

BIOSOCIAL ARCHAEOLOGY: WHEN ANCIENT DNA OPENS THE DISCUSSION TO SOCIAL STRUCTURES

Theme: 5. Assembling archaeological theory and the archaeological sciences

Author: Maïté Rivollat

Co-Author(s): Anna Szécsényi-Nagy, Daniela Hofmann, Lara Cassidy, István Koncz

Keywords: ancient DNA, social structures, kinship, site organisation, interdisciplinarity

Over the last years, methodological advancements in ancient DNA allowed more specific studies, either at individual levels with high-covered genomes, or at group levels with extensive sampling. The evolution of the field makes now possible finer analysis at local scales, exploring in particular kinship and site organization. This increasing power of resolution offers new elements of analysis for the investigation of social structures, such as marital rules, female/male mobility, population size, consanguinity, networks at local or regional scales... As one can always object that biological kinship or affinities do not necessarily demonstrate that the individuals either recognized this connection or bonded based on it, these elements open the discussion about the relationship between biological and social kinship. Developments of new analysis tools to explore these biological structures are actively in progress and will contribute to deeply improve our knowledge in this regard.

In parallel, the discussion now must include insights from social anthropology as well as archaeology to critically assess these new results in the light of human behavior. It also highlights our biases as modern societies and which we must question when coming to interpret social systems in ancient societies.

Many different perspectives can be brought together in this session to discuss this growing and exciting panel of ancient DNA data, with the aim to help building a critical and integrative research.

We welcome all researchers involved in genetics, archaeology, anthropology and social anthropology who want to contribute to an interdisciplinary discussion about biosocial archaeology. Contributions can address the following questions and research topics, for any time period:

- Case studies including analyses of social structures, kinship and site studies;
- New tools to explore genetic, archaeological or anthropological data in a social perspective;
- Theoretical discussions related to biosocial archaeology about interpretative choices, vocabulary, historical records and ethnoarchaeology.

Abstract book ISBN:

978-80-907270-8-3

Abstracts for session #468

MAKING KIN: THE ARCHAEOLOGY AND GENETICS OF HUMAN RELATIONSHIPS

Catherine Frieman¹, Joanna Bruck²

¹ *Australian National University*

² *University College Dublin*

Kin-making is a key part of how humans structure their relations with each other, with their wider community and with the non-human world. Kin relations are constituted by shared values, shared experience, as well as by shared cultural or biological lineage. In recent years, archaeogenetics has offered us a startling level of clarity into biological relationships between individuals and groups of past people. At this crucial moment for our discipline, when archaeogenetic studies are being heralded as offering extraordinary insights into the social and political organisation of past communities, it is imperative that archaeologists retain a critical stance on the assumptions that so often underpin interpretations of archaeogenetic data.

In this paper, we argue that blood and biology are key elements of kin-making only in so far as they are contextualised and made sense of through social relations. The naturalisation of biological relatedness as the basis of kinship has its origins in the legacies of colonialism, which employed a particularly restrictive definition of kinship as a means of legitimating access to land and controlling the bodies of women and indigenous groups. Instead, taking as our inspiration the work of Indigenous scholars, we argue that the kinship produced through social relations and the kinship produced by genetic studies are not identical but can be complimentary.

Archaeology, with its focus on the material remains of the past, provides particular opportunities to examine how other forms of material and technological intervention (including ritual, exchange, and the sharing of food) facilitated the creation of kinship links not solely rooted in the human body. Here, we consider the extent to which the social salience of biological relationships identified through aDNA analysis can be addressed without imposing contemporary forms of familial structure and gender ideology onto the past.

