

UNIVERSITI TEKNOLOGI MARA

**GENETIC DIVERSITY AND
PHYLOGENETIC RELATIONSHIP OF
SIX MALAYS SUB-ETHNIC GROUPS IN
PENINSULAR MALAYSIA AS INFERRED FROM
AUTOSOMAL *ALU* INSERTION
POLYMORPHISM**

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ABSTRACT

Alu insertion polymorphisms is referred to those relatively several elements that presence in the genomes of some individuals and absence from others. The insertions of *Alu* elements are approximately 300 bp in length that mobilise via the process of retroposition. *Alu* insertion has several advantages as compared to other polymorphic markers. Firstly, they are identical by descent (IBD), mean all chromosomes carrying a polymorphic *Alu* element are inherited from common ancestor and once inserted they do not appear to be subject to loss or rearrangement. Thus it will reflect both the maternal and paternal history of a population. Malays are the largest ethnic groups in Malaysia which can be divided into 14 sub-ethnic groups based on their migration history hundred years ago. Even though Malays ethnic have believed to be one of genetically diverse population but the number of studies which focus on their genetic information and population structure is very limited. In this study we showed the genetic diversity and phylogenetic tree of six Malays sub-ethnic groups from eight autosomal *Alu* loci that frequently use in population genetic studies (A25, ACE, APO, DI, B65, FXIIB, PV92, and TPA25). The eight *Alu* loci were typed in 208 of healthy and unrelated individuals from six Malays sub-ethnic groups (Minangkabau-Malays, Jawa-Malays, Bugis-Malays, Banjar-Malays, Rawa-Malays, and Kelantan-Malays). All selected individual were restricted to inclusion factor of three pure generations. All *Alu* loci were polymorphic in all sub-ethnics. Analyses of, eight *Alu* insertion markers generate differentiation variation pattern among six Malays sub-ethnic groups studied. The F_{ST} value of all *Alu* loci for populations in this study was 0.0464 which demonstrate there is little genetic subdivision occur as the value was less than 0.05. The positive value of F_{IS} and F_{IT} indicate that there was an excess of homozygotes and the population might be inbred. The phylogenetic tree constructions from A25, ACE, APO, DI and FXIIB *Alu* loci for six Malays sub-ethnic groups in this study reveal that Bugis-Malays, Banjar-Malays and Jawa-Malay were closely grouped together whereas Minangkabau-Malays was group with Rawa-Malays. Meanwhile, Kelantan-Malays population might have separated earlier than Java Sea population and could have had ancestry which more divergent as they present at a more basal position for all phylogenetic trees constructed compared to other Malays sub-ethnic. The information obtained from this study could be used as additional information for genetic differentiation among Malays sub-ethnic groups and essential data in order determine the origin of Malays in Peninsular Malaysia.

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