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В № 20 «Записок ИИМК РАН» публикуются научные исследования, представленные на российско-финляндском симпозиуме «Торговля, обмен и взаимовлияния в доисторическое время и средневековье/историческое время». В разделах «Новейшие открытия и разработки ИИМК РАН» и «Из истории науки» представлены статьи Н. Ф. Соловьёвой и А. В. Полякова, посвященные полевым открытиям на Ыылгыны-депе в Южном Туркменистане и анализу данных радиоуглеродного датирования фёдоровской культуры на Енисее, а также работа С. О. Ремизова, обобщающая информацию об изучении памятников каменного века Волгоградской обл.

Издание адресовано археологам, культурологам, историкам, музейоведам, студентам исторических факультетов вузов.

The 20th issue of the “Transactions of IHMC RAS” contains the Proceedings of the Russian-Finnish Symposium “Trade, Exchange and Contacts in Prehistory and in the Medieval/post-Medieval Times”. The sections “Newest discoveries and developments” and “From the history of science” present the papers by N. F. Solovyova and A. V. Polyakov devoted to field discoveries at Ilgynly-depe in South Turkmenistan and to the analysis of radiocarbon dates obtained for the Fyodorovo culture on the Yenisei river, respectively, as well as the work by S. O. Remizov who summarizes the information about the Stone Age sites of the Volgograd oblast.

The volume is intended for archaeologists, culturologists, historians, museum workers, and students of historical faculties.

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ANCIENT HUMAN GENES OF NORTH-EASTERN EUROPE

P. ONKAMO, K. MAJANDER, S. PELTOLA, E. SALMELA, K. NORDQVIST¹

Keywords: *archaeogenetics, ancient DNA, archaeology, anthropology, population genetics, North-Eastern Europe.*

The SUGRIGE-project (University of Helsinki) aims at getting a whole genomic picture of the ancient inhabitants of North-Eastern Europe, a previously un(der)studied region in terms of ancient DNA (Fig. 1). This is accomplished by sequencing whole genomes from archaeological human remains from the region, representing different time periods and archaeological cultures. In addition, we incorporate views from linguistic data (Fig. 2) — are the observed genetic changes connected to simultaneous linguistic shifts, or are the phenomena mainly independent of each other?

For these purposes, we gather samples of ancient human remains from the north-east European region, in collaboration with the Max Planck Institute for the Science of Human History (Jena, Germany). The genomes are compared in a population genetic framework to other ancient and modern people throughout the world.

We have very recently published our first results on 11 ancient individuals from a Bronze Age site of Bolshoy Oleniy Ostrov and Čalmn-Varré, a Saami burial site from the 18th century, in the Kola Peninsula, together with an Iron Age site of Levänluhta in western Finland (Lamnidis et al. 2018). Another manuscript, focusing on ancient mitochondrial (maternal) lineages in Finland and with full mtDNA sequences from over 100 individuals, is currently under review. Novel sample sets from various areas of Russia, like Karelia and Don-Volga (forest) steppes, and ranging from the Eneolithic until the medieval are being analysed for an ongoing study, the first publication of which is planned for fall 2019.

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Introduction

Studies of ancient DNA (aDNA) open a direct window into the past human populations. However, most published aDNA studies have focused on central and southern

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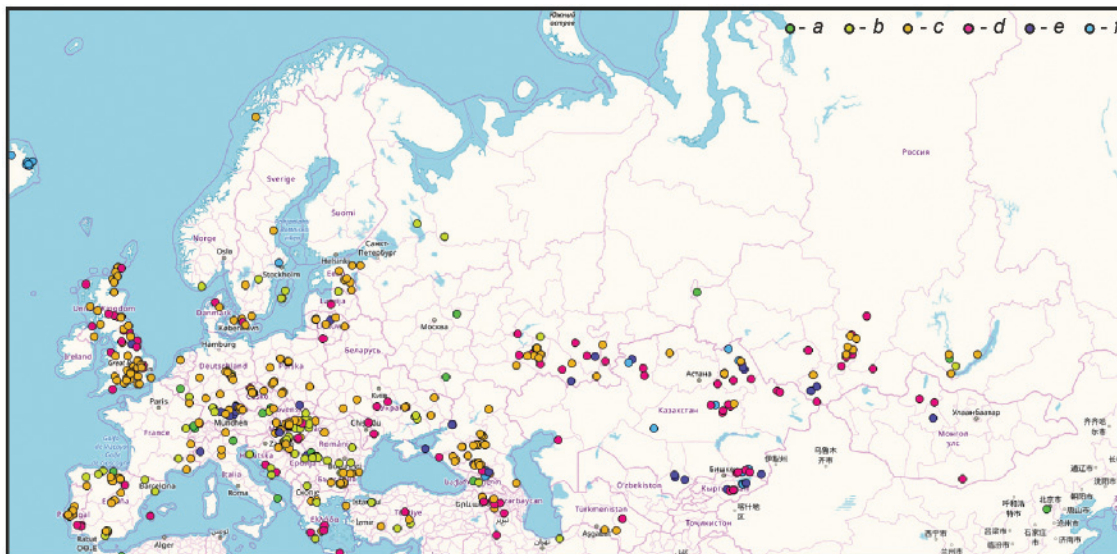


