Mitochondrial DNA hypervariable region (HVS-I) analysis of Semoq Beri population in Peninsular Malaysia

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Abstract

Orang Asli is the earliest inhabitants that still practicing traditional lifestyle and has been recognised as indigenous to the country. The molecular interest on Orang Asli started from dispersal of prehistoric population by the ancient “Out of Africa” migration to other continents. In this study, DNA sequence of the mitochondrial hypervariable region I (HVS-I) was analysed among 40 unrelated Semoq Beri population in Hulu Terengganu as an initial effort to determine the sequence variation and haplogroup identification. Totally, seven haplotypes containing 18 polymorphic sites and neither deletion nor insertion were found in 481 bp long. A total of five haplogroups were identified which are haplogroups M74 (35,078.9 ± 7,152.0 ya), M21a (22,822.7 ± 7,891.2 ya), H2a3 (5,203.8 ± 3,219.3 ya), R21 (4,100 – 5,100 ya) and N9a6b (171 ya). The earliest age estimations were within Late Pleistocene until the end of Last Glacial Maximum period. The distribution of those haplogroups except H2a3 located within the Southern Mongoloid and South East Asia, thus showing bottleneck population. This study speculated that: (1) a total of five series of prehistoric migration occurred; (2) there was a possibility that the Semoq Beri ancestry was originated from Sunda shelf and (3) there was likely a minor Late Glacial/early postglacial dispersal from Sunda shelf into Peninsular Malaysia and Southern Borneo.

Keywords: Orang Asli; Semoq Beri; hypervariable segment; haplogroup; migration

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