



# Genetic study of the Rurik Dynasty

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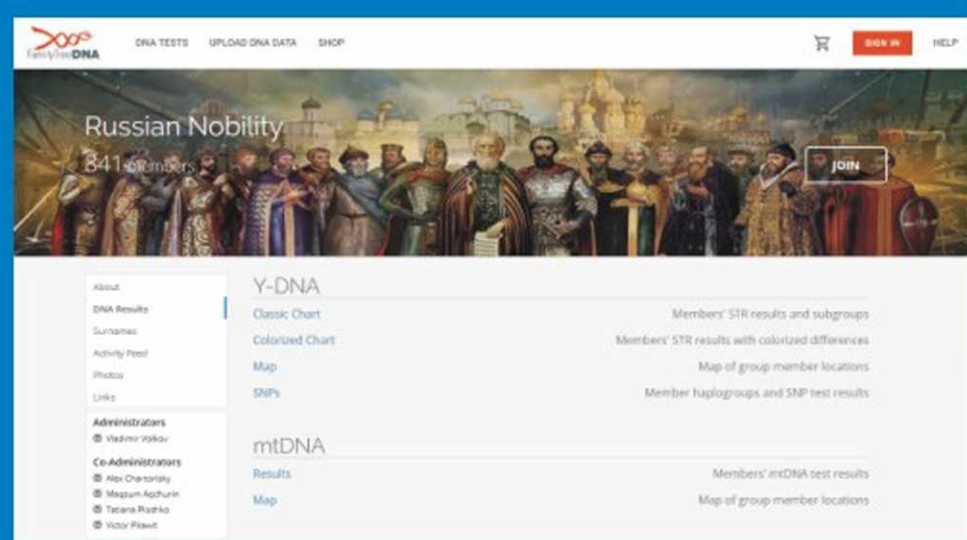
## Introduction

The House of Rurik (Rurikids) is one of the oldest dynasties of Europe. Rurik the founder of the dynasty lived at the end of the IX century. The House of Rurik ruled Kievan Rus' and its successor states, including the Grand Duchy of Moscow and the Tsardom of Russia, until the 17th century. Presently the descendants of Rurik live in various locations across the globe.



Initiated in 2006 by Nikita Maksimov and Andrey Seslavin the "Rurikid Genome" project was started with candidates being selected (based on their documented genealogy as being descendants of Rurik) to undergo DNA testing.

Most of the samples were obtained by Andrey Seslavin the head of the international DNA research project "Rurikids - Russian princes". Also considerable work on the collection and financing of the processing of samples was carried out by Polish colleagues: Andrzej Bajor, Tomasz Lenczewski and Marek Jerzy Minakowski.



The main work of organizing the sequencing process and on financing the project was carried out by the heads of the "Russian Nobility DNA Project": Vladimir Volkov and Alex Chartorisky.

## Materials and methods

From 2006 to 2017 over 40 DNA samples were obtained from living members of the Rurikid Dynasty and processed through DNA testing, the eventual results grouped the participants into 3 haplogroups (N1c1, R1a1, and I2a1). The group that had the highest frequency and was also the most interrelated was the group belonging to subclade N-Y4339 (40%) represented by the following genealogical lines (Massalsky, Puzyna, Lobanov-Rostovsky, Khilkov, Gagarins, Putyatin, Rzhhevsky, Tatishchev, Kropotkin, and Shakhovskiy).

