

Genetic relatedness of indigenous ethnic groups in northern Borneo to neighboring populations from Southeast Asia, as inferred from genome-wide SNP data

ABSTRACT

The region of northern Borneo is home to the current state of Sabah, Malaysia. It is located closest to the southern Philippine islands and may have served as a viaduct for ancient human migration onto or off of Borneo Island. In this study, five indigenous ethnic groups from Sabah were subjected to genome-wide SNP genotyping. These individuals represent the "North Borneo"-speaking group of the great Austronesian family. They have traditionally resided in the inland region of Sabah. The dataset was merged with public datasets, and the genetic relatedness of these groups to neighboring populations from the islands of Southeast Asia, mainland Southeast Asia and southern China was inferred. Genetic structure analysis revealed that these groups formed a genetic cluster that was independent of the clusters of neighboring populations. Additionally, these groups exhibited near-absolute proportions of a genetic component that is also common among Austronesians from Taiwan and the Philippines. They showed no genetic admixture with Austro-Melanesian populations. Furthermore, phylogenetic analysis showed that they are closely related to non-Austro-Melanesian Filipinos as well as to Taiwan natives but are distantly related to populations from mainland Southeast Asia. Relatively lower heterozygosity and higher pairwise genetic differentiation index (F_{ST}) values than those of nearby populations indicate that these groups might have experienced genetic drift in the past, resulting in their differentiation from other Austronesians. Subsequent formal testing suggested that these populations have received no gene flow from neighboring populations. Taken together, these results imply that the indigenous ethnic groups of northern Borneo shared a common ancestor with Taiwan natives and non-Austro-Melanesian Filipinos and then isolated themselves on the inland of Sabah. This isolation presumably led to no admixture with other populations, and these individuals therefore underwent strong genetic differentiation. This report contributes to addressing the paucity of genetic data on representatives from this strategic region of ancient human migration event(s).