Fig. 1. A map of published ancient DNA studies from Europe. The small dots indicate sites with one or more published individuals: *a* — prior to 10 000 BC; *b* — 10 000–5000 BC; *c* — 5000–2000 BC; *d* — 2000–1 BC; *e* — 1–650 AD; *f* — 650–1500 AD. The stars indicate the sites (Bolshoy Oleniy Ostrov, Čalmn-Varrè, and Levänluhta) included in our published study (Lamnidis et al. 2018). Map coordinate data extracted from http://umap.openstreetmap.fr/en/map/ancient-human-dna_41837; map created using QGIS version 2.18 (QGIS Development Team 2016); base map: Open Street Map

Рис. 1. Карта опубликованных исследований древней ДНК в Европе. Маленькие точки соответствуют памятникам, для которых опубликованы данные как минимум по одному индивиду: *a* — ранее 10 000 лет до н. э.; *b* — 10 000–5000 лет до н. э.; *c* — 5000–2000 лет до н. э.; *d* — 2000–1 гг. до н. э.; *e* — 1–650 гг. н. э.; *f* — 650–1500 гг. н. э. Звездочками отмечены памятники Большой Олений Остров, Чальмн-Варрэ и Левянлухта, включенные в наше опубликованное исследование (Lamnidis et al. 2018). Координатные данные взяты с сайта http://umap.openstreetmap.fr/en/map/ancient-human-dna_41837; карта создана с помощью QGIS version 2.18 (QGIS Development Team 2016); топографическая основа: Open Street Map

Europe (Fig. 1), with very few samples analysed from North-Eastern Europe. The studies on central and southern Europe have revealed successive waves of major population movements during the last 10,000 years. In fact, the modern central European gene pool can be well-explained by a combination of just two such waves: first the early-farming-associated genetic population mixing heavily with local hunter-gatherer population (Skoglund et al. 2012; Lazaridis et al. 2014; Haak et al. 2015), and then the steppe population gene flow from the east, in the Early Bronze Age, again replacing a large portion of the previous two-way mix population (Allentoft et al. 2015; Haak et al. 2015). These genetic components alone, however, cannot sufficiently explain the modern north-east European gene pool, including both Russian and Finno-Ugric speakers: additional Asian-related ancestry is needed (Lazaridis et al. 2014; Haak et al. 2015) to complete the observed genetic combination. From the viewpoint of archaeology this is rather obvious: material culture clearly indicates that several waves of influence from the east have taken place during the past millennia.

In the north-east of Europe, the hunter-gatherer population that prevailed from the end of the Ice Age until the Late Neolithic, has in genetic terms been denoted “eastern hunter-gatherers” (EHG). Even though only four individuals from two locations (Karelia and Samara, approximately 8000 years ago) (Haak et al. 2015) have been published as of now, they are genetically quite alike, and show a genetic continuum all the way from the Siberian Palaeolithic individual, Ma’lta boy, from 20,000 years ago (Raghavan et al. 2014).

Nevertheless, even as near as in Estonia and Latvia, the Mesolithic population harboured a prominent component from another group, so-called “western hunter-gatherers” (WHG), who were otherwise constrained to western Europe — the eastern Baltic region seems to have served as a contact zone for human populations deriving from eastern and western Ice Age refugia. Much like in central Europe, the appearance of Corded Ware Culture here coincides with the emergence of a new genetic component, coming from the steppes (Saag et al. 2017; Mittnik et al. 2018). Some more early farmer-related ancient European genes were locally introduced in the Bronze Age, but yet, the Siberian kind of genetic legacy, though observed in low levels in, e.g., modern Estonians, has not been presented in the studied ancient individuals of this region (Saag et al. 2017; Mittnik et al. 2018). Until the project presented in this paper, basically no studies concerning North-Western Russia or Finland have been published.