Keywords

Kinship, archaeogenetics, lineage, relationality

Note/comment

INVESTIGATING NEOLITHIC SOCIAL STRUCTURES ON THE BASIS OF UNPRECEDENTEDLY LARGE FAMILY TREES FROM THE SITE GURGY “LES NOISATS” IN FRANCE

Maité Rivollat^{1,2}, Harald Ringbauer³, Ainash Childebayeva², Mélie Le Roy⁴, Léonie Rey¹, Gwenaëlle Goude⁵, Vincent Balter⁶, Stéphane Rottier¹, Marie-France Deguilloux¹, Wolfgang Haak²

¹ *University of Bordeaux, PACEA, France*

² *Max Planck Institute for the Science of Human History, Department of Archaeogenetics, Jena, Germany*

³ *Max Planck Institute for the Science of Human History, Department of Archaeogenetics, Leipzig, Germany*

⁴ *Queen's University Belfast, School of Natural and Built Environment, ArcPal, Belfast, UK*

⁵ *Aix Marseille University, CNRS, Ministry of Culture, LAMPEA, Aix-en-Provence, France*

⁶ *Ecole Normale Supérieure, Laboratoire de Géologie de Lyon, Lyon, France*

The elucidation of kinship structure in past societies has been at the center of intra-group studies in archaeology and anthropology. However, the reconstruction of genetic relatedness in archaeological contexts has rarely been feasible. With the development of ancient DNA methods, it is now possible to obtain genome-wide data for multiple individuals from a single group, even in the presence of poor DNA preservation. Here, we present new data from the Middle Neolithic French site of Gurgy “les Noisats”. Thanks to an extensive sampling and use of the 1240K capture array, we obtained genomic data for 94 out of 128 individuals. We reconstructed two large pedigrees, one of them spanning seven generations and connecting 62 individuals. These unprecedentedly large genealogies allowed us to look beyond the immediate genetic relatedness, and to explore the potential social structure of the group, its size, and its funerary and mobility practices.

We observed a strong patrilocal and patrilineal system with a single male lineage for the main family. The group practiced female exogamy, as no adult daughters were buried at the site (except for three females), and all mothers in the pedigree (except one) came from genetically-unrelated external groups, suggesting a wide regional network.

Accompanying Strontium analyses confirm the non-local origin of adult females, but also reveal a non-local signature of the first-generation founders of the site. Biological relatedness reveals a spatial organization of the graveyard, showing chronological and nuclear family groupings that were not visible through archaeological elements. The seven-generations pedigree also allowed us to constrain the chronological range of the site use and led us to propose a narrower occupation phase.

In the case of Gurgy, biological relatedness opens a previously inaccessible window into the Neolithic and provides numerous insights into the social structure of this group.

Keywords

Neolithic, ancient DNA, large pedigrees, social insights

Note/comment

I would like to add one author, as we are actually a team of eleven people and each of us participated to this work. Then I would like to add in the 4th position:

Adam Benjamin Rohrlach,

1st affiliation: Max Planck Institute for the Science of Human History, Department of Archaeogenetics, Jena, Germany

2nd affiliation: ARC Centre of Excellence for Mathematical and Statistical Frontiers, School of Mathematical Sciences, The University of Adelaide, Adelaide, SA, 5005, Australia

Thanks for your consideration.

ANCESTRY CHANGE AND KINSHIP ORGANISATION IN CHALCOLITHIC-EARLY BRONZE AGE BRITAIN: A CRITICAL ASSESSMENT OF MALE-DOMINATED MODELS

Joanna Bruck¹, Tom Booth²

¹ *School of Archaeology, University College Dublin*

² *Francis Crick Institute*

Large-scale archaeogenetic studies of people from prehistoric Europe tend to be broad in scope and difficult to resolve with local archaeologies. Drawing together a critical anthropological perspective with the details of the archaeological record, we show how information provided in the supplementary information of Olalde et al. (2018) can provide new insights into patterns of ancestry change and genetic relatedness in the past. Olalde et al. identified a >90% shift in ancestry of people who lived in Britain during the Chalcolithic and Early Bronze Age. We assess suggestions that such changes were the result of swift and large-scale migration of 'war bands' of young men from continental Europe who practised exogamous marriage with women from local groups and introduced patriarchal forms of social organisation. While ancestry change was certainly influenced by movements of communities carrying novel ancestries into Britain, this was unlikely to have been a simple, rapid process, potentially taking up to 17 generations, during which time there is evidence for the synchronous persistence of groups largely descended from the Neolithic populations. Insofar as genetic relationships can be assumed to have had social meaning, identification of genetic relatives in cemeteries suggests paternal relationships were important, but there is substantial variability in how genetic ties were referenced and little evidence for strict patrilocality or female exogamy. It is evident, too, that relations with maternal kin were significant and that kinship was not solely predicated on genetic relatedness.

