

# Genome analysis shows common origin of Pskov, Novgorod and Yakutia populations

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Scientists have for the first time compared complete genome data of different ethnic groups in Russia. Using a special algorithm, they traced the genetic history for some groups. In the future, such data can be used

in other important studies. For example, it can help to identify genetic risk factors in various populations of Russian people. The results are published in *Genomics*.

The Russian Federation is a large country uniting many nationalities and populations. However, their genetic diversity is still understudied. Existing studies have considered either a specific population or a part of the [genome](#). At the same time, a comparison of whole genome data from different populations can reveal information about the spread of diseases and resistance. Therefore, St. Petersburg State University initiated the Russian Genomes project, in which scientists from various organizations have created a database of Russian population genetic data.

The scientists analyzed 204 genome datasets of different populations from other papers and added 60 new genomes from Pskov, Novgorod and Yakutia. In all, 264 representatives of 55 ethnic groups were examined during the study.

The researchers used a special program written at ITMO University to predict the [demographic history](#) for three of these populations. This demographic history describes the population development: How and when they were one ancestral population, how the population size changed, and the rates of their migration.

"We developed a program to search for the optimal demographic [history](#) according to the genomes of samples of the populations. This required calculation and analysis of the occurrence frequency of different alleles. The program then built many demographic histories to find out which of them is more appropriate for this data," says Ekaterina Noskova from the Laboratory of Computer Technologies at ITMO University.

It turned out, for example, that in the past, the current inhabitants of Pskov, Novgorod and Yakutia were one [population](#) of about 2000

people. But 7000 years ago, the Yakuts separated from it, and about 1,200 years ago, representatives of Pskov and Novgorod divided. Since then, all three populations began to grow sharply in numbers.

According to scientists, comparing the genomes of [different populations](#), as well as their development histories, helps to understand which gene variants cause diseases, and which protect from them. Therefore, for the next step of this study, the researchers plan to carefully analyze the data and look for correlations with diseases.

**More information:** Daria V. Zhernakova et al, Genome-wide sequence analyses of ethnic populations across Russia, *Genomics* (2019). DOI: [10.1016/j.ygeno.2019.03.007](https://doi.org/10.1016/j.ygeno.2019.03.007)

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