[2] New Insights on the Peopling History of East Asia according to HLA Markers

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The genetic and linguistic differentiation between northern and southern East Asians has been revealed in many studies on human peopling history of the region. Genetics has shown its power in tracing the origin of East Asian populations as well as that of linguistic families. In our study, we collected and analyzed the data of five highly polymorphic HLA loci. These data include the genetic makeup of about 127,000 individuals belonging to 84 distinct populations representing all the main East Asian linguistic families. We observe a generally continuous differentiation from the northernmost Altaics to the Sino-Tibetans, and to speakers of other southern linguistic families. Some HLA alleles are unevenly distributed: while some alleles observed in northern populations are widespread at the global level, some alleles observed in southern populations are virtually unique in Asia. The general HLA genetic variation is also characterized by a decrease of diversity from north to south, although a reverse pattern appears when only those alleles restricted to Asia are considered. These results reflect a more complex migration history than that assumed by the ‘‘southern-origin’’ hypothesis, in that a genetic contribution of ancient human migrations through a northern route has probably been quite substantial. We thus propose a new model where northward and southward opposite migrations occurring at different periods overlapped. We suggest that present speakers of Altaic and other linguistic families may represent the descendents of migrants from the northern and southern routes, respectively. During the last 5,000 years, a main southward expansion of Altaics and Sino-Tibetans eventually shifted an initially more northern genetic boundary to its actual location along Yangtze River.