

## **A Genetic Focus on the Peopling History of East Asia**

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Past human migrations throughout the world have left significant signatures in the genetic patterns of present human populations, such as sharp genetic clines, tight correlations between genetic and geographic distances, and/or relevant relationships with linguistic families. In particular, genetic studies on the peopling history of East Asia have revealed a complex genetic structure with a main differentiation between northern and southern populations, heterogeneous levels of genetic diversity and uneven distributions of some genetic lineages. These results have led to competing hypotheses on the settlement history of the area that are still disputed today.

In this presentation, we summarize alternative scenarios put forward by different geneticists on the peopling history of East Asia, and we present our recent findings based on the analyses of the major histocompatibility complex (MHC) in humans, the HLA polymorphism. We propose a model where human populations followed two main migration routes from western Asia eastwards along both sides of the Himalayas, followed by northward and southward migrations overlapping in East Asia. The likelihood of this scenario is currently tested by computer simulation analyses against an alternative scenario of a unique southern route. We also propose to discuss with linguists and archaeologists alternative models of human migrations, e.g. those related to the domestication of rice and/or the expansion of linguistic families, that would be worth testing by computer simulations with different sets of genetic markers.