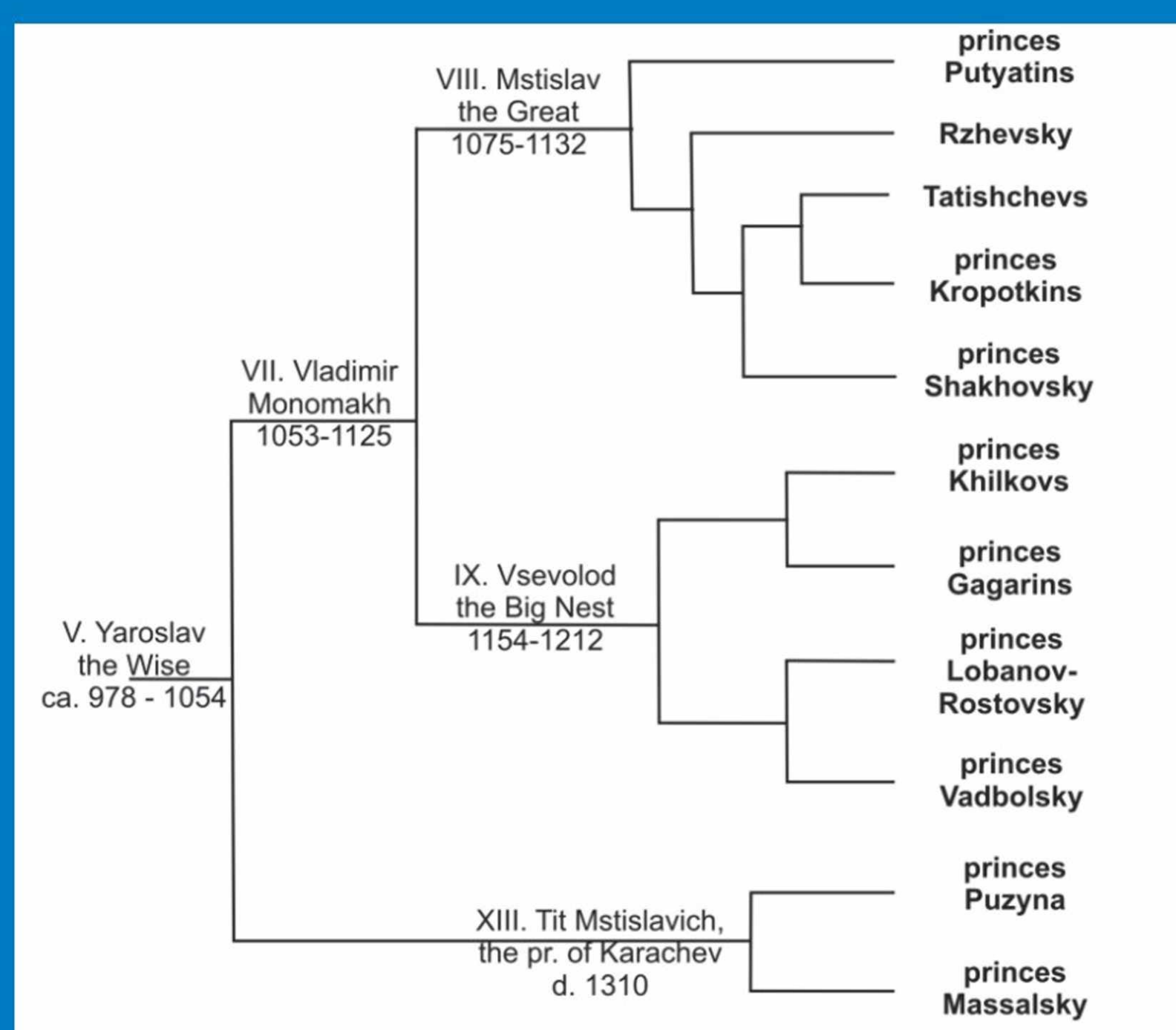


Figure 1. A brief version of the Rurikid pedigree according to P.V. Dolgorukov. The ancestors of the genealogical lines and the generation of Rurik are indicated.

The DNA samples of these genealogical lines of Rurikid underwent extensive sequencing of the Y chromosome (BigY test) in the laboratories of Family Tree DNA in Houston (USA), and the concluding results established the degree of paternal kinship.

## Results and Discussion

Within the haplogroup N-Y4339 there is a common SNP shared by the entire Rurikid group, that SNP being Y10931 and while the presences of other certain SNP's convincingly shows that the Rurikid group N-Y10931 is divided into three branches. One branch determined by SNPs VL15, VL16, VL17 and VL18 (princes Massalsky and Puzyna), the second by VL11 (princes Lobanov-Rostovsky, Gagarin and Putyatin) and the third by VL12 (princes Kropotkin and Shakhovskiy, Rzhhevsky and Tatishchev).