Keywords

Ancestry, Genetic relatedness, Social kinship, Chalcolithic and Early Bronze Age Britain

Note/comment

SALVAGING aDNA KINSHIP RESEARCH: A NECESSARY WAKE UP CALL AND REORIENTATION

Bradley Ensor¹

¹ *Eastern Michigan University*

Archaeology, bioarchaeology, and genomics are challenging the dominance of ethnological approaches to prehistoric kinship. Unlike today's kin term evolutionism, they have data that actually date to prehistory and can avoid dubious normative cultural models interpreted through discredited 19th century phylogenetics or 1960s neoevolutionism. Though largely ignored or misunderstood in Europe, archaeological kinship analysis is the most developed and can detect intra- and inter-community variation and change. Bioarchaeological kinship analysis - using strontium isotope ratios or phenotypic traits - needs more informed interpretive models. From a social anthropological perspective, European genomic research has the most impoverished understanding of kinship, is ethnocentrically obsessed with uninformative nuclear family relations, and some is alarmingly mired in pre-WWII essentialism - particularly disturbing in an era of reemerging racist nationalism. At stake is whether genomics will become relevant to kinship research or serve as a precautionary tale as it is currently headed. Because kinship is always a social construction, aDNA researchers need models for interpreting how different kinds of corporate kin groups socially distribute biological relatedness within and across settlements and cemeteries. This paper illustrates how common kinship practices manipulate intra- and intergroup/cemetery biological compositions and re-analyzes published aDNA, strontium, and archaeological data from Central European Neolithic sites (patrilocality is not supported). Far from the sensationalist image of aDNA providing a definitive source, different kinship practices produce difficult to distinguish aDNA distribution patterns - a problem compounded by inappropriate cemetery sampling. However, aDNA results can be clarified when combined with strontium isotope ratios for individual life histories. In turn, archaeological kinship analyses can further clarify those results. Ancient DNA can potentially contribute productively to prehistoric kinship research but only if scholars familiarize themselves with the subject, adopt informed interpretive models and appropriate sampling, and combine their data with other sources.

Keywords

ancient DNA, Kinship, Bioarchaeology, Archaeology, Europe, Neolithic

Note/comment

EARLY BRONZE AGE FAMILIES IN THE NORTHWESTERN CARPATHIAN BASIN

Anna Szecsenyi-Nagy¹, Alena Šefčáková², Inigo Olalde³, Harald Ringbauer⁴, Juraj Bartík⁵, Zdeněk Farkaš⁵, Pavol Jelínek⁵, Klaudia Daňová⁶, Ron Pinhasi⁷, David Reich^{8,9}

¹ *Institute of Archaeogenomics, Research Centre for the Humanities, Eötvös Loránd Research Network*

