Eastern Finnic populations: genetic structure inferred from genome-wide and Y-chromosome data in light of historical data Natalia Kuznetsova[1], Vyacheslav Kuleshov[2]

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There is a certain consensus between archaeologists, linguists and geneticists that the Proto-Finnic populations have developed about 3000 years ago (Lang 2024: 416). Eastern Finnic populations, including Karelians, Veps, Votes, Ingrians, and Ingrian Finns, are a significant component of the Finnic history. However, they still remain understudied, also from the genetic point of view (but see e.g. Ilumäe et al. 2016; Tambets et al. 2018; Balanovska, Chernevskiy & Balanovsky 2021; Németh & Szeverényi 2024 mentioning some of those groups).

In this work (cf. Agdzhoyan et al. 2024), we explore the gene pools of Karelians (Northern, Tver, Ludic, and Livvi), Veps, Ingrians, Votes, and Ingrian Finns using both Y-chromosome markers (N=357) and genome-wide autosomes (N=123). The data is analysed with statistical, bioinformatic, and cartographic methods.

The autosomal gene pool of eastern Finnic populations can be divided into two large categories based on our results of PCA and ADMIXTURE modeling:

a) “Karelia” — Veps, Northern, Ludic, Livvi, and Tver Karelians;
b) “Ingria” — Ingrians, Votes, Ingrian Finns.

This clustering reflects the major areal groupings of the populations in question.

The Y-chromosomal gene pool of Eastern Finnic populations is more diverse than the autosomal gene pool and contains three main genetic components:

a) “Northern” — prevails in Northern Karelians and Ingrian Finns;
b) “Karelian” — prevails in Livvi, Ludic, and Tver Karelians;
c) “Southern” — prevails in Votes.

Ingrians and Veps occupy intermediate positions. Both are close to Northern Russians (which are outside the aforementioned three clusters) but also gravitate towards each other and to Novgorod Russians (which are part of the “Southern” cluster, together with Votes), while Ingrians additionally gravitate towards the “Northern” and the “Karelian” cluster.

We argue that this general Y-chromosome clustering reflects the genetic ancestry of all the popupations in question. In particular, our phylogeographic analysis has found that the Y-haplogroup N3a4-Z1927 carriers are frequent among most Eastern Finnic populations, as well as among some Northern Russian and Central Russian populations. This haplogroup is also frequent on the territory of Finland (Preussner et al. 2024). The founder of this haplogroup lived about 2400 years ago, but a rapid population growth among his descendants, according to the analysed data, occurred about 1700-2000 years ago. This growth chronologically corresponds to the archaeological period of the so-called “typical” *Tarand* graves (I-IV c. AD), characteristic of Estonia, northern and western Latvia, south-western Finland and north-western Russia during the Roman Iron Age (Lang 2018: 174-77, 306-7). The Y-haplogroup N3a4, however, is relatively rare among Estonians (Ilumäe et al. 2016), so its founder might have rather originated from a territory outside the center of the Tarand culture, potentially from its easternmost part which was a starting point for the Finnic migrations to the east.

In the talk, our genetic findings will be discussed in the context of what is known about the Eastern Finnic groups from the archaeological, linguistic, and other historical sources.

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