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## Admixture Patterns and Genetic Differentiation in Negrito Groups from West Malaysia Estimated from Genome-wide SNP Data

Timothy A. Jinam

*Department of Genetics, School of Life Science, Graduate University for Advanced Studies (SOKENDAI), Mishima, Japan*

Maude E. Phipps

*School of Medicine and Health Sciences, Monash University (Sunway Campus), Selangor, Malaysia*

Naruya Saitou

*Division of Population Genetics, National Institute of Genetics, Mishima, Japan, [saitounr@lab.nig.ac.jp](mailto:saitounr@lab.nig.ac.jp)*

The Hugo Pan-Asian SNP Consortium

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## **Abstract**

Southeast Asia houses various culturally and linguistically diverse ethnic groups. In Malaysia, where the Malay, Chinese, and Indian ethnic groups form the majority, there exist minority groups such as the "negritos" who are believed to be descendants of the earliest settlers of Southeast Asia. Here we report patterns of genetic substructure and admixture in two Malaysian negrito populations (Jehai and Kensiu), using ~50,000 genome-wide single-nucleotide polymorphism (SNP) data. We found traces of recent admixture in both the negrito populations, particularly in the Jehai, with the Malay through principal component analysis and STRUCTURE analysis software, which suggested that the admixture was as recent as one generation ago. We also identified significantly differentiated nonsynonymous SNPs and haplotype blocks related to intracellular transport, metabolic processes, and detection of stimulus. These results highlight the different levels of admixture experienced by the two Malaysian negritos. Delineating admixture and differentiated genomic regions should be of importance in designing and interpretation of molecular anthropology and disease association studies.

## **Keywords**

Admixture, Negrito, Indigenous, Structure

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## ***Admixture Patterns and Genetic Differentiation in Negrito Groups from West Malaysia Estimated from Genome-wide SNP Data***

TIMOTHY A. JINAM,<sup>1,2,\*</sup> MAUDE E. PHIPPS,<sup>3</sup> NARUYA SAITOU,<sup>2,1,4†</sup> AND THE HUGO PAN-ASIAN SNP CONSORTIUM

**Abstract** Southeast Asia houses various culturally and linguistically diverse ethnic groups. In Malaysia, where the Malay, Chinese, and Indian ethnic groups form the majority, there exist minority groups such as the “negritos” who are believed to be descendants of the earliest settlers of Southeast Asia. Here we report patterns of genetic substructure and admixture in two Malaysian negrito populations (Jehai and Kensiu), using ~50,000 genome-wide single-nucleotide polymorphism (SNP) data. We found traces of recent admixture in both the negrito populations, particularly in the Jehai, with the Malay through principal component analysis and STRUCTURE analysis software, which suggested that the admixture was as recent as one generation ago. We also identified significantly differentiated nonsynonymous SNPs and haplotype blocks related to intracellular transport, metabolic processes, and detection of stimulus. These results highlight the different levels of admixture experienced by the two Malaysian negritos. Delineating admixture and differentiated genomic regions should be of importance in designing and interpretation of molecular anthropology and disease association studies.

The Southeast Asian region represents an intriguing avenue into the study of human population genetics, given the rich ethnic diversity of the region. The general consensus from various population genetic studies are the African origin of modern human populations based on mitochondrial, Y-chromosomal, and autosomal DNA markers (e.g., Underhill 2003; Li et al. 2008; Stoneking and Delfin 2010). With

<sup>1</sup>Department of Genetics, School of Life Science, Graduate University for Advanced Studies (SOKENDAI), Mishima, Japan.

<sup>2</sup>Division of Population Genetics, National Institute of Genetics, Mishima, Japan.

<sup>3</sup>School of Medicine and Health Sciences, Monash University (Sunway Campus), Selangor, Malaysia.

<sup>4</sup>Department of Biological Sciences, School of Science, University of Tokyo, Tokyo, Japan.

\*Present address: Division of Human Genetics, National Institute of Genetics, Mishima, Japan.

†Correspondence to: Naruya Saitou, Division of Population Genetics, National Institute of Genetics, Mishima, 411-0831 Japan. E-mail: [saitounr@lab.nig.ac.jp](mailto:saitounr@lab.nig.ac.jp).