

Genes and language in the prehistory of Uralic-speaking peoples

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Abstract

Recent work on the genetic background of Uralic speaking populations provides a new example of the correlation of genetic and linguistic histories. Tambets et al. (2018) and Lamnidis et al. (2018) indicate that bulk of studied Uralic speaking populations has retained a trace of common genetic origins, as well as identifying the cases where this does not hold true.

Examples of *superstrata* influence includes first of all the influence Proto-Germanic has had on Proto-Finno-Saamic. The Germanic speakers are presumed to have had stronger linguistic influence as the higher prestige community even though the type of archeological finds associated with Germanic peoples are restricted to very small area of the speaker area. However, the associated genetic admixture has to be specifically tested with genetic work.

Estonian instead is an example of *genetic replacement* within a language population. When the speakers of the proto-Finnic language arrived from the east to the Baltic Sea coasts they encountered speakers of Proto-Balto-Slavic. Current DNA studies show that Estonians resemble their Baltic neighbours more than they resemble other Uralic speaking populations.

Within North Russia *language shift* can be demonstrated clearly: The place names and historical sources indicate a large distribution of some western Uralic language variants, but currently the area is Russian speaking. The genetic studies support this by showing that the North Russian population resembles Uralic speaking populations more than Slavic speaking populations. Other potential cases of ancient language shift demonstrated by a combination of linguistic, genetic and archaeological evidence include a shift of a non-Uralic speaking population to Saamic languages in the Bronze Age in Eastern Scandinavia, followed by later linguistic and genetic admixture with Finnic speakers.

Despite significant differences in the ways of visualising genetic and linguistic relationships (modern population geneticists compare genetic distances rather than family trees), comparison of these results can provide important evidence for clarifying and explaining pattern of diversity, as well as generating testable hypotheses about historical scenarios in the less well documented languages and populations to the east.

Lamnidis, T.C., et al. 2018. "Ancient Fennoscandian Genomes Reveal Origin and Spread of Siberian Ancestry in Europe." *BioRxiv*, March, 285437. <https://doi.org/10.1101/285437>.

Tambets, K., et al. 2018. Genes reveal traces of common recent demographic history for most of the Uralic-speaking populations. *Genome Biology* 19:139. <https://doi.org/10.1186/s13059-018-1522-1>