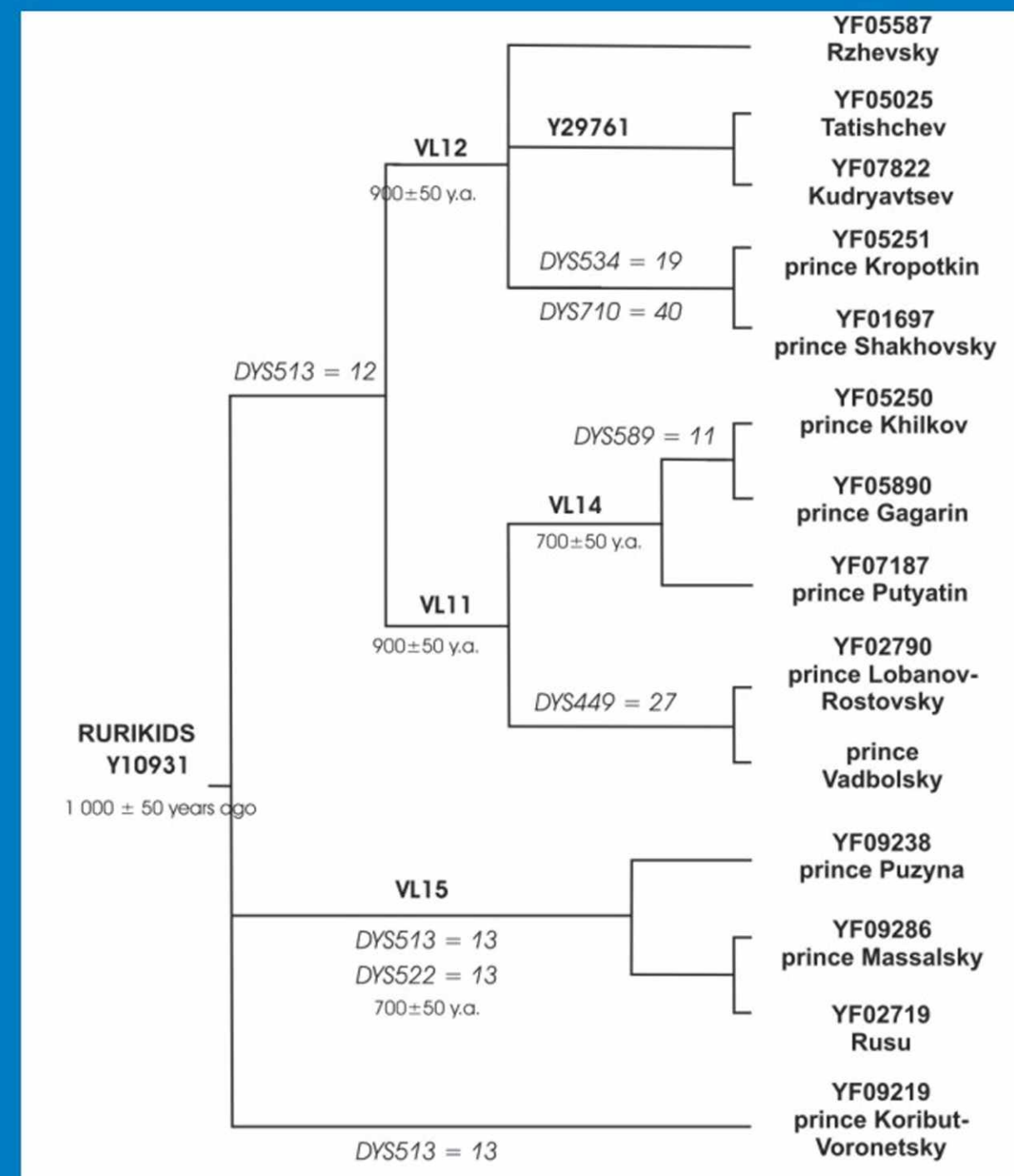
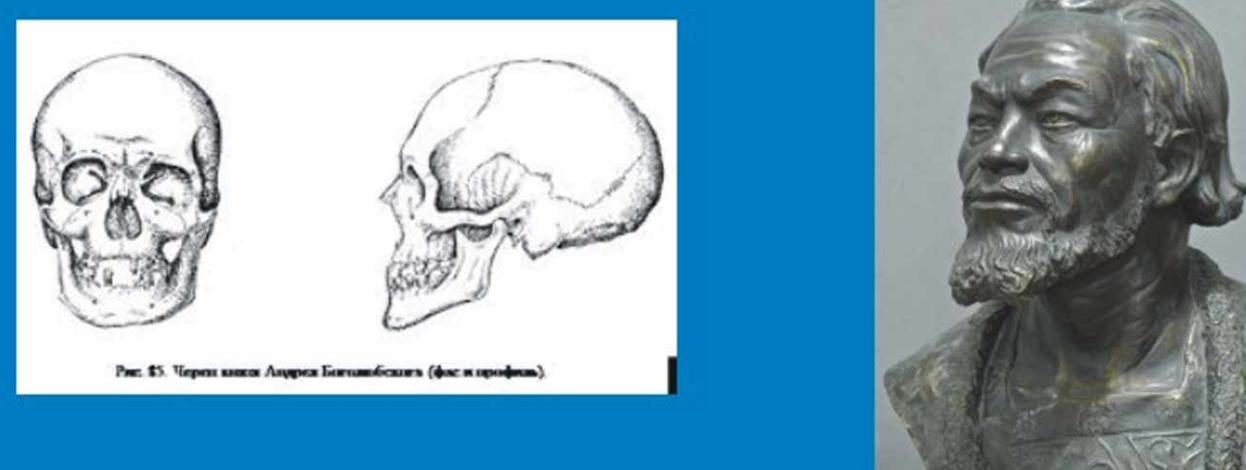