Our project, called SUGRIGE (Fi. Suomalais-ugrilainen muinaisgenomi), focuses specifically on north-east European region, with its fascinating mosaic of various populations carrying unique genetic characteristics and historical background. The work is carried out by a team of geneticists and archaeologists from the Universities of Helsinki and Turku (Finland), and the Max Planck Institute for the Science of Human History (Jena, Germany), in collaboration with several archaeological institutes and museums in Russia.

More information of the project can be found at blogs.helsinki.fi/paleogenetics.

Aims

The overall objective of the project is to elucidate human population genetic prehistory in north-east Europe, a previously un(der)studied region. This is carried out by DNA sequencing of bone samples from archaeological human remains from the area. The methodology is further elaborated in chapter “Materials and methods” below.

The specific aims of the project are following:

1) *Characterise genetic population history in north-east Europe* through time. To create an overview of human genetic variation both spatially and temporally, we aim to sequence a minimum of 3–5 individuals from each site/time period. In general, one individual yields some hundreds of thousands of markers genome wide, of which each marker is a realisation of all possible routes of inheritance from ancestors into an individual. Thus, even one individual has the potential to yield a statistically relevant sample set.

2) *Assess possible correlations of genetic events with archaeological and linguistic transitions in the area; do such exist?* Do observed genetic changes coincide with known cultural or linguistic changes? Does the same geographical area carry various patterns of genetic make-up and how does the material culture coincide with these findings? For this aim, we work in close collaboration with archaeologists and linguists.

3) *Shed further light on genetic origins and relatedness of Finno-Ugric peoples.* A recent study has shown that all Fenno-Ugric populations do carry a genomic component that is

most prevalent in the modern-day Khanty and Mansi (Tambets et al. 2018). Can clues to this relationship be found in ancient individuals of the Volga-Ural region?

4) *Assess the genetics of adaptation to climate and environment in North-Eastern Europe.* In the north, this means the duress to adapt to long periods of reduced sunlight, cold climate, and occasionally enduring a diet limited in variation and nutrients, such as vitamin C. Globally, a transition in subsistence strategies — from the hunter-gatherer lifestyle into an agricultural one — has had an effect on metabolic genes such as fatty acid desaturases (FADS) (Mathieson et al. 2015) and amylases (AMY) (Perry et al. 2007). Thus, we seek for functional gene variants, which natural selection has acted on, in the ancient populations of the north.

5) *Screen for infectious disease agents in ancient individuals.* We utilise routine screening methodology for more than 100 pathogens, including, for example, the causative agents for plague, leprosy, and tuberculosis.

6) *Evaluate genetic data on sex, relatedness between individuals, and phenotypes.*

Materials and methods

Laboratory workflow. The samples selection is dependent on the condition of the skeletal elements. Typically teeth, and other well preserving parts, such as the inner ear structure (petrous part) of the skull, are collected for sampling. Prior to sampling, all materials are carefully decontaminated to minimise the amount of DNA originating from other sources than the individual under study. Approximately 50 mg of bone powder is drilled out of the target bone element under sterile conditions and strict safety measures in a clean room facility. DNA is extracted following standard protocols and turned into NGS libraries. The libraries are indexed with a unique synthetic oligonucleotide, which serves as a barcode to trace the sequenced reads back to the individual sample source and to eliminate any downstream contamination. All libraries are amplified with PCR technique, and aliquots of the initial amplified product are used for the initial shotgun sequencing for human and pathogen screening methods and for the possible subsequent enrichment methods. Enrichments targeted for mitochondrial, Y-chromosomal, or for a whole genome scale selection of SNPs (single nucleotide polymorphism) are possible, as well as specific pathogen enrichments for samples, where infectious agents are suspected. The DNA is sequenced on Illumina technologies, on a HiSeq, NextSeq or MiSeq platform.

Data analysis. Genome assemblies, as well as phylogenetic comparisons, are carried out with state-of-the-art bioinformatics methods. A pipeline for aDNA-specific analysis has been developed and tested. Java-based EAGER pipeline contains multiple tools and functions, such as merging of the fragmented DNA, aligning the sequenced aDNA to a reference genome, and mapping for circular genomes (bacterial genomes, mtDNA). It can also be used to conduct statistical analyses, such as genomic coverage and provide quality control estimates, such as plotting the damage to verify the age of the samples and calculating the percentage of endogenous DNA in the sample.

