

# Unravelling the Genetic History of Negritos and Indigenous Populations of Southeast Asia

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## Abstract

Indigenous populations of Malaysia known as Orang Asli (OA) show huge morphological, anthropological, and linguistic diversity. However, the genetic history of these populations remained obscure. We performed a high-density array genotyping using over 2 million single nucleotide polymorphisms in three major groups of Negrito, Senoi, and Proto-Malay. Structural analyses indicated that although all OA groups are genetically closest to East Asian (EA) populations, they are substantially distinct. We identified a genetic affinity between Andamanese and Malaysian Negritos which may suggest an ancient link between these two groups. We also showed that Senoi and Proto-Malay may be admixtures between Negrito and EA populations. Formal admixture tests provided evidence of gene flow between Austro-Asiatic-speaking OAs and populations from Southeast Asia (SEA) and South China which suggest a widespread presence of these people in SEA before Austronesian expansion. Elevated linkage disequilibrium (LD) and enriched homozygosity found in OAs reflect isolation and bottlenecks experienced. Estimates based on  $N_e$  and LD indicated that these populations diverged from East Asians during the late Pleistocene (14.5 to 8 KYA). The continuum in divergence time from Negritos to Senoi and Proto-Malay in combination with ancestral markers provides evidences of multiple waves of migration into SEA starting with the first Out-of-Africa dispersals followed by Early Train and subsequent Austronesian expansions.

**Key words:** Negritos, Senoi, Proto-Malay, population genetics, SNPs.

## Introduction

The events and period of prehistoric peopling of Southeast Asia (SEA) have been controversial. Human remains from archeological sites such as Callao Cave in Philippines (Mijares et al. 2010) and Niah Cave in Malaysia (Barker et al. 2007) suggest that SEA was populated by anatomically modern humans approximately 50–70 kilo years ago (KYA). In 2009, a large-scale genome-wide study by the HUGO-Pan Asia consortium showed that all East Asians and Southeast Asians originated from a single wave “Out-of-Africa” via a southern coastal route (HUGO Pan-Asia SNP Consortium 2009). Thereafter, two models have been proposed to explain subsequent migrations involved in shaping today's SEA populations. The Out-of-Taiwan model refers to the Austronesian language expansion that occurred around 5,000–7,000 years before the present. This replaced the pre-existing

Australoid people with Austronesian agriculturists (Diamond and Bellwood 2003; Bellwood 2005). In the long period between the first initial Out-of-Africa and the recent “Out-of-Taiwan” migrations, recent genetic studies on mitochondrial DNA (mtDNA) suggest an Early Train wave of migration during the late Pleistocene to early Holocene (Hill et al. 2006, 2007; Soares et al. 2008; Karafet et al. 2010; Jinam et al. 2012).

The rich ethnological diversity that exists in Peninsular Malaysia provides a great opportunity to study SEA prehistory. The current Malaysian population comprises three major ethnic groups including Malay, Chinese, and Indians. In addition to these groups, Peninsular Malaysia is home to other ethnicities including several minor indigenous communities collectively known as “Orang Asli” (OA) or “Original People.” Making up approximately 0.6% of Malaysian population, OA has been classified into three groups, namely