriginals of Papua New Guinea based on morphological features but genetic studies to support Negritos as a branch of African origin are still unavailable (Enfield et al. 2011; Ismail et al. 2013).

The Negritos which is one of the sub-tribes of orang asli are easily recognisable by their morphological features such as dark pigmentation, short stature and wide nose that largely resemble the people in Papua New Guinea aborigines in general (Schurr & Wallace 2002). Besides that, the 'Out of Africa' model suggested Homo Sapiens original in Africa and then dispersed around the world human population (Aghakhanian et al. 2015). The branch of macrohaplogroup M and N found among Malay population are originated from superhaplogroup L3 found mainly in Africa (Ricaut et al. 2009). The argument is that all modern people are ultimately descendants of African. However, there is no documented evidence in research studies to prove that Malays in Malay Peninsula are originated directly from Africa (Ismail et al. 2013).

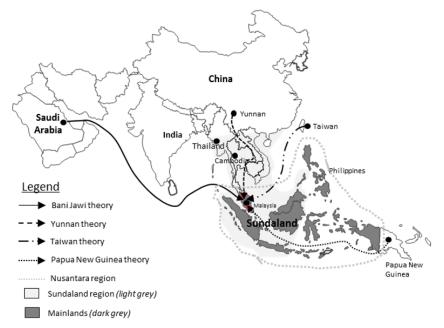


Figure 2. Migration pattern showing the origin of Malays according to developed theories. The highlighted light grey region shows Sundaland during Last Glacial Maximum before the rise of sea levels. The rise in ocean level had submerged Sundaland and spread people to mainlands (Indonesia, Borneo, Philippines and Malaysia) today.

3. The Taiwan theory (1997)

About 6,000 years ago, a certain group of Southern Chinese migrated to Taiwan, then to Philippines and later to Borneo (Lipson et al. 2014). Thereafter, they split into different parts of Malay Archipelago such as Sulawesi, Java, Sumatra and Malay Peninsula all of which speak Austronesian language. The final migration to Malay Peninsula occurred approximately 5,500 years ago (Hill et al. 2007). This migration was proved by a Taiwanese archaeologist, Hsiao Chun Hung and her team when they found green nephrite artifacts from a source in eastern Taiwan that were distributed through the Philippines, East Malaysia, southern Vietnam and peninsular Taiwan between 500 B.C and 500 A.D (Hung et al. 2007). Besides that, all these groups share traceable DNA and linguistic origins in southern China (Isa & Zen 2014).

4. Contradiction to main theories

The three main theories suggested origin of Malays into Peninsular Malaysia are from North to Southeast Asia. However, these theories were rejected by many researchers by saying that the human migration pattern occurred from Southeast Asia to the North. Norliza & Ismawi (2014) highlighted three more theories that show origin of Malays from Sundaland, Nusantara and Bani Jawi. Besides that, recent studies on mitochondrial DNA lineages also show that Malays evolving in Southeast Asia longer than as mentioned in previous theories.

The theory of expansion from Sundaland was suggested by Oppenheimer which depicted the population migration were most likely driven by climate change during the last ice age (Jin et al. 2000). He outlines the rise in ocean levels during the period 14,000 to 7,000 years ago had submerged the Sundaland. This diaspora spread the people westward creating Java, South China Indonesia and the Philippines today. Besides that, the Austronesian language is also believed to be originated from Sundaland and Neolithic revolution might have started from there. This theory was supported by the DNA findings from HUGO (Human Genome Organization) which showed that human movement could only have been northwards during prehistoric times.

Moreover, theory of Malays originated in the Malay Archipelago (Nusantara) was depicted after the great ice age occurred around 2 million to 500,000 years ago. The gradual melting of ice had caused seawater to flood the lowlands and highlands turned into islands. Besides that, volcanic eruptions were actively happening in the mountains a hundred thousand years ago. This caused a separation of Peninsular Malaysia, Sumatra, Java, Borneo and other islands in Indonesia. Human population also have been separated and each sub-populations followed their own customary and traditions.

Furthermore, another theory from an Arab Muslim portrayed the origin of Malays from Bani Jawi/Bangsa Mala. 'Bani Jawi' is an Arabic term referring to people who are from the family of Prophet Abraham who migrated from Arab and settled in Malay Archipelago. The descendants of Prophet Abraham went through the continent of Indian ocean and straight to Malay land. Thereafter, Prophet's children were believed to be the founder of Malay race in Malay Archipelago because the Malay word was derived from the word 'Mala' which is the basis race name of Quanturah (Prophet's third wife).

GENETIC ADMIXTURES OF MALAY SUB-ETHNIC GROUPS

The enigmatic origin of Malays from different regions of Malay Archipelago (Andaman and Nicobar Islands, Brunei, East Malaysia, East Timor, Indonesia, Philippines, Singapore) had reflected various ethnicities and diversified cultures which made them a uniquely complex population to be studied (Yahya et al. 2017). Deutero Malays (ancestors of modern Malays) in Peninsular Malaysia are sub-divided into ten (10) sub-ethnic groups according to their different ancestral lineages that occurred during migrations centuries ago (Embong et al. 2016). The Malay Peninsula was once a strategic trading centre for seafarers through the Straits of Malacca and South China Sea. Therefore, the intermarriages and integration that happened between the locals and seafarers had caused complex genetic admixtures of Malays. In this context, we have reconstructed the historical events of each sub-ethnic group based on the DNA analysis conducted from previous studies (Hatin et al. 2011, 2014). Furthermore, the settlement and distribution of each subethnic groups are indicated as in Figure 3.