² *Department of Anthropology, Slovak National Museum–Natural History Museum*

³ *Department of Genetics, University Pompeu Fabra*

⁴ *Department of Archaeogenetics, MPI EVA, Leipzig*

⁵ *Slovak National Museum–Archaeological Museum*

⁶ *Archaeological Institute of the Slovak Academy of Sciences*

⁷ *Department of Evolutionary Anthropology, University of Vienna*

⁸ *Department of Genetics, Harvard Medical School*

⁹ *Department of Human Evolutionary Biology, Harvard University*

Fine-scale ancient DNA analyses provide not only insights to prehistoric demographic processes, but also a deeper understanding of the studied communities' structure and organization. Here we present intensively sampled Early Bronze Age graveyards (assigned to the Nitra and Únětice cultures) from the north-west part of the Carpathian Basin, and compare the new genomic data with anthropological and archaeological records and theories. Several families are reconstructed based on the genome-wide capture data, and attempts on reconstructing distant relatedness is also presented. A comprehensive analyses of the paternal and maternal lineages, together with the autosomal DNA results enable to reformulate the current knowledge about the social system of the Nitra (Nitrianska) culture's population, that culture was disseminated in present-day southwest Slovakia and southern Moravia. The Nitra culture followed epi-Corded Ware traditions in many ways, and most of the burials showed emphasis on highlighting the gender and social status of the buried individuals. The homogeneity of the male lineages of the Nitra culture's population, the detected distinct ancestry components and the comparison of the male and female admixture signals all contribute to a new way of understanding of the social changes at the dawn of the Bronze Age in East-Central Europe.

Keywords

Early Bronze Age, archaeogenetics, Carpathian Basin, Nitra culture, Únětice culture, social archaeology

Note/comment

HOME IS WHERE THE HEARTH IS: EXPLORING SEX BIAS IN GENETICALLY-ATTESTED MIGRATIONS IN PREHISTORIC EUROPE

Lindsey Büster¹, Ian Armit¹
¹ *University of York*

Recent large-scale ancient DNA studies have transformed our understandings of past population dynamics and, coupled with multi-proxy approaches such as stable isotope analysis, provide us with new insights into movement and mobility at a number of scales. Particularly striking has been the significance of population movement as a vector of cultural change. For many, this realisation carries uncomfortable echoes of early twentieth century archaeology, when migration, often implicitly presented as violent colonisation by a dominant group, was too easily invoked as the primary driver of change. Migration, however, as we can see from the world today, takes many forms, and can be a long-term process rather than a single event. Movement can be voluntary or forced, and is often undertaken by desperate or marginalised individuals and groups. Migratory pressures are also typically bound up with issues of age, class and gender. Indeed, recent aDNA analyses have demonstrated the major role of female mobility in Neolithic and Bronze Age societies. Traditional interpretations of prehistoric mobility have tended to focus on long-distance, male-dominated networks, but—drawing on the results of recent work on the Middle-Late Bronze Age in southern Britain—this paper argues that female mobility was crucial in instigating significant changes in language and culture. While the large-scale movement of women does not necessarily negate the presence of male-dominated power structures, it forces us to consider the lived realities of these migrants and the ways in which their own agency transformed their host communities from the inside out.

Keywords

migration, mobility, gender, aDNA, language, Bronze Age

Note/comment

SOCIAL BELONGING BETWEEN GENES AND PRACTICES

Philipp Stockhammer^{1,2}

¹ *LMU Munich*

² *MPI Jena*

Recent breakthroughs in archaeogenetics have not only produced ground-breaking new insights into the deep past, but also raised the risk of reinforcing biological determinism in the constitution of social structure. Whereas New Kinship Studies have demonstrated the usual complexity of “feeling related”, the challenge of tracing such “feelings” in the archaeological record has instigated us to emphasize the notion of “biologically related”. However, we need to take into account that past human world views were shaped by completely different assumptions about being human in the world and that present-day world views shaped by current scientific knowledge present only one way of understanding belonging. In my paper, I will first present my approach to linking scientific and archaeological datasets in order to understand the dynamics of social belonging out of the dialogue of genes and social practices like gender, age, mobility, nutrition and status. Subsequently, I will discuss case studies from Central Europe and the Eastern Mediterranean, where bioarchaeological datasets have recently enabled fascinating new insights into past social structures. Finally, I aim to show how we might use these datasets to take a further step towards the understanding of past social belonging and consequently past world views.

