



UNIVERSITI
TEKNOLOGI
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Institut
Pengajian
Siswazah

THE DOCTORAL RESEARCH ABSTRACTS

Volume: 13, Issue 13

April 2018

13th ISSUE



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Title : HAPLOTYPE PROFILING AND PHYLOGENETIC TREE DEVELOPMENT OF *ORANG ASLI* POPULATION IN PENINSULAR MALAYSIA USING Y-STR AND AUTOSOMAL STR

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The aborigines are only 0.5% of the entire population of Peninsular Malaysia, typically living secluded together in their own tribe. This reduces inter-tribal marriage and mating. They have been assigned to tribes and sub tribes through physical appearances such as the colour of their skin, the structure of their nose and their hair. Short tandem repeats (STR) that can be found in Y-chromosome of human male is called Y chromosome short tandem repeat (Y-STR) while the microsatellites found in the autosomal chromosomes are called the autosomal STR. The objective of this study were to construct haplotypes, to calculate allele frequency and haplotype frequency, to calculate the haplotype diversity and discrimination capacity of the haplotype, to calculate gene diversity and locus diversity and to construct phylogenetic network for *Orang Asli* using SWGDAM-recommended Y-STRs and CODIS recommended autosomal STRs. Y-STR used in this study were SWGDAM-recommended haplotype consisted of DYS19, DYS385 a/b, DYS389 I/II, DYS390, DYS391, DYS392, DYS393, DYS438 and DYS439. Markers of autosomal STR are from the Combined DNA Index System (CODIS) database selected by American Federal Bureau of Investigation. After ethical approval of JAKOA and UiTM were obtained, buccal swabs of 276 *Orang Asli* individuals were collected and saved on FTA cards. All samples were run through Polymerase Chain Reaction (PCR) and the fragments obtained were analyzed. Several samples were selected for sequencing for number of repeats validation. Haplotype profiling revealed 164 distinct haplotypes obtained from 184 samples using Y-STR while 167 haplotype were found

from 167 samples using autosomal STR. The haplotypes showed 100% discrimination capacity for autosomal STR markers while only 90.76% for Y-STR with haplotype diversity for Y-STR and autosomal STR 0.9987 and 1.000 respectively. Average heterozygosity was found to be the highest in Proto Malay. Senoi and Negrito showed the least genetic distance between tribe when analyzed using both markers which were 0.064 and 0.039 when using Y-STR and autosomal STR respectively. Y-STR revealed Senoi and Proto Malay to be the most distant tribes with genetic distance value of 0.165. On the other hand, the most distant tribes according to autosomal STR were Negrito and Proto Malay with the value 0.106. AMOVA analyses showed that the differences were found to be more abundant within populations for both type of markers with the range of percentage variance between 82-98%. Percentages of variances obtained among the populations were between 2-18%. Phylogenetic analysis showed clusters that reflect the tribes affiliation better when using Y-STR pairwise distances compared to autosomal STR distances. Y-STR markers are better than autosomal STR in grouping *Orang Asli* individuals into their respective tribes as assigned by physical attributes. In conclusion, Y-STR and autosomal STR can be used to find the differences between tribes. However, the subtribes are too close to one another, no clear pattern can be obtained using said markers. However, more samples of *Orang Asli* that includes more subtribes from different locations should be included in future studies to provide better conclusion.