

Population Data and Forensic Evaluation of Six Alu insertions in Indigenous groups from Sabah, Malaysia

Abstract

Background and aim: The present study is the first to report the genetic relatedness of indigenous populations of Sabah, Malaysia, using a set of Indel markers (HS4.32, TPA25, APO, PV92, B65 and HS3.23). The primary aim was to assess the genetic relationships among these populations and with populations from other parts of the world by examining the distribution of these markers. Subjects and methods: A total of 504 volunteers from the three largest indigenous groups, i.e. Kadazan-Dusun, Bajau and Rungus, were recruited for the study. Six Alu insertions were typed by PCR with specific primer sets. Results: All insertions were found to present at different frequencies, ranging from 0.170–0.970. The heterozygosity of most of the markers was high (.0.4), with the exception of HS3.23 and APO. A genetic differentiation study revealed that these populations are closely related to each other ($G_{ST} \approx 0.006$). A principle component plot showed that these populations have higher affinity to Mainland South East Asia/East Asia populations, rather than Island Southeast Asia (ISEA) populations. Conclusion: In summary, these indigenous groups were closely associated in terms of their genetic composition. This finding also supports the colonization model of ISEA, which suggests that the inhabitants of this region were mostly descendants from Southern China.