

Evolutionary History of Continental Southeast Asians: “Early Train” Hypothesis Based on Genetic Analysis of Mitochondrial and Autosomal DNA Data

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The complete mtDNA sequences for all 86 individuals have been submitted to DDBJ/EMBL/Genbank (accession nos. AP012346–AP012431).

Abstract

The population history of the indigenous populations in island Southeast Asia is generally accepted to have been shaped by two major migrations: the ancient “Out of Africa” migration ~50,000 years before present (YBP) and the relatively recent “Out of Taiwan” expansion of Austronesian agriculturalists approximately 5,000 YBP. The Negritos are believed to have originated from the ancient migration, whereas the majority of island Southeast Asians are associated with the Austronesian expansion. We determined 86 mitochondrial DNA (mtDNA) complete genome sequences in four indigenous Malaysian populations, together with a reanalysis of published autosomal single-nucleotide polymorphism (SNP) data of Southeast Asians to test the plausibility and impact of those migration models. The three Austronesian groups (Bidayuh, Selatar, and Temuan) showed high frequencies of mtDNA haplogroups, which originated from the Asian mainland ~30,000–10,000 YBP, but low frequencies of “Out of Taiwan” markers. Principal component analysis and phylogenetic analysis using autosomal SNP data indicate a dichotomy between continental and island Austronesian groups. We argue that both the mtDNA and autosomal data suggest an “Early Train” migration originating from Indochina or South China around the late-Pleistocene to early-Holocene period, which predates, but may not necessarily exclude, the Austronesian expansion.

Key words: Austronesian, Negrito, mitochondrial DNA, Southeast Asia, Orang Asli.

Introduction

The Southeast Asian region is home to a rich variety of human populations, each with their own ethnic cultures and traditions. The history and diversity of the various indigenous groups that still populate the region had been described by using archaeological, linguistic, and most recently, genetic data. Archaeological evidence points to the presence of modern humans in Southeast Asia at least 40,000 years before present (YBP) (Brothwell 1960; Barker et al. 2007). Those early migrants eventually reached the Sahul landmass, which today is split into Papua New Guinea, Australia, and Tasmania (Leavesley and Chappell 2004; O’Connell and Allen 2004). That ancient wave of migration was believed to have brought the ancestors of several “Australoid” populations found in Southeast Asia and Australia. These include the Papuans and Australian Aboriginals, as well as several groups in the Andaman,

Philippines, and West Malaysia, which are collectively known as Negritos (Cavalli-Sforza et al. 1994). Up until the Last Glacial Maximum approximately 20,000 YBP, the current islands of Sumatra, Java, and Borneo were joined together to the Asian mainland, forming a landmass known as Sundaland (Glover and Bellwood 2004), which was separated from the Sahul landmass by multiple islands collectively referred to as Wallacea; Wallace’s line separates Wallacea and Sundaland (fig. 1).

Another significant epoch with respect to human migrations in island Southeast Asia occurred much later during the mid-Holocene period (5,000–7,000 YBP). With Taiwan as the probable starting point, this migration wave eventually spread southward throughout island Southeast Asia and into the islands of Oceania, bringing with it agriculture, domesticated livestock, and Austronesian languages (Bellwood 2005). This “Out of Taiwan” migration was largely supported by