Insight of the Orang Asli population in Peninsular Malaysia

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Abstract

Peninsular Malaysia is a part of the mainland Southeast Asia with multi-racial ethnic groups including the Orang Asli population. Orang Asli is believed to be the earliest inhabitants of Malaysia Peninsula and distributed mostly in central, northern and southern part of the peninsular. They were grouped into the Semang, Senoi and Proto Malay based on linguistic and culture diversity. The objective of this research is to study the genetic variation of Orang Asli population in Peninsular Malaysia using high throughput SNP genotyping method. A total of 154 unrelated individuals from 14 sub tribes of Orang Asli were genotyped using Affymetrix Genome Wide Human 6.0 Array. We also included the Yoruba, Indian Telugu and Malay population data as the additional study population. Based on the genetic differences among the 14 sub-tribes of Orang Asli, Semang Lanoh shows a greater divergence from the other Semang tribes but significantly closer to Senoi Temiar. Semang Kensiu and Semang Kintaq were genetically closer to each other (Fst = 0.019). The Proto Malay tribes; Jakun, Semelai and Temuan are closer to each other while Senoi Jah Hut and Semai shows to be genetically closer to Proto Malay Temuan. The genetic variations of 14 tribes of Orang Asli were presented in 2D and 3D model of MDS analysis. Semang subgroups cluster closely together with exception for Lanoh which dispersed at the centre of the plot near to Senoi Temiar. The Semaq Beri distributed upwards on the right side of the plot, Semai and Temiar form their own cluster at the centre and bottom right of the plot. The Proto Malay tribes form a cluster together with the Senoi Che Wong and Jah Hut. The distance genetic data provide a brief view into the Orang Asli sub-tribes however by applying model based approach, the ancestry and the admixture of the population can be link providing new insights into their backgrounds.

Keywords: Orang Asli; SNP genotyping; genetic variations

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