Figure 3.Settlement and distributions of Malay subethnic groups in Peninsular Malaysia

Kedah Malays

Kedah was previously known as Kadaram by the ancient Tamils. Historically, it was one of the biggest empires from Myanmar until the North of Peninsular Malaysia. The Empire of Sri Vijaya and later the Cholas had extended their rule over this kingdom around the 4th century. The Bujang Valley in Kedah was well known as an international hub for traders awaiting the change of current and monsoon winds of Indian Ocean (Kuroda 2019; Musa 2015). The first Kedah ruler was Maharaja Merong Mahawangsa had expanded Hindu-Buddhism among his people. Thereafter, he converted his religion to Islam where he subsequently ruled as Sultan Mudzafar Shah (Mohd Fadli Ghani 2020).

The Malay sub-ethnic in Kedah was the biggest and earliest settler in Peninsular Malaysia. There are about 15% of Malays were settled in Kedah state (Anon n.d.). The historical contact of Kedah with Indians, Arabs and other traders had created wide genetic influxes which were proved by the existence of Indian haplogroups in gene pool of northern Malays such as haplogroups M3, K, U2b, R30 and R8 (Maruyama et al. 2010). Furthermore, phylogenetic tree structure and haplotypes sharing analyses conducted by Hatin et al. (2014) also show a major contribution of Indian haplotypes in northern Malays. Besides that, Deutero Malays who are known as present day Malays had genetic admixture with Arab, Sumatran and Siamese (Samri Sainuddin. 2003).

Kelantan Malays

The Kelantan Malays were genetically different from other Malay sub-ethnic groups. A mitochondrial DNA analysis among Kelantan Malays showed high genetic diversity with 76 haplotypes found from 79 individuals. The presence of Mongoloid markers (M7c1c, F, M-C and M-D) along with Polynesian motifs (16217T/C and 16261C/T) and indigenous haplogroups (R11, N21, N22, M21a, M21b, M21d, M45, M45a, M46) depicted that this sub-ethnic group has high affinity towards the Proto-Malay lineage (Edinur et al. 2009).

Besides that, another researcher had established a close genetic relationship of the Kelantan Malays with Indians (especially Telugu and Marathi) and *Orang Asli Semang*. The *Semang* haplogroup is one of the oldest genetic influx from indigenous population centuries ago and is still found among Kelantan Malays (Hatin et al. 2014). This might be due to the culture of Kelantan Malays that is quite firm in choosing life partners among their sub-ethnic group which retains their ancestral genetic flow. Furthermore, archaeological evidence showed that Kelantan Malays have existed in Peninsular Malaysia since Mesolithic era and indigenous Malay populations are found here (Abd Gani et al. 2015).

Minang Malays

The Minang Malays are descendants of Minangkabau people from West Sumatra, Indonesia later who settled mainly at Negeri Sembilan especially in Naning, Sungai Ujong and Rembau. They are adhered to "Adat Perpatih" custom where the descents and inheritance are passed down through matrilineal lineage (Mrazek & Siegel 2002; Reid 2001). In this unique sociological culture, daughters are strongly encouraged to marry their partner from the same sub-ethnic group or else they are not allowed to live on family land. This custom was implemented to ensure the safety of women. This strict wedding culture had retained a similar genetic flow through each generation.

A study found that Minang Malays slightly shared admixture of Indian component, probably occurred before they migrated to Peninsular Malaysia (Hatin et al. 2014). However, the analysis of mitochondrial DNA autosomal single nucleotide polymorphisms (SNPs) shows Minang Malays exhibit none of Chinese ancestral components (SyedHassan et al. 2018). The result is concordance with another study using human leukocyte antigen (HLA) shows DRB1*15-DQB1*05 is the most frequent haplotype among Minang Malays (26%) (Edinur et al. 2009). This haplotype is found common in Indonesian Nusa Tenggara (32%) and Indonesian Molucca (44%) which proved the origin of this sub-ethnic from Indonesia (The Allele Frequency Net Database: http://www.allelefrequencies.net).

Jawa Malays

The modern Jawa Malays in Peninsular Malaysia are descendants from Indonesian Island of Java. They migrated to Johor and Selangor states around 17th century to avoid conflicts with the Dutch colonists who ruled Indonesia in the era between 1880 to 1930 (Joshua Project 2021). Thereafter, this sub-ethnic group had dispersed throughout Peninsular Malaysia in parts of Selangor, Perak and Johor. There are also Jawa Malays living in coastal areas of Sabah (Siti Zainatul Umaroh 2019). A study conducted based on genetic distance measures shows that Melayu Jawa and Indonesian Jawa postulated widespread admixtures with the Chinese population which probably happened before the migrations of Jawa Malays to Peninsular Malaysia (Hatin et al. 2011).

Jawa people have brought economic and social development in Peninsular Malaysia since the 19th century. This was proved by the emergence of their villages known as Kampung Jawa and Parit Jawa in Malacca during the Malacca Sultanate (Khazin Mohd Tamrin 1984). Research conducted on Jawa Malays Y-STR plot showed that close genetic relationship between them and Indonesian Java, suggesting a common ancestry (Syed Hassan et al. 2018). Besides that, a study conducted based on Human Neutrophil Antigen (HNA) loci 5a shows that Jawa Malays have a high HNA-5a allele frequency (0.910) compared with other sub-ethnic groups (Manaf et al. 2015).

Bugis Malays

Bugis Malays are originated from South Sulawesi around 17th century and migrated to Johor. They were sea traders and legendary warriors from Indonesia (Joshua Project 2021). Later on, Bugis people settled in Selangor and dominated politics and economy by establishing the Sultanate of Selangor. A researcher found a close linked genetic relationship between Bugis Malays and Indonesian Teroja since there were originated from the same geographic origin even though geographically separated for hundred years (Hatin et al. 2014).

