ANALYSIS OF THE GENETIC STRUCTURE OF THREE SARAWAKIAN ETHNIC GROUPS FROM EAST MALAYSIA

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The population of Malaysia is shaped by multi-ethnic complexity. The majority of the population is formed by Malay people, while nearly one third is Chinese and approximately ten percent is Indians. Malaysia, therefore, is a blend of languages, religions, and cultures in which the Malays are thought to be admixed descendants of Proto-Malays by intermarriages with late arrival populations. Complex historical events and a number of migration waves may have contributed to the complexity of genetic lineages and admixture in Peninsular Malaysia. Nevertheless, the genetic make-up of sub-populations currently living in Malaysia is still poorly explored.

In the presented study, we performed analysis of the genetic structure of three ethnic groups (Iban, Bidayuh, and Melanau) of Sarawak, an East Malaysia state on the island of Borneo, where more than half of the population is composed of indigenous people. The ForenSeq DNA Signature Prep kit (Verogen) which includes autosomal, X and Y STR markers, and identity-, ancestry- and phenotype-informative SNPs was used to exhibit the genetic pattern of studied groups. The sequencing was performed on an Illumina MiSeq FGx system.

Low F_{st} values, based on the variation in autosomal STR loci, suggest an extensive rate of the gene flow among the three ethnic groups and thus reduced genetic differentiation among individuals. The ForenSeq UAS principal component analysis (PCA) specifies the East Asian biogeographical ancestry of most DNA samples. The results contribute to a more complex characterization of the genetic structure of the population of Malaysia. The analysis will be complemented by exploration of Y-chromosome markers and mitochondrial DNA (mtDNA). Finally, the study will supplement forensic databases of autosomal STR, Y-STRs, and mtDNA.