Figure 2. Phylogenetic tree of lineage N-Y10931 according to Y-SNP and Y-STR markers.

The extensively sequenced Y-chromosome data clearly shows an extremely accurate correlation between the distribution of distinctive mutations within the different groups of Rurik's descendants and the traditional documented pedigree of Rurikid. The results clearly testify that the documentary genealogy of Rurikid as a whole truly reflects that of the interrelated genetic structure of the participants within the study.

## Perspectives



The final determination of which genetic lineage did Rurikid belong to can be established on the basis of paleogenetics. In this regard, it is necessary to complete the sequencing of the genome of the ancient Rurikid.

## Genetic origin of Rurikid

A separate issue for consideration is the genetic origin of the whole group of Rurikid N-Y10931, i.e. connection to a common ancestor of this group with certain geographic regions.



According to the Russian Primary Chronicle, Rurik came from the sea at the head of the Varangians, who "were known as Rus, just as some are called Swedes, and others, Normans, Angles, Gotlanders ..."



Thus according to the sources Rurik was of Scandinavian origin.

The genetic lineage of N-Y10931 is derived from the subclade N-Y4339, and distribution of this subclade is primarily found in Sweden (52%) followed by Finland (14%), Russia (10%), Britain (10%) with a smaller frequency in Norway (5%) and Ukraine (5%).

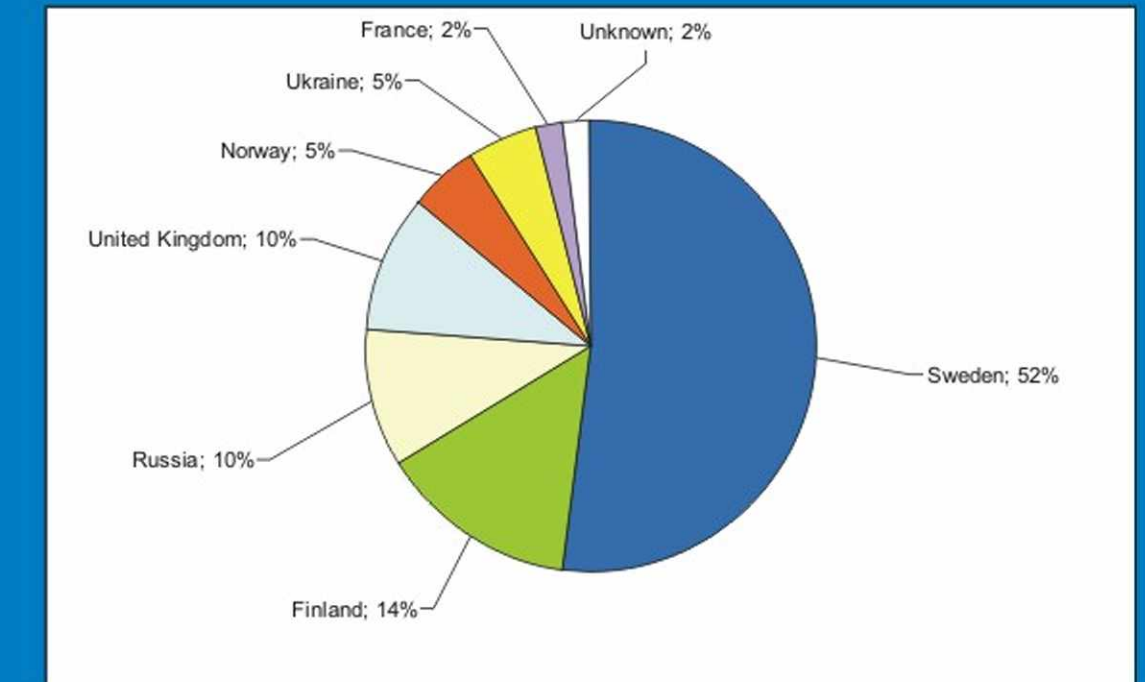


Figure 3. Frequency of genetic lineage N-Y4339 in Europe.