The assimilation of Bugis into the Malay community through intermarriage causes admixtures events in the genome (Máñez & Ferse 2010). A study conducted based on killer cell immunoglobulin-like receptor (KIR) genes show unique haplotypes among Bugis Malays which are AB23, AB202 and BB71. The presence of these KIR genotypes among this sub-ethnic group shows genetic admixtures between the Malays with Chinese, Arab, Indian and African populations (Wu et al. 2019). Nevertheless, based on Y-STR plot by Syed Hassan et al. (2018) shows that Bugis Malays show less genetic linkage with other Malay sub-ethnic groups which might be due to founder effects. This is because Bugis Malays migrated from Sulawesi to several settlements including, Singapore, Sumatra, Riau and Peninsular Malaysia which could result in a significant decrease in genetic diversity (Abdul Fattah et al. 2011).

Aceh Malays

The relationship between Aceh and Malaysia started when Aceh ruler, Sultan Husain Ali Riayat Syah had defeated Perak ruler, Sultan Mansur Shah I to expand their empire in the year 1573. Thereafter, Perak ruler's eldest son, Raja Alauddin was married to an Aceh princess, Raja Puteri and he was appointed as "Sultan of Aceh". Then, Aceh government sent back Sultan Mansur Shah to rule Perak state under the control of Aceh's government (Encyclopaedia Britannica 2018).

Aceh Malays in Peninsular Malaysia was originated from Sumatra Island which is the province of Aceh. The Aceh people practiced Islam religion and speak Aceh language. This language belongs to the group of Malayo-Polynesian of the Austronesian language family (Yusuf et al. 2013). During the ruling of Perak government by Aceh, many Aceh Malays had migrated to Perak state and settled in villages nearby coastal areas (Abdul Halim Nasir 1999). The evolutionary process had shaped Aceh Malays subethnics in Peninsular Malaysia. Evidence of Aceh stone found at Langkawi Island, Kedah had proved the Islamization of Malay rulers during 13th century (Bustami et al. 2016).

Banjar Malays

Banjar people is a non-Malay ethnic group originated from Banjarmasin, Indonesia. In 1526, the Banjar Prince Samudera has converted his religion to Islam as a condition of receiving help from Jawa army in overthrowing his uncle. Later, he was known as Sultan Suriansyah and spread Islamism throughout South Kalimantan, then followed by his ruling people. The trading and seafaring way of life had caused Banjar people migrated to Peninsular Malaysia by the end of 19th and early 20th century then settled on the west coast (Johor Selangor, Perak) (Noriah Mohamed & Ghazali Basri 2012). In the context of genetic, studies regarding Banjar Malays in Peninsular Malaysia remains scarce. Nevertheless, medical-based studies on Human Neutrophil Antigen and Human Leukocyte Antigen have been conducted showing allele frequencies of Banjar Malays is closely linked to other Asian populations compared with Europeans and Africans (Abd Gani et al. 2015; Edinur et al. 2009; Wan Syafawati et al. 2015).

Rawa Malays

Rawa Malays are a group of Minangkabau people who originated from Pasaman, West Sumatera in between 1773 to 1848. They are also called Ughang Rawo and Ughang Rao. They were farmers, traders, skilled miners, administrators and religious preachers. Fathil et al. (2018) mentioned that Rawa people had left their provinces to search for more profitable activities in Malay Archipelago. Thereafter, the migration between Peninsular Malaysia and Sumatra was more prominent in the era of Malacca Sultanate when it rose as new political power, commercial and Islamic centre in the Malay Archipelago (Yasin et al. 2019).

Rawa Malays entered through coastal ports in Negeri Sembilan first thereafter followed by dissemination to Pahang, Selangor, Perak and Penang by the year 1876. A small town in Perak named Gopeng is well known town for Rawa community who is still preserving their tradition and dialect. Besides that, Raub in Pahang also has the largest concentration of Rawa population because this place was abundant in gold mining activities Suhaila Megat (2020) mentioned that Rawa subethnic is a distinct group whom different from other communities in Sumatra based on the spoken dialect. However, studies using Human Leukocyte Antigen show Minangkabau and Rawa Malays exhibited high similarities in haplotype frequencies suggesting a common origin from Sumatera (Edinur et al. 2009).

Champa Malays

Cham people are descendants of Champa (present day central Vietnam) who migrated to Malaysia between 1975 and 1982. Hinduism was practiced first in Champa, followed by introduction of Islam religion by the mid-19th century. Champa's success in maritime trade wealth had created conflict with the Vietnamese (Danny Wong Tze Ken 2004). This continuous conflict had disappeared Champa from the political map of Southeast Asia and Cham people became refugees (Angie Ngoc Tran 2016). Thereafter, they migrated to neighboring countries especially Cambodia. Thereafter, they suffered great violence in Cambodia during the second Indochina war (1954 – 1975) causing most of the refugees migrated to Kelantan (Rie Nakamura 2019).

During the era of Malay civilization, Malaysia government had decided to treat Cham refugees as Malaysian nationals and integrated into the construction of Cham ethnic identity of Champa Malays. They established Cham colony in Malacca and the evolutionary process causes genetic admixtures between Cham and local Malays (Joachim Schliesinger 2011). There are more than 50,000 Champs Malays in Malaysia. A study conducted based on Human Platelet Antigen shows common genotype HPA -3a/3a and HPA -15a-15b among Champa Malays. Nevertheless, this genotype was also found similar to other Asian populations (Wan Syafawati et al. 2015).