Population genetic analyses of the data are done by standard methods of population history inference, such as PCA and Admixture (Alexander et al. 2009). Additionally, as the nature of aDNA data limits the range of possible analysis methods, we also use tools specifically designed for ancient DNA, for example, F statistics (Patterson et al. 2012) and related methods. They are more tolerant to, and can make better use of, the typical

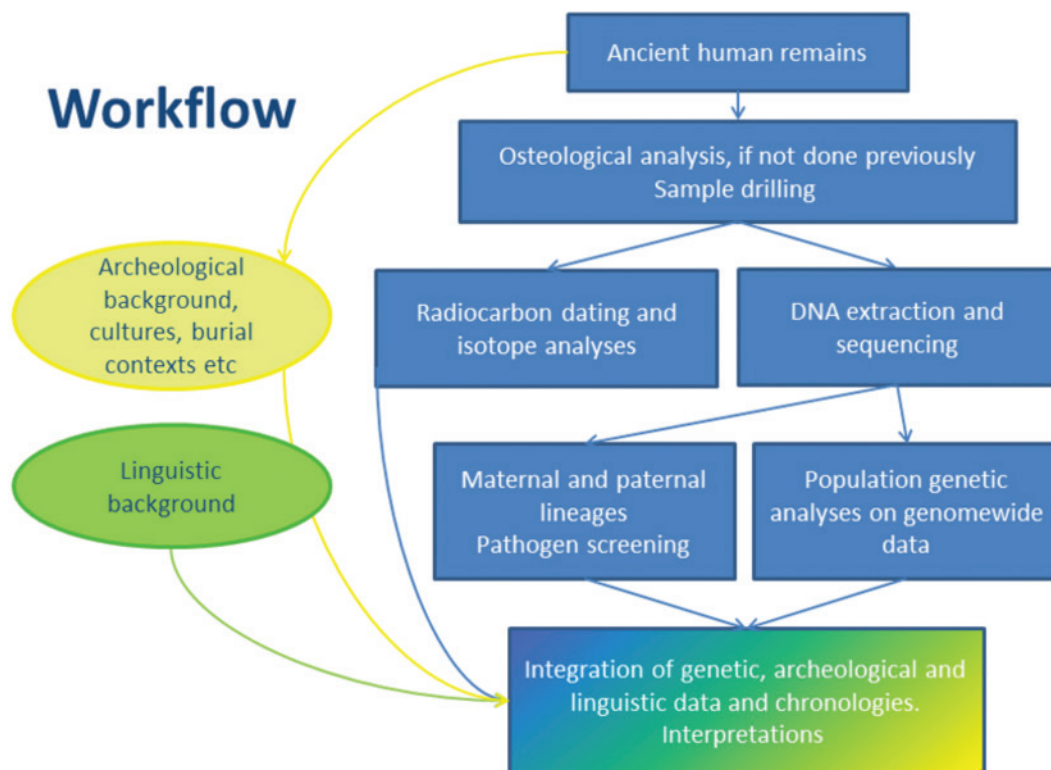


Fig. 2. Project workflow

Рис. 2. Процесс выполнения проекта

features of the data — such as the pseudohaploid genotypes necessitated by the usually very low coverage of the sequencing data — than many methods developed for modern DNA data would be. As reference data in the analyses, we use other ancient as well as modern populations, including publicly available datasets and those available through our collaborators.

We will also estimate the individuals' sexes based on the relative sequencing coverage of the sex chromosomes and the rest of the genome (Skoglund et al. 2013), and infer the individuals' relatedness by multiple methods (Lipatov et al. 2015; Monroy Kuhn et al. 2018). Inference of morphological and other phenotypes of the individuals and their susceptibility to certain genetic diseases will be assessed based on the presence of genetic variants contributing to said phenotypes and diseases. Of interest is, for example, the presence and time of appearance of the variants that yield adult lactose tolerance, as it deepens our understanding of the potential phenotypic adaptation to the introduction of livestock.

Comparison of sex determination methods. Traditional sex estimations based on osteological analysis of the bones will be made based on internationally approved and standardised methods (Buikstra, Ubelaker 1994; Brickley, McKinley 2004). Their results will be compared to the results from molecular sexing, and the comparisons, in turn, used to determine the skeletal elements most reliable for estimating the biological sex. The genetic sexes will be further compared to the archaeological gender estimations based on artefacts, such as jewellery or weapons found as grave goods. Possible discrepancies will open new views to gender roles present in the past societies.

Non-genetic analyses. We also analyse our sample material using a variety of non-genetic methods in order to obtain information about the age of our samples (radiocarbon dating), as well as their lifetime migration and diet (isotopic analyses) and morphology and paleopathology (osteological evaluation). Combined to the results of the genetic analyses, these analyses will complement our knowledge of the ancestry, subsistence strategies, and life histories of our study individuals (Fig. 2).