The phylogenetic tree convincingly shows that the origin of the lineage N-Y4339 is rooted in the territory of Sweden, and the results clearly show that the closest to Rurikid are the representatives of the lineage N-Y85136 whose ancestors lived in the Uppsala region of Sweden and having a common ancestor who lived 1200-1350 years ago, clearly showing a good correlation with the main genealogy of Rurikid and Rurik's lifetime.

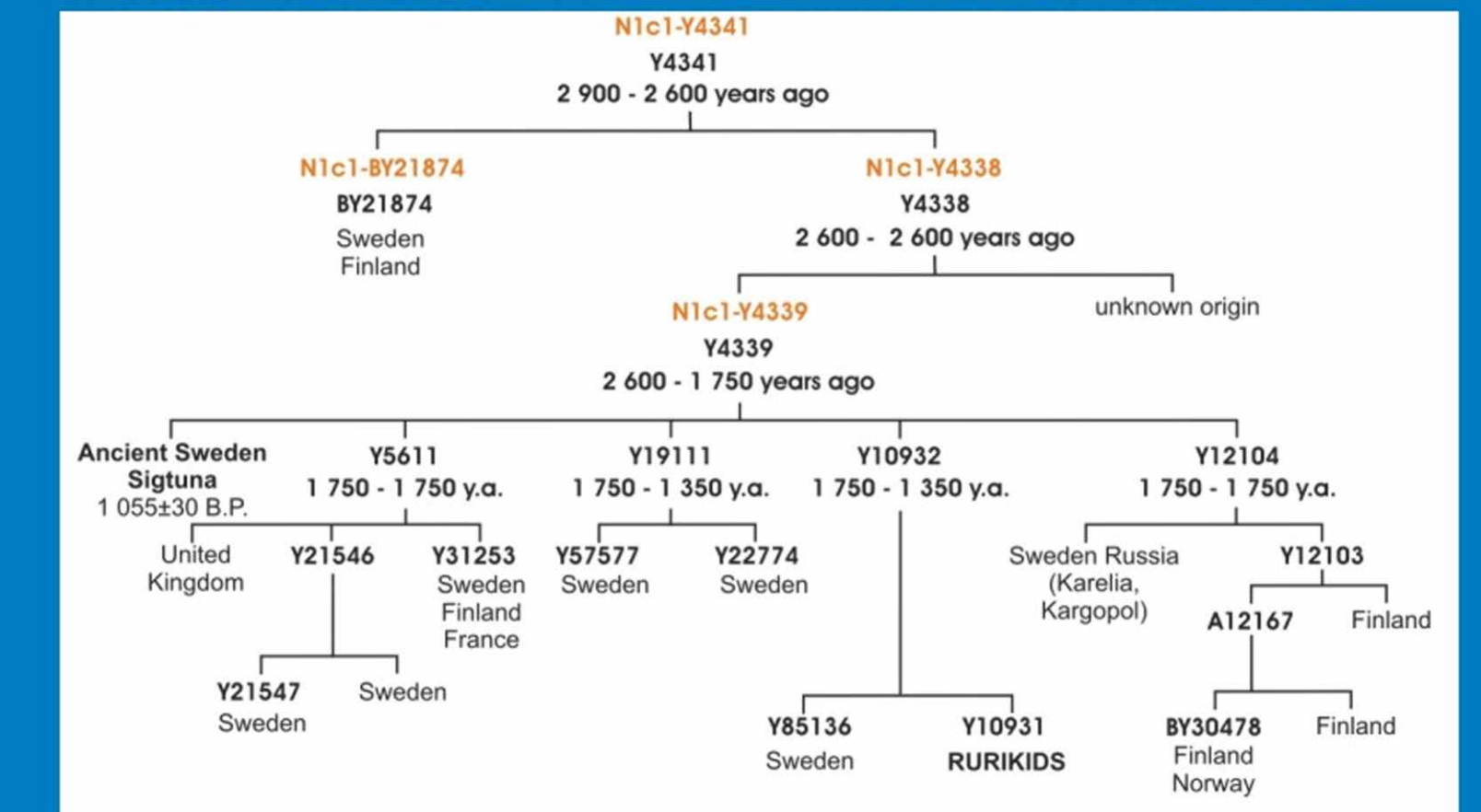


Figure 4. Phylogenetic tree of subclade N-Y4341.

In general, the genetic data indicates that the most likely region of residence of the closest paternal ancestors of Rurik to be that of the Uppsala region of Sweden.

