



Short population report

The pattern of HLA-A, -B and -DRB1 alleles and haplotypes of four Malay sub-ethnic groups namely Kelantan, Champa, Patani and Mandailing Malays of Peninsular Malaysia

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A B S T R A C T

“Bumiputra” or “son of the soil” is a term used to represent the Malays and other indigenous populations of Malaysia. The Malays are Austronesian speaking population and originated from different parts of the Indo-Malay Archipelago. The migration of Malay population from different parts of Indo-Malay Archipelago were mainly due to trading purposes which shaped the current Malay sub-ethnic groups with unique culture and with distinctive dialects. In this study, HLA typing was carried out using Sequence-based Typing (SBT) method on 109 individuals comprising of four Malay sub-ethnic groups namely Kelantan (n = 28), Champa (n = 29), Patani (n = 25) and Mandailing (n = 27) Malays. The HLA data is available in the Allele Frequencies Net Database (AFND).

Malays are an Austronesian language speaking population living in the geographical region extending from the west of Indochina to the Bismark Island, known as Indo-Malay Archipelago [1]. Archaeological and linguistic studies have suggested that the movements of Austronesian speakers were from Taiwan (1500BC) to Philippines, Indonesia and further to Borneo and finally reached Peninsular Malaysia by 500BC [1]. However, this finding is contested by studies using genetic approach. Study by Oppenheimer using mitochondrial genetic markers suggested that the origin of Austronesian speaking population is actually within Southeast Asia 13,000 to 17,000 years ago and expansion from Southeast Asia to Philippines and Taiwan happened 7,000 to 14,000 years ago [2].

The early Malay speaking groups settled in the Malay Peninsula and founded several ancient maritime trading states and kingdoms. Due to trading activities, there were migrations of populations within the Indo-Malay Archipelago, which contributed to the presence of various Malay sub-ethnic groups in Malaysia [1]. In this study, Kelantan, Mandailing, Champa and Patani Malay sub-ethnic groups were studied.

Kelantan is located at the north-eastern coast of Malay Peninsula. The geographic location of Kelantan provided opportunity for the Kelantan Malays to interact with population in the north part of Malay Peninsula [3]. Patani is a district in Thailand located in close proximity with the Malaysia-Thailand border. Patani was once a strong Malay empire before it fell to the Siamese government in the 1785. As a result of this, there was a population exodus from Patani to Malaysia [3]. Champa Malays are originated from Vietnam and they are Austronesian speaking population. By the 1490s, Champa was absorbed by

Vietnamese government and due to this, many Champa people migrated out of their original homeland to different countries [4]. Mandailing people originated from the northern part of Sumatra Island in Indonesia. Civil war in West Sumatera from 1821 until 1838 further increased the migration of the Mandailing people to the West of Peninsular Malaysia [5]. Study on the genetic makeup of these Malay sub-ethnic groups could give a more refined information on the genetic diversity exhibited in the Malay population. In addition to that, the genetic relationship between these Malay sub-ethnic groups could be studied and correlated with the historical information.

Kelantan (n = 28), Champa (n = 29), Patani (n = 25) and Mandailing (n = 27) Malays were studied using HLA-Sequence Based Typing (SBT) method. The inclusion criteria for sample selection were; Malay descendent from three un-admixed generations and healthy. The locations where the samples were collected are shown in Fig. 1. Ethical approval for this study was obtained from the Research Ethics Committee, Universiti Sains Malaysia.

HLA-A, -B and -DRB1 loci were typed using Secore® HLA Sequencing kit by Invitrogen Corp., and the alleles were identified using uType® software by Thermo Fisher Scientific Incorporation. IMGT/HLA database release 3.13.1 was used. Samples that produced ambiguous results were sent to Life Technologies at Wisconsin, United States in order to resolve the ambiguity.

Several statistical parameters were studied namely the allele and haplotype frequencies and Hardy Weinberg Equilibrium (HWE) using Arlequin software version 3.5 [6]. The exact test of HWE shows no deviation except for Kelantan Malays for HLA-A locus.

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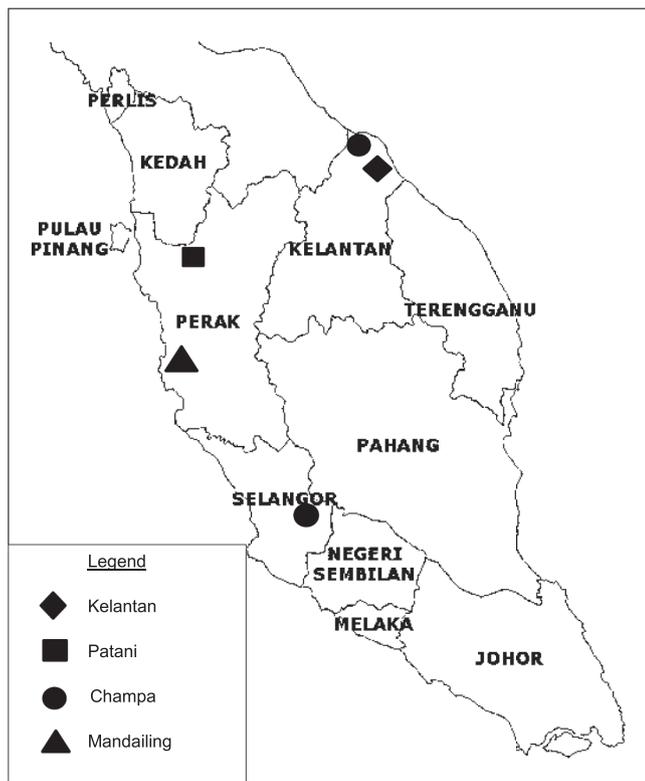


Fig. 1. Map of Peninsular Malaysia showing the approximate geographical locations of the sample collection.

The HLA genotypes, allele frequencies (see Supplementary Tables 1–3) and haplotypes frequencies (see Supplementary Tables 4–7) of the studied Malay sub-ethnic groups are available in the Allele Frequency

Net Database (AFND) under the population name “Malaysia Kelantan” (AFND3438), “Malaysia Champa” (AFND3424), “Malaysia Patani” (AFND3437) and “Malaysia Mandailing” (AFND3439) [7].

Conflict of interest

There is no conflict of interest.

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Appendix A. Supplementary material

Supplementary data to this article can be found online at <https://doi.org/10.1016/j.humimm.2019.02.015>.

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