Research environments and infrastructure. The project is mainly carried out at the Department of Biosciences, University of Helsinki, and the Department of Biology, University of Turku (Finland). However, the main bulk of the laboratory work will be conducted at the Max Planck Institute for the Science of Human History in Jena, Germany. The aDNA sequencing for pathogens will be done in a specialised laboratory at the Institute for Evolutionary Medicine, University of Zürich, Switzerland. The radiocarbon dating and isotope analyses will be carried out in the Laboratory of Chronology, University of Helsinki. Computational analyses of the ancient data will be done in Jena, Turku, and Helsinki, utilising the local and national computational facilities. For the computation and long-time storage of data in Finland, CSC (IT Center for Science Ltd.) will provide the resources needed. Large genomic aDNA datasets will be stored in the IDA research data storage service operated by CSC. These facilities provide an excellent support network for both the molecular and the computational analyses of our project.

First results of the project

In our article “Ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe”, published in Nature Communications November 2018 (Lamnidis et al. 2018), we show a significant gene flow from Siberia into the north Fennoscandian population, starting already 4000 years ago. Approximately 50–60 % of the genomes of individuals buried in the Bronze Age Bolshoy Oleniy Ostrov cemetery (3500 BP; Fig. 2) derive from Siberia, from a source that genetically resembles most the modern-day Nganasan population. This is not contradicted by the archaeological evidence, where certain similarities in ceramics as well as in some other artefact types have been proposed between Northern Fennoscandia and Northern Siberia, including the Taimyr Peninsula (Carpelan 2003; 2004; Murashkin et al. 2016).

We also found Siberian genomic contribution in individuals from the 1500-year-old lake burial site of Levänluhta in Southern Ostrobothnia, Finland. These Iron Age people resemble most closely the current-day Saami. If Saami-like genes and the Saami languages have occurred together, it is fair to assume that people speaking Saami lived in Finland much further south than today. Noteworthy, Siberian admixture is still visible in the present-day Saami, Finns and northern Russians. The evidence points towards several instances of genetic admixture of Siberian genetic legacy to these populations. Of all European populations, the modern Saami are the most evident representatives of the Siberian ancestry.

The work of the project is currently ongoing, and new results are to be published in the near future. For example, a manuscript focusing on ancient mitochondrial (maternal) lineages in Finland and with full mtDNA sequences from over 100 individuals, is currently under review. Similarly, samples from various areas of Russia, like Karelia and Don-Volga (forest) steppes, and ranging from the Eneolithic until the medieval are being analysed for a publication planned for late 2019.

Impact beyond academia

Our project increases the knowledge of population history in the area of North-Eastern Europe, which is traditionally of great interest to the general public of the region. On societal level, additional information on the genetic past also contributes to the better understanding and acknowledgement of the local population histories. More generally, acquiring a more comprehensive view of population history can prove pivotal in today's world of increasing nationalism, by emphasising the key role of migrations and admixture in forming the modern nations.

Advantages of aDNA studies

Obviously, aDNA studies are a new potent tool for archaeology. Beyond population-level questions, they can illuminate factors that are of interest at the level of individuals and communities. For example, estimating the sex of individuals can be accomplished from very limited quantities of sample material, and genetic relatedness between individuals can bring new insights into the gender roles and kinship practices within the respective communities.

We acknowledge that genes, cultures and languages do not always travel hand in hand. One of our large-scale aims is to compare the existing archaeological record and local contexts of our samples to their genetic make-up for possible correlations. Where it is possible to track down the historical development of languages, we will study the genetic differences between language groups and the possible co-occurrence of genetic turnovers and language shifts. Ultimately, by combining evidences from several fields of inquiry, our goal is to contribute to better and more comprehensive understanding of the population histories of past and present North-Eastern Europe.