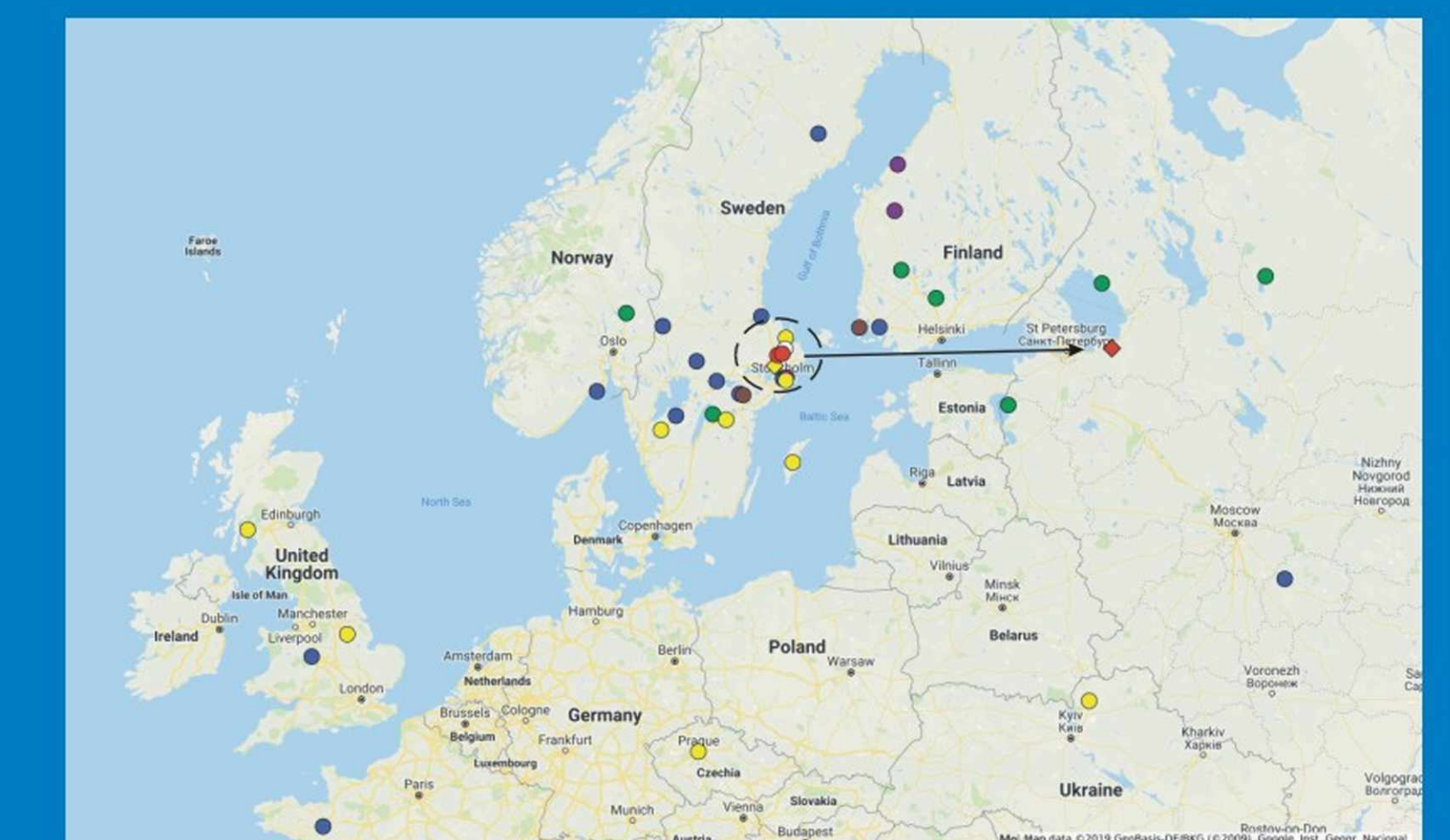


Figure 5. Residences of ancestors different lines N-Y4339

- ◆ - Old Ladoga - residence of Rurik
- - N-Y85136 - close genetic relatives of Rurikid
- - N-Y5611
- - N-Y12104
- - N-Y19111
- - N-Y4339 (xY10932, Y5611, Y12104, Y19111)
- ◆ - N-Y4339\* (Sigtuna, Sweden)

Again the genetic results fully confirm the historical accounts of the early Russian chronicles about the Scandinavian origin of Rurik.

## Acknowledgements

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