Patani Malays

During the prehistoric time, Patani empire ruled southern part of Thailand (Songkhla, Hat Yai, Satun) until north of Kelantan, Peninsular Malaysia. The Patani Malays are devout Muslim people descended from Malaysian Muslims. They live at the border of cultural ecotone between Thai and Muslim Malay cultures. The differences in cultures caused conflict between Patani Malays and Thai government where situations arose for Patani Malays to fight for their freedom. Thus, some of them had migrated to Peninsular Malaysia to avoid these conflicts (TRT World 2004).

Genetic study conducted by Yahya et al. (2017) found that 20% of analyzed 250 Malay SNPs show Patani and Kedah Malays have genetic influx from Indians. Nevertheless, further researches to find the most informative SNP marker is needed to differentiate Patani Malays from other sub-ethnic groups.

Mandailing Malays

The Mandailing is an ethnic group that originated from Indonesia's North Sumatra Province. They have been Muslims since Minangkabau Malays introduced Islam in Indonesia (Abdur Razzaq Lubis 2003). Mandailing Malays worked as miners and farmers in the middle of 19th century. In the process of evolution, most of Mandailing Malays migrated to West Malaysia through Klang or Penang and then moved inland to lower hill area of Negeri Sembilan, Selangor or Perak (Donald Tugby & Brian Embury 1973). Nevertheless, the population of Mandailing ethnic is the minority which is about 31,000 in Malaysia today (Joshua Project 2021). Thus, the genetic markers of this sub-ethnic group have yet to study.

HAPLOGROUP DIVERSITY AND GENETIC MARKERS USEFUL IN FORENSIC APPLICATION

In this section, we gathered data based on the genetic studies conducted from 2000 to 2021. We noted that haplogroups and haplotypes of Malay population are very wide in Peninsular Malaysia due to various genetic admixtures from Arab, Sundaland, China, Nusantara and India during prehistoric times. Therefore, we have only highlighted some common and unique genetic markers found widely among the indigenous and Malay population in Peninsular Malaysia which has been found in previous studies.

Variants at low frequency could have been difficult to detect without studying the indigenous populations. Orang asli are indigenous people found to be the earliest settlers in Peninsular Malaysia. The genetic discrimination power among them is low because many individuals share the same haplotypes. This might be due to their maintained wedding cultures among orang asli tribes. M21a, M21b and M22 haplogroups are reported consistently observed among aboriginal people (Hill et al. 2006; Jinam et al. 2012; Maruyama et al. 2010; Yew et al. 2018). Besides that, haplogroup R21 was observed at high frequency of 48.28 among analyzed 58 samples from two orang asli population (Kensiu and Jehai) (Jinam et al. 2012; Zainuddin & Goodwin 2004). A research conducted from ancient Negrito hair samples found that their maternal lineage belongs to B4c2 sub-branch of haplogroups B which have mutations at C16147T, A16235G and C16184A (François Xavier Ricaut et al. 2006).

Besides that, Orang Asli is categorized into nineteen sub-tribes as mentioned earlier (Ang et al. 2012; Norhalifah et al. 2016). Eventhough many haplotypes among Negritos are common but discrimination of phylogenetic haplogroups between their sub-tribes must be taken into account for human identification in forensic application. Bidayuh has higher percentage of F1a'c and N9a6a haplogroups frequencies meanwhile Temuan has highest 14 haplotype diversity compared to other sub-tribes and haplogroups M21a, N22 and N21 found to be common among them (Hill et al. 2006; Macaulay et al. 2005). Moreover, Seletar has only five number of haplotypes but their frequency towards haplogroup N9a6 is the highest (71.4%) and unique compared with other sub-tribes (Jinam et al. 2012).

The polymorphism occurred at 16294 region in haplogroup N9a6a were observed among 6.5% of

aboriginal Malays (Hill et al. 2006) meanwhile 9.6% of aboriginal Malay population has haplogroup R9b. Orang asli Mendriq was assigned to F1a1a then Semai carried to M51 and B5a haplogroups respectively. Haplogroup F1a1a is mainly found in aboriginal Senoi groups of the Malay Peninsula (Hill et al. 2007). Sub-groups of Malaysia Negritos were clearly different from East Asia populations where this distinct pattern might be resulted from genetic drift (Aghakhanian et al. 2015).

The evolution of aboriginal Malays had shaped the modern Malay population today. The several waves of migrations among Malay population had caused their genetic haplogroups were widely diversified at 99.47% (Nur Haslindawaty et al. 2010). A study conducted by Zainuddin & Goodwin 2004 had found that the wide haplotype diversity of Malay population had increased the discrimination power to make it useful tool in forensic analysis. Therefore, determination of genetic markers is vital among the diversified Malay population whom are majority in Peninsular Malaysia. Researcher found a common haplotypes among Malay population where mitochondrial DNA mutations occurred at positions of 73, 146, 150, 195, 263, 315.1C, 16140, 16182C, 16183C, 16189, 16217, 16274, 16335 (Nur Haslindawaty et al. 2010). These genetic markers can be used to distinguish Malay population with other population, but differentiation between sub-ethnic groups of Malay needed more markers to increase the discrimination power.

Furthermore, sequencing control region polymorphisms in mitochondrial DNA of modern Malays noted that some individuals have unclassified M* haplogroup suggest the presence of old genetic influxes among them (Maruyama et al. 2010). This unclassified haplogroup proved the unique nature and highly diverse for the modern Malay population. Their research also found that Malay population may constitute new branch of R30 haplogroup. Nevertheless, R30 lineage can only be determined using coding region mutations because non-coding region mutations were different from reported Indian haplotype. Besides that, Mörseburg et al. 2016 found haplogroups B4a1a and M7b1a2a1 are typical markers of Malayo-Polynesian speaking populations like Malays.