Keywords

Bioarchaeology, Bronze Age, Social Belonging, Social Practices, Biological Relatedness, New Kinship Studies

Note/comment

GENETIC INSIGHTS INTO KINSHIP AND SOCIAL STRUCTURE OF AN IRON AGE COMMUNITY FROM TUVA, SOUTHERN SIBERIA

Marcel Keller¹, Gino Caspari^{2,3}, Marco Milella⁴, Timur Sadykov⁵, Jegor Blochin⁵, Sönke Szidat^{6,7}, Lehti Saag⁸, Toomas Kivisild^{9,8}, Sandra Lössch⁴, Christiana Scheib^{8,10}

¹ *Institute of Genomics, University of Tartu*

² *Department of Archaeology, University of Sydney, Australia*

³ *Institute of Archaeological Sciences, University of Bern, Switzerland*

⁴ *Department of Physical Anthropology, Institute of Forensic Medicine, University of Bern, Switzerland*

⁵ *Institute for the History of Material Culture, Russian Academy of Sciences, St. Petersburg, Russia*

⁶ *Department of Chemistry and Biochemistry, University of Bern, Switzerland*

⁷ *Oeschger Centre for Climate Change Research (OCCR), University of Bern, Switzerland*

⁸ *Institute of Genomics, University of Tartu, Estonia*

⁹ *Department of Human Genetics, KU Leuven, Belgium*

¹⁰ *St John's College, University of Cambridge, United Kingdom*

The site of Tunnug1 (Republic of Tuva, Southern Siberia) is prominent for its 'Scythian' kurgan (9th c. BCE) but includes also significantly younger features such as a funerary complex of the Kokel culture (2nd–5th c. CE). The skeletal material of this cemetery is remarkable for the high incidence rate of perimortem trauma due to interpersonal violence interpreted as signs of warfare, executions or rituals. However, the single and multiple graves including grave goods indicate a careful funerary treatment, and radiocarbon dating suggests usage of this cemetery over several centuries.

In this case study, we aim to explore the social structure and kinship of this population through ancient DNA analyses on more than 50 individuals. Genome-wide sequencing data revealed a heterogeneous genetic background of these individuals forming a cline with different proportions of Western hunter-gatherer and Han-like ancestry, reflecting the high mobility of this nomadic steppe culture. However, first- and second-degree relationships among the individuals support the interpretation as one or multiple social communities.

Dating to the period following the fall of the Xiongnu Empire, this site offers valuable insights into the social organization of a 'Hunno-Sarmatian' population in the face of political instability.

Keywords

Ancient DNA, Palaeogenetics, Iron Age, Steppe, Kinship

Note/comment

**GENETIC METHODS IN ARCHAEOLOGICAL RESEARCH
(FUNDED BY GOVERNMENT GRANT NO. 075-15-2019-1879)**

Maria Ochir-Goryaeva¹

¹ *Kalmyk Research Center Russian Academy of Sciences*

The introduction of genetic methods in archaeological research, has brought the studies of blood relations and social hierarchies of archeological societies to a new level. The results obtained by these methods have often the force of irrefutable facts. However, it may be quite useful to remember that cultural and historical interpretations are impossible without detailed analyses and examinations of archaeological sites, the only sources of information about prehistoric individuals and entire ethno-cultural communities.

To illustrate, the genetic analysis of twenty individuals from five burial mounds of the Scythian era located in the Sayan Highlands indicated that thirteen of them were first-degree relatives [Mary, et al., 2020]. In another work the examination of a Hunnic necropolis in Mongolia has allowed to establish that it comprised the representatives of five generations of two family clans buried in the same necropolis [Keyser et al., 2020]. Unfortunately, these and a number of similar articles discuss only the results of the work of geneticists. They shed no light on the planigraphy of the kurgan groups under study or on the analysis of their burial structures; there is no data concerning the chronology of the burials. When archaeology with its rich experience in the field is left neglected, the results of geneticists may appear less convincing or even doubtful. Archaeology has a whole arsenal of reliable methods and approaches, which can be illustrated