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Presentation Title: Investigating the origin of Transeurasian languages: common ancestry hypothesis or language contact theory.

Research Focus: Anthropology, Population Genetic, Language Contact, Historical Linguistics

Abstract

Striking lexical and grammatical similarities found among the Japonic, Koreanic, Turkic, Tungusic, and Mongolic languages have been a topic of intense interest among linguists. The Transeurasian hypothesis has been formulated to explain these similarities. This hypothesis suggests that Turkic, Tungusic, and Mongolic form an Altaic macro-language family. Altaic, Japonic and Koreanic then form a Transeurasian macro-language. As such, linguistic similarities are explained by the evolution of Japonic, Koreanic, Turkic, Tungusic, and Mongolic from a common proto-Transeurasian language. An alternative socio-linguistic language contact approach to the Transeurasian hypothesis would view Japonic, Koreanic, Turkic, Tungusic, and Mongolic as part of a northeast Asian *Sprachbund*. As such, linguistic similarities stem from close geographical proximity and borrowing that has evolved over a prolonged period of time due to intense contact between the speakers of these languages. Here, we attempted to examine the complex question of the origin of Transeurasian languages from a multiplicity of disciplinary perspectives.

Within the context of genetics, we studied Y-chromosomal haplogroup frequency distribution in Japonic-, Koreanic-, Turkic-, Tungusic-, and Mongolic-speaking populations. The results of principal component and correspondence analyses revealed three distinct clusters on the genetic landscape of Central and East Asia, namely Turkic, Koreanic-Japonic, and Tungusic-Mongolic groups. We also investigated haplotype diversity within the haplogroup C2-M217, which is considered as a putative genetic marker for exploring the Transeurasian hypothesis. While the haplogroup is one of the most frequently encountered lineages in most of the Turkic-, Tungusic-, and Mongolic-speaking populations, the highest rates of its haplotype diversity were detected in the Japonic, Koreanic and Turkic groups. Additionally, we revealed a strong clustering of Korean and Japanese haplotypes, with the former ones being widely scattered on a network.

We also considered the archaeological and historical record. The ancestors of contemporary Transeurasian language speaking populations survived and thrived due to complex combination of factors that may have begun with successful adaptation to climate change during the Last Glacial Maximum. Altaic languages flourished due to mobile pastoralism, the successful domestication of the horse in Central Asia and reindeer in Northern Eurasia, the adoption of sedentary agriculture in some regions, and the expansion and demise of nomadic societies such as the Mongol Empire. The phenomenon of language shift stands as another factor that should not

be neglected. In contrast to Altaic languages, the archaeological and historical records reflect that geographical and cultural isolation played a substantial role in the evolution of Koreanic and Japonic language families. Furthermore, rice cultivation clearly distinguishes the evolution of Koreanic and Japonic with that of Altaic. Korean and Japanese now occupy a huge corner of the global linguistic tapestry because their ancestors found a survival strategy that supports a very high population density.

The Transeurasian hypothesis presupposes that contemporary Japonic-, Koreanic-, Turkic-, Tungusic-, and Mongolic-speaking populations all diverged from a common ancestral population. Our research suggests that such an assumption is inconsistent with the genetic, archaeological and historical evidence. We would expect closer genetic distances between the populations and more similar archaeological and historical data. Rather, language contact theory seems to better explain linguistic similarities shared by these languages families.