Literature

- Alexander et al. 2009 — *Alexander D. H., Novembre J., Lange K.* Fast model-based estimation of ancestry in unrelated individuals // *Genome Research*. 2009. Vol. 19. P. 1655–1664.
- Allentoft et al. 2015 — *Allentoft M. E., Sikora M., Sjögren K.-G., Rasmussen S., Rasmussen M., Stenderup J., Damgaard P. B., Schroeder H., Ahlström T., Vinner L., Malaspina A.-S., Margaryan A., Higham T., Chivall D., Lynnerup N., Harvig L., Baron J., Della Casa P., Dąbrowski P., Duffy P. R., Ebel A. V., Epimakhov A., Frei K., Furmanek M., Gralak T., Gromov A., Gronkiewicz S., Grupe G., Hajdu T., Jarysz R., Khartanovich V., Khokhlov A., Kiss V., Kolář J., Kriiska A., Lasak I., Longhi C., McGlynn G., Merkevicius A., Merkyte I., Metspalu M., Mkrtychyan R., Moiseyev V., Paja L., Pálfi G., Pokutta D., Pospieszny Ł., Price T. D., Saag L., Sablin M., Shishlina N., Smrčka V., Soenov V. I., Szeverényi V., Tóth G., Trifanova S. V., Varul L., Vicze M., Yepiskoposyan L., Zhitenev V., Orlando L., Sicheritz-Pontén T., Brunak S., Nielsen R., Kristiansen K., Willerslev E.* Population genomics of Bronze Age Eurasia // *Nature*. 2015. Vol. 522. P. 167–172.
- Brickley, McKinley 2004 — *Brickley M., McKinley J. I.* (eds.). *Guidelines to the Standards for Recording Human Remains*. Reading: British Association for Biological Anthropology and Osteoarchaeology and Institute of Field Archaeologists. 2004. 62 p. (CIFA Paper. No. 7).
- Buikstra, Ubelaker 1994 — *Buikstra J. E., Ubelaker D. H.* (eds.). *Standards for Data Collection from Human Skeletal Remains*. Fayetteville: Arkansas Archaeological Survey, 1994. 272 p. (Arkansas Archaeological Survey Research Series. No. 44).

- Carpelan 2003 — *Carpelan C.* Inarilaisten arkeologiset vaiheet // Lehtola V.-P. (ed.). Inari–Aanaar. Inarin historia jääkaudesta nykypäivään. Inari: Inarin Kunta, 2003. S. 28–95.
- Carpelan 2004 — *Carpelan C.* Environment, archaeology and radiocarbon dates. Notes from the Inari region, northern Finnish Lapland // Lavento M. (ed.). Early in the North. Helsinki: Finnish Antiquarian Society and Archaeological Society of Finland, 2004. Vol. 5. P. 30–36 (Iskos. 13).
- Haak et al. 2015 — *Haak W., Lazaridis I., Patterson N., Rohland N., Mallick S., Llamas B., Brandt G., Nordenfelt S., Harney E., Stewardson K., Fu Q., Mittnik A., Bánffy E., Economou C., Francken M., Friederich S., Garrido Pena R., Hallgren F., Khartanovich V., Khokhlov A., Kunst M., Kuznetsov P., Meller H., Mochalov O., Moiseyev V., Nicklisch N., Pichler S. L., Risch R., Rojo Guerra M. A., Roth C., Szécsényi-Nagy A., Wahl J., Meyer M., Krause J., Brown D., Anthony D., Cooper A., Alt K. W., Reich D.* Massive migration from the steppe was a source for Indo-European languages in Europe // *Nature*. 2015. Vol. 522. P. 207–211.
- Lamnidis et al. 2018 — *Lamnidis T. C., Majander K., Jeong C., Salmela E., Wessman A., Moiseyev V., Khartanovich V., Balanovsky O., Ongyerth M., Weihmann A., Sajantila A., Kelso J., Pääbo S., Onkamo P., Haak W., Krause J., Schiffels S.* The ancient Fennoscandian genomes reveal origin and spread of Siberian ancestry in Europe // *Nature Communications*. 2018. Vol. 9: 5018. P. 1–12.
- Lazaridis et al. 2014 — *Lazaridis I., Patterson N., Mittnik A., Renaud G., Mallick S., Kirsanow K., Sudmant P. H., Schraiber J. G., Castellano S., Lipson M., Berger B., Economou C., Bollongino R., Fu Q., Bos K. I., Nordenfelt S., Li H., de Filippo C., Prüfer K., Sawyer S., Posth C., Haak W., Hallgren F., Fornander E., Rohland N., Delsate D., Francken M., Guinet J.-M., Wahl J., Ayodo G., Babiker H. A., Bailliet G., Balanovska E., Balanovsky O., Barrantes R., Bedoya G., Ben-Ami H., Bene J., Berrada F., Bravi C. M., Brisighelli F., Busby G. B. J., Cali F., Churnosov M., Cole D. E. C., Corach D., Damba L., van Driem G., Dryomov S., Dugoujon J.-M., Fedorova S. A., Gallego Romero I., Gubina M., Hammer M., Henn B. M., Hervig T., Hodoglugil U., Jha A. R., Karachanak-Yankova S., Khusainova R., Khusnutdinova E., Kittles R., Kivisild T., Klitz W., Kučinskás V., Kushniarevich A., Laredj A., Litvinov S., Loukidis T., Mahley R. W., Melegh B., Metspalu E., Molina J., Mountain J., Näkkäläjärvi K., Nesheva D., Nyambo T., Osipova L., Parik J., Platonov F., Posukh O., Romano V., Rothhammer F., Rudan I., Ruizbakiev R., Sahakyan H., Sajantila A., Salas A., Starikovskaya E. B., Tarekegn A., Toncheva D., Turdikulova S., Uktveryte I., Utevska O., Vasquez R., Villena M., Voevoda M., Winkler C. A., Yepiskoposyan L., Zalloua P., Zemunik T., Cooper A., Capelli C., Thomas M. G., Ruiz-Linares A., Tishkoff S. A., Singh L., Thangaraj K., Vilems R., Comas D., Sukernik R., Metspalu M., Meyer M., Eichler E. E., Burger J., Slatkin M., Pääbo S., Kelso J., Reich D., Krause J.* Ancient human genomes suggest three ancestral populations for present-day Europeans // *Nature*. 2014. Vol. 513. P. 409–413.
- Lipatov et al. 2015 — *Lipatov M., Sanjeev K., Patro R., Veeramah K. R.* Maximum likelihood estimation of biological relatedness from low coverage sequencing data // *bioRxiv*. 2015. P. 1–20.
- Mathieson et al. 2015 — *Mathieson I., Lazaridis I., Rohland N., Mallick S., Patterson N., Roodenberg S. A., Harney E., Stewardson K., Fernandes D., Novak M., Sirak K., Gamba C., Jones E. R., Llamas B., Dryomov S., Pickrell J., Arsuaga J. L., Bermúdez de Castro J. M., Carbonell E., Gerritsen F., Khokhlov A., Kuznetsov P., Lozano M., Meller H., Mochalov O., Moiseyev V., Rojo Guerra M. A., Roodenberg J., Vergès J. M., Krause J., Cooper A., Alt K. W., Brown D., Anthony D., Lalueza-Fox C., Haak W., Pinhasi R., Reich D.* Genome-wide patterns of selection in 230 ancient Eurasians // *Nature*. 2015. Vol. 528. P. 499–503.

- Mittnik et al. 2018 — *Mittnik A., Wang C.-C., Pfrengle S., Daubaras M., Zarina G., Hallgren F., Allmäe R., Khartanovich V., Moiseyev V., Törv M., Furtwängler A., Valtueña A. A., Feldman M., Economou C., Oinonen M., Vasks A., Balanovska E., Reich D., Jankauskas R., Haak W., Schiffels S., Krause J.* The genetic prehistory of the Baltic Sea region // *Nature Communications*. 2018. Vol. 9: 442. P. 1–11.
- Monroy Kuhn et al. 2018 — *Monroy Kuhn J. M., Jakobsson M., Günther T.* Estimating genetic kin relationships in prehistoric populations // *Plos One*. 2018. Vol. 13, no. 4: e0195491. P. 1–21.
- Murashkin et al. 2016 — *Murashkin A. I., Kolpakov E. M., Shumkin V. Ya., Khartanovich V. I., Moiseyev V. G.* Kola Oleneostrovskiy grave field: a unique burial site in the European Arctic // *Uino P., Nordqvist K. (eds.). New Sites, New Methods: Proceedings of the Finnish-Russian Archaeological Symposium, Helsinki, 19–21 November 2014.* Helsinki: Suomen muinaismuistoyhdistys, 2016. P. 185–199 (Iskos. No. 21).
- Patterson et al. 2012 — *Patterson N., Moorjani P., Luo Y., Mallick S., Rohland N., Zhan Y., Geneschoreck T., Webster T., Reich D.* Ancient admixture in human history // *Genetics*. 2012. Vol. 192. P. 1065–1093.
- Perry et al. 2007 — *Perry G. H., Dominy N. J., Claw K. G., Lee A. S., Fiegler H., Redon R., Werner J., Villanea F. A., Mountain J. L., Misra R., Carter N. P., Lee C., Stone A. C.* Diet and the evolution of human amylase gene copy number variation // *Nature Genetics*. 2007. Vol. 39. P. 1256–1260.
- Raghavan et al. 2014 — *Raghavan M., Skoglund P., Graf K. E., Metspalu M., Albrechtsen A., Moltke I., Rasmussen S., Stafford T. W. Jr., Orlando L., Metspalu E., Karmin M., Tambets K., Rootsi S., Mägi R., Campos P. F., Balanovska E., Balanovsky O., Khusnutdinova E., Litvinov S., Osipova L. P., Fedorova S. A., Voevoda M. I., DeGiorgio M., Sicheritz-Ponten T., Brunak S., Demeshchenko S., Kivisild T., Villems R., Nielsen R., Jakobsson M., Willerslev E.* Upper Palaeolithic Siberian genome reveals dual ancestry of Native Americans // *Nature*. 2014. Vol. 505. P. 87–91.
- Saag et al. 2017 — *Saag L., Varul L., Christiana L., Stenderup J., Allentoft M. E., Saag L., Pagani L., Reidla M., Tambets K., Metspalu E., Kriiska A., Willerslev E., Kivisild T., Metspalu M.* Extensive farming in Estonia started through a sex-biased migration from the steppe // *Current Biology*. 2017. Vol. 27, no. 14. P. 2185–2193.
- Skoglund et al. 2012 — *Skoglund P., Malmström H., Raghavan M., Storå J., Hall P., Willerslev E., Gilbert M. T. P., Götherström A., Jakobsson M.* Origins and genetic legacy of Neolithic farmers and hunter-gatherers in Europe // *Science*. 2012. Vol. 336, no. 6080. P. 466–469.
- Skoglund et al. 2013 — *Skoglund P., Storå J., Götherström A., Jakobsson M.* Accurate sex identification of ancient human remains using DNA shotgun sequencing // *JAS*. 2013. Vol. 40, no. 12. P. 4477–4482.
- Tambets et al. 2018 — *Tambets K., Yunusbayev B., Hudjashov G., Ilumäe A.-M., Rootsi S., Honkola T., Vesakoski O., Atkinson Q., Skoglund P., Kushniarevich A., Litvinov S., Reidla M., Metspalu E., Saag L., Rantanen T., Karmin M., Parik J., Zhadanov S. I., Gubina M., Damba L. D., Bermisheva M., Reisberg T., Dibirova K., Evseeva I., Nelis M., Klovins J., Metspalu A., Esko T., Balanovsky O., Balanovska E., Khusnutdinova E. K., Osipova L. P., Voevoda M., Villems R., Kivisild T., Metspalu M.* Genes reveal traces of common recent demographic history for most of the Uralic-speaking populations // *Genome Biology*. 2018. Vol. 19: 139. P. 1–20.

References

QGIS Development Team 2016 — QGIS Geographic Information System. Open Source Geospatial Foundation Project. <https://qgis.org>.

ГЕНЫ ДРЕВНЕГО НАСЕЛЕНИЯ СЕВЕРО-ВОСТОЧНОЙ ЕВРОПЫ

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Ключевые слова: археогенетика, древняя ДНК, археология, антропология, популяционная генетика, Северо-Восточная Европа.

Проект SUGRIGE (университет Хельсинки) нацелен на получение целостного представления о геноме древних обитателей Северо-Восточной Европы — региона, который ранее был обойден вниманием исследователей древней ДНК (рис. 1). Задача решается посредством секвенирования полных геномов из человеческих костей с археологических памятников региона, относящихся к разным периодам и культурам. Кроме того, мы учитываем и лингвистические данные (рис. 2) и стремимся выяснить, связаны ли наблюдаемые генетические изменения с одновременными лингвистическими сдвигами, или же эти явления в основном независимы друг от друга.

Для достижения этих целей мы в сотрудничестве с Институтом изучения истории человека Общества Макса Планка (Йена, Германия) собираем образцы древних человеческих останков с северо-востока Европы. Выявленные геномы сопоставляются в рамках популяционно-генетического подхода с геномами других древних и современных людей со всего мира.

Совсем недавно мы опубликовали свои первые результаты, которые получены по костям 11 индивидов с памятника бронзового века Большой Олений Остров и с саамского могильника XVIII в. Чальмн-Варрэ на Кольском п-ове, а также с памятника железного века Левянлухта в Западной Финляндии (Lamnidis et al. 2018). Рукопись еще одной работы, посвященной древним митохондриальным линиям Финляндии и представляющей полные последовательности мтДНК более чем ста индивидов, находится в настоящее время на рассмотрении. Новые группы образцов из разных частей России, таких как Карелия и Волго-Донской регион, варьирующие во времени от энеолита до средневековья, являются объектом анализа в нашем текущем исследовании, первая публикация результатов которого запланирована на осень 2019 г.