Furthermore, Tuladhar et al. (2015) found the most frequent mitochondrial DNA HVI haplotype (3.88%) is defined by mutation at nucleotide position 16233 C \rightarrow T transition in Malay population which also found in South Indians, Argentine, Taiwanese Han, Japanese, Russian, Korea ethnic Chinese and indigenous Indian tribe populations. Meanwhile, the most frequent mitochondrial DNA HVII haplotype (6.79%) was defined by polymorphism at nucleotide position 73 and 263 A \rightarrow G transition, 249 A-del and the insertion of a C-residues at 309.1C and 315.1C in Malay population.

CONCLUSION

In conclusion, we must agree that human origin in Malaysia is complex especially among Malay population in Peninsular Malaysia. The theories relating origin of Malays are shackled by speculations and archeological evidences. However, researcher should be cautious for interpreting the origin of Malays based on the stone tools found at excavation sites because migration happen as continuous process. Thus, stone tools found by archaeologists might not indicate the actual origin and lead to false-positive results. Based on the literature review the theory of Nusantara is closely linked to genetic findings about origin of Malays. Despite of the theories developed, the migration and dispersal of Malays are most relatable during the Malacca Sultanate since 15th century which rooted from Srivijaya-Jambi government.

Based on the review above, Peninsular Malaysia comprises different genetic or ancestral lineages of people from Semang, Senoi, Proto-Malays, Chinese and Indian. The several waves of migration in pre-historic times caused genetic admixtures in the descendants of ancient subpopulations in Peninsular Malaysia. The history of subethnic groups among Malay population in Peninsular Malaysia is fairly contentious with different perspectives being held by different scholars. Therefore, genetic analysis must be conducted on each sub-ethnic groups of Malay population to identify their ancestral lineages and informative markers which can be used in future forensic application for human identification.

We have highlighted several genetic studies conducted on Malay sub-population in Peninsular Malaysia. Researchers have successfully found few informative markers which are common and unique within Malays. Nevertheless, there are few limitations in these studies that drives the urge to conduct an improved genetic research in future. Ishar et al. (2019) mentioned that more variations needed to be analyzed to increase the discrimination power of SNP markers. Besides that, low number of samples can lead false positive results by giving higher percentage of haplogroup frequencies. Macrohaplogroups contain similar pattern of mutations in the gene pool, but mutations which can distinguish each branch of specific haplogroups are necessary to differentiate Malay sub-population.

Last but not least, further studies have to be conducted to build more genetic markers and larger sample size may provide an extensive view on the composition structure of Malay population in Peninsular Malaysia. Close genetic linkage exists between shared haplotype among population could aid in in forensic identification of victims.

ACKNOWLEDGMENT

We are thankful to Universiti Kebangsaan Malaysia for the financial assistance and also for providing the facilities to carry out this project.

FUNDING

This study was supported by UKM GGPM grant (GGPM 2020-025)

AVAILABILITY OF DATA AND MATERIALS

The datasets generated during and analyzed during the current study are available from the corresponding author on reasonable request.

CONSENT FOR PUBLICATION

Written informed consent was obtained from all participants for the publication of this report and any accompanying images.

COMPETING INTEREST

The authors decline that they have no competing interest.

REFERENCES

- Abd Gani, R., Manaf, S. M., Zafarina, Z., Panneerchelvam, S., Chambers, G. K., Norazmi, M. N. & Edinur, H. A. 2015. Molecular blood group typing in Banjar, Jawa, Mandailing and Kelantan Malays in Peninsular Malaysia. *Transfusion and Apheresis Science* 53(1): 69–73.
- Abdul Halim Nasir. 1999. *Sejarah Perak.* Kuala Lumpur: Jabatan Muzium.
- Abdur Razzaq Lubis. 2003. Transformation of Mandailing Cultural Identity and Leadership. *Journal of the Malaysian Branch of the Royal Asiatic Society* 76(1): 55–79.
- Aghakhanian, F., Yunus, Y., Naidu, R., Jinam, T., Manica, A., Hoh, B. P. & Phipps, M. E. 2015. Unravelling the genetic history of Negritos and Indigenous populations of Southeast Asia. *Genome Biology and Evolution* 7(5): 1206–1215.
- Andaya, L. Y. 2008. Leaves of the same tree: Trade and ethnicity in the straits of Melaka. Honolulu, Hawaii: University of Hawai'i Press.
- Ang, K. C., Ngu, M. S., Reid, K. P., Teh, M. S., Aida, Z. S., Koh, D. X. R., Berg, A., et al. 2012. Skin color variation in Orang Asli tribes of Peninsular Malaysia. *PLoS ONE* 7(8).

- Anon. (n.d.). Orang Melayu Kedah. Wikipedia Bahasa Melayu, ensiklopedia bebas. https://ms.wikipedia. org/wiki/Orang Melayu Kedah [20 July 2021].
- Benjamin, G. 2013. Why have the peninsular "Negritos" remained distinct? *Human Biology* 85(1–3): 445–484.
- Benjamin, G. 2018. On Being Tribal in the Malay World. Dlm. Benjamin (pnyt.) & Chou (pnyt.). Tribal Communities in the Malay World, hlm. 7–76. Singapore: Institute of Southeast Asian Studies.
- Breurec, S., Guillard, B., Hem, S., Brisse, S., Dieye, F. B., Huerre, M., Oung, C., et al. 2011. Evolutionary history of helicobacter pylori sequences reflect past human migrations in southeast Asia. *PLoS ONE* 6(7).
- Bustami, R., Suyatno & Wekke, I. S. 2016. Migrants in Nusantara: Indonesian and Malaysian Perspectives. *Journal of Nusantara Studies* 1(2): 63–74.
- Danny Wong Tze Ken. 2004, March. Vietnam-Champa Relations and the Malay-Islam Regional Network in the 17th–19th Centuries | Kyoto Review of Southeast Asia. Kyoto Review of Southeast Asia. https:// kyotoreview.org/issue-5/vietnam-champa-relationsand-the-malay-islam-regional-network-in-the-17th-19th-centuries/ [20 July 2021].
- Donald Tugby & Brian Embury. 1973. The Persistence of the Mandailing Languae in West Malaysia. Southeast Asian Journal of Social Science 1(2): 29–33. Retrieved from https://www.jstor.org/ stable/24489988
- Donohue, M. & Denham, T. 2011. Languages and genes attest different histories in Island Southeast Asia. *Oceanic Linguistics* 50(2): 536–542.
- Edinur, H. A., Zafarina, Z., Spínola, H., Nurhaslindawaty, A. R., Panneerchelvam, S. & Norazmi, M. N. 2009. HLA polymorphism in six Malay subethnic groups in Malaysia. *Human Immunology* 70(7): 518–526.
- Embong, A. M., Jusoh, J. S., Hussein, J. & Mohammad, R. 2016. Tracing the Malays in the Malay Land. *Procedia - Social and Behavioral Sciences* 219: 235–240. doi:10.1016/j.sbspro.2016.05.011
- Encyclopaedia Britannica. 2018, April 27. Aceh | province, Indonesia. Encyclopedia Britannica. https://www. britannica.com/place/Aceh [20 July 2021].
- Enfield, N. J. 2011. *Dynamics of Human Diversity in Mainland Southeast Asia*. Pacific Linguistics, Research School of Pacific and Asian Studies, The Australian National University
- Fahmi, W. 2004. Origin of Malay People. The Malay Adventurer. https://themalayadventurer.wordpress. com/2014/05/03/origin-of-malay-people/ [19 July 2021].
- Fathil, F., Sulong, W. S. W. & Manaf, N. F. A. 2018. Rawa Migration to the Malay Peninsula In The 19th Century: The Case of Pahang, Perak and Selangor. Al-Shajarah: *Journal of Islamic Thought and Civilization* 27–50.

- Fattah, R. A. A., Rusdi, M. & Abdullah, M. A. 2011. Penghijrahan Masyarakat Bugis ke Alam Melayu: Kajian Kes Bugis di Indragiri Hilir Riau. Seminar Serumpun Melayu V, hlm. 1–21. Makassar: Universitas Hasanuddin Makassar Indonesia.
- Ghani, M. F. 2020. Kedah: Kerajaan Islam pertama di Tanah Melayu. Harakah Daily. https://harakahdaily. net/index.php/2020/01/15/kedah-kerajaan-islampertama-di-tanah-melayu/ [20 July 2021].
- Hatin, W. I., Nur-Shafawati, A. R., Etemad, A., Jin, W., Qin, P., Xu, S., Jin, L., et al. 2014. A genome wide pattern of population structure and admixture in peninsular Malaysia Malays. *HUGO Journal* 8(1): 1–18.
- Hatin, W. I., Nur-Shafawati, A. R., Zahri, M. K., Xu, S., Jin, L., Tan, S. G., Rizman-Idid, M., et al. 2011. Population genetic structure of peninsular Malaysia Malay sub-ethnic groups. *PLoS ONE* 6(4): 2–6.
- Hays, J. 2015. Semang (Negritos), Senoi, Temiar and Orang Asli of Malaysia. Facts and Details. https:// factsanddetails.com/southeast-asia/Malaysia/ sub5_4c/entry-3647.html#chapter-9 [17 July 2021].
- Hill, C., Soares, P., Mormina, M., Macaulay, V., Clarke, D., Blumbach, P. B., Vizuete-Forster, M., et al. 2007. A mitochondrial stratigraphy for Island Southeast Asia. *American Journal of Human Genetics* 80(1): 29–43.
- Hill, C., Soares, P., Mormina, M., Macaulay, V., Meehan, W., Blackburn, J., Clarke, D., et al. 2006. Phylogeography and ethnogenesis of aboriginal Southeast Asians. *Molecular Biology and Evolution* 23(12): 2480–2491.
- Hung, H. C., Iizuka, Y., Bellwood, P., Kim, D. N., Bellina, B., Silapanth, P., Dizon, E., et al. 2007. Ancient jades map 3,000 years of prehistoric exchange in Southeast Asia. *Proceedings of the National Academy of Sciences of the United States of America* 104(50): 19745–19750.
- Isa, N. M. & Zen, I. H. 2014. The Making of Malaysian Heterogeneous Society and Theories of the Origin of Malays. Dlm. Z.F.Nordin (pnyt.). Bahasa Melayu Sebagai Bahasa Agama : Daripada Klasik kepada Moden, hlm. 272–287. Sintok, Kedah: Pusat Pengajian Umum, UUM.
- Ishar, S. M., Parameswaran, K., Masduki, N. S. & Rus Din, R. D. 2019. Variations in mitochondrial DNA control region among Malay and Chinese subpopulations (sequence 16000–16200). *Mitochondrial DNA Part* A: DNA Mapping, Sequencing, and Analysis 30(8): 843–847.
- Ismail, E., Amini, F., Razak, S. A., Zaini, H. M., Farhour, R. & Zilfafalil, B. A. 2013. Peninsular Malaysia's negrito orang asli and its theory of african origin. *Sains Malaysiana* 42(7): 921–926.

- Jin, L., Seielstad, M. & Xiao, C. 2000. Genetic, Linguistic and Archaeological Perspectives on Human Diversity in SouthEast Asia. Recent advances in human biology. Yunnan, China: World Scientific Publishing Company.
- Jinam, T. A., Hong, L. C., Phipps, M. E., Stoneking, M., Ameen, M., Edo, J. & Saitou, N. 2012. Evolutionary history of continental southeast asians: Early train hypothesis based on genetic analysis of mitochondrial and autosomal DNA data. *Molecular Biology and Evolution* 29(11): 3513–3527.
- Jinam, T. A., Phipps, M. E., Aghakhanian, F., Majumder, P. P., Datar, F., Stoneking, M., Sawai, H., et al. 2017. Discerning the Origins of the Negritos, First Sundaland People: Deep Divergence and Archaic Admixture. *Genome Biology and Evolution* 9(8): 2013.
- Joshua Project. 2021. People Groups. Ministry of Frontier Ventures. https://joshuaproject.net/people_groups/ MY [20 July 2021].
- Khazin Mohd Tamrin. 1984. Orang Jawa di Selangor, penghijrahan dan penempatan, 1880-1940. Kuala Lumpur: Dewan Bahasa dan Pustaka, Kementerian Pelajaran, Malaysia.
- Khoo, S. N. & Lubis, A.-R. 2005. *Kinta Valley: Pioneering Malaysia's Modern Development*. Ipoh: Perak Academy.
- Kossak, S. M. & Watts, E. W. 2001. The Art of South and Southeast Asia. (S. M. Kossak, Ed.). New York: The Metropolitan Museum of Art.
- Kuroda, K. 2019. A Migrants 'World from South Thailand to Kedah — A History of Inland Kedah. *Journal of General Studies* 3: 15–39.
- Lipson, M., Loh, P. R., Patterson, N., Moorjani, P., Ko, Y. C., Stoneking, M., Berger, B., et al. 2014. Reconstructing Austronesian population history in Island Southeast Asia. *Nature Communications* 5: 1–7.
- Macaulay, V., Hill, C., Achilli, A., Rengo, C., Clarke, D., Meehan, W., Blackburn, J., et al. 2005. Single, rapid coastal settlement of Asia revealed by analysis of complete mitochondrial genomes. *Science* 308(5724): 1034–1036.
- Manaf, S. M., NurWaliyuddin, H. Z. A., Panneerchelvam,
 S., Zafarina, Z., Norazmi, M. N., Chambers, G. K.
 & Edinur, H. A. 2015. Human neutrophil antigen profiles in Banjar, Bugis, Champa, Jawa and Kelantan Malays in Peninsular Malaysia. *Blood Transfusion* 13(4): 610–615.
- Máñez, K. S. & Ferse, S. C. A. 2010. The history of Makassan trepang fishing and trade. *PLoS ONE* 5(6).
- Maruyama, S., Nohira-Koike, C., Minaguchi, K. & Nambiar, P. 2010. MtDNA control region sequence polymorphisms and phylogenetic analysis of Malay population living in or around Kuala Lumpur in Malaysia. *International Journal of Legal Medicine* 124(2): 165–170.

- Md-Zain, B. M., The, M. S., Ang, K. C., Lim, L. S. & Yaakop, S. 2017. Phylogenetic relationships of the Orang Asli (Proto Malay) tribe based on the HVS II gene sequences. *Malaysian Applied Biology* 46(4): 35–42.
- Mörseburg, A., Pagani, L., Ricaut, F. X., Yngvadottir, B., Harney, E., Castillo, C., Hoogervorst, T., et al. 2016. Multi-layered population structure in Island Southeast Asians. *European Journal of Human Genetics* 24(11): 1605–1611.
- Mrazek, R. & Siegel, J. T. 2002. Engineers of Happy Land: Technology and Nationalism in a Colony. *Indonesia* 74(4): 167.
- Musa, M. 2015. The Memory of the Word Register: The Sultan Abdul Hamid Correspondence and Kedah History. *Kajian Malaysia* 32(1): 53–74.
- Nakamura, R. 2019. Becoming Malay: The Politics of the Cham Migration to Malaysia. *Studies in Ethnicity* and Nationalism 19(3): 289–306.
- Norhalifah, H. K., Syaza, F. H., Chambers, G. K. & Edinur, H. A. 2016. The genetic history of Peninsular Malaysia. *Gene* 586(1): 129–135.
- Noriah Mohamed & Ghazali Basri. 2012. Masyarakat Banjar Johor. Johor: Yayasan Warisan Johor.
- Nur Haslindawaty, A. R., Panneerchelvam, S., Edinur, H. A., Norazmi, M. N. & Zafarina, Z. 2010. Sequence polymorphisms of mtDNA HV1, HV2, and HV3 regions in the Malay population of Peninsular Malaysia. *International Journal of Legal Medicine* 124(5): 415–426.
- Rahman, N. H. S. N. A. 2016. A Commentary on the Relationship between Peninsular Malaysia and Yunnan During the Prehistoric Era. *Jurnal Arkeologi Malaysia* 7(0).
- Reid, A. 2001. Understanding Melayu (Malay) as a source of diverse modern identities. *Journal of Southeast Asian Studies* 32(3): 295–313.
- Ricaut, François X., Razafindrazaka, H., Cox, M. P., Dugoujon, J. M., Guitard, E., Sambo, C., Mormina, M., et al. 2009. A new deep branch of eurasian mtDNA macrohaplogroup M reveals additional complexity regarding the settlement of Madagascar. *BMC Genomics* 10: 1–9.
- Ricaut, François Xavier, Bellatti, M. & Lahr, M. M. 2006. Ancient mitochondrial DNA from Malaysian hair samples: Some indications of Southeast Asian population movements. *American Journal of Human Biology* 18(5): 654–667.
- Samri Sainuddin. 2003. *Titas : Tamadun Melayu. Tanjong Malim*, Perak: Quantum Books.
- Schliesinger, J. 2011. *Ethnic groups of Cambodia*, hlm. Vol. 3. White Lotus Press.
- Schurr, T. G. & Wallace, D. C. 2002. Mitochondrial DNA diversity in Southeast Asian populations. *Human Biology* 74(3): 431–452.

- Siti Zainatul Umaroh. 2019, November 17. Kisah Orang Jawa yang tak jadi bagian dari Melayu. Antara News. https://www.antaranews.com/berita/1167079/kisahorang-jawa-yang-tak-jadi-bagian-dari-melayu [20 July 2021].
- Spriggs, M. 2011. Archaeology and the Austronesian expansion: Where are we now? *Antiquity* 85(328): 510–528.
- Suhaila Megat. 2020, November 28. Asas dialek Bahasa Rawa di Perak . The Malaya Post. https://www. themalayapost.my/asas-dialek-bahasa-rawa-diperak/ [20 July 2021].
- SyedHassan, S. R., Aedrianee, A. R., Sundararajulu, P., Mohd, N. N. & Abdullah, Nur Azeelah Zainuddin, Z. 2018. Paternal lineage affinity of the Malay subethnic and Orang Asli populations in Peninsular Malaysia. *International Journal of Legal Medicine* 132(4): 1087–1090.
- Tran, A. N. 2016. Weaving Life Across Borders: The Cham Muslim Migrants Traversing Vietnam and Malaysia.
 Dlm. Lian Kwen Fee (pnyt.), Mizanur Rahman (pnyt.), & Yabit bin Alas (pnyt.). International Migration in Southeast Asia - Continuities and Discontinuities, hlm. 1st Edisi ., Vol. 2, 13–37. California: Springer.
- TRT World. 2004, October 25. How Patani-Malay Muslims refuse to be swallowed by Thailand's mainstream. TRT World. https://www.trtworld.com/ magazine/how-patani-malay-muslims-refuse-tobe-swallowed-by-thailand-s-mainstream-40837 [20 July 2021].
- Tuladhar, B. S., Rashid, N. H. A., Panneerchelvam, S. & Nor, N. M. 2015. Sequence Polymorphism of Mitochondrial Dna Hypervariable Regions I and Ii in Malay Population of Malaysia. *Scientific World* 12(12): 24–29.
- Tweedie, M. W. F. 1953. The Stone Age in Malaya. Journal of the Malayan Branch of the Royal Asiatic Society 26(162): 3–90.
- Van Nguyen, L., Ta, T. K. O. & Tateishi, M. 2000. Late Holocene depositional environments and coastal evolution of the Mekong River Delta, Southern Vietnam. *Journal of Asian Earth Sciences* 18(4): 427–439.
- Wain, A. 2012. Chinese Muslims and the Conversion of Melaka to Islam. *International Proceedings of Economics Development and Research* 51(9): 35–40.
- Wan Syafawati, W. U., Norhalifah, H. K., Zefarina, Z., Zafarina, Z., Panneerchelvam, S., Norazmi, M. N., Chambers, G. K., et al. 2015. Allele frequencies of human platelet antigens in Banjar, Bugis, Champa, Jawa and Kelantan Malays in Peninsular Malaysia. *Transfusion Medicine* 25(5): 326–332.
- Wey, A. L. K. & Harun, A. L. 2018. Grand strategy of the Malacca Sultanate, 1400–1511. *Comparative Strategy* 37(1): 49–55.

- Wu, D., Dou, J., Chai, X., Bellis, C., Wilm, A., Shih, C. C., Soon, W. W. J., et al. 2019. Large-Scale Whole-Genome Sequencing of Three Diverse Asian Populations in Singapore. *Cell* 179(3): 736-749.e15.
- Y.Andaya, L. 2014. Orang Asli and the Melayu in the History of the Malay Peninsula. *Journal of the Malaysian Branch of the Royal Asiatic Society* 75(282): 23–48.
- Yahya, P., Sulong, S., Harun, A., Wan Isa, H., Ab Rajab, N. S., Wangkumhang, P., Wilantho, A., et al. 2017. Analysis of the genetic structure of the Malay population: Ancestry-informative marker SNPs in the Malay of Peninsular Malaysia. *Forensic Science International: Genetics* 30: 152–159.
- Yasin, Z., Hwai, A. T. S., Abdullah, A. L. & Razalli, N. 2019. The Ocean Legacy of Malaka and Sustainability in the Straits of Malacca. *Journal of Ocean and Culture* 2: 59–73.
- Yew, C. W., Lu, D., Deng, L., Wong, L. P., Ong, R. T. H., Lu, Y., Wang, X., et al. 2018. Genomic structure of the native inhabitants of Peninsular Malaysia and North Borneo suggests complex human population history in Southeast Asia. *Human Genetics* 137(2): 161–173.
- Yusuf, Y. Q., Pillai, S. & Najwa, N. T. A. 2013. Speaking Acehnese in Malaysia. *Language and Communication* 33(1): 50–60. doi:10.1016/j.langcom.2012.08.004
- Zainuddin, Z. & Goodwin, W. 2004. Mitochondrial DNA profiling of modern Malay and Orang Asli populations in peninsular Malaysia. *International Congress Series* 1261(C): 428–430.

Shalini Parthipan

Forensic Science Program, Faculty of Health Sciences,

Forensics UKM, Basement 1 PTSL,

Universiti Kebangsaan Malaysia,

43600 Bangi

Selangor, Malaysia

*Seri Mirianti Ishar

Forensic Science Program, Faculty of Health Sciences,

Forensics UKM, Basement 1 PTSL,

Universiti Kebangsaan Malaysia,

43600 Bangi,

Selangor, Malaysia.

*Corresponding author:

Seri Mirianti Ishar Email: seri.ishar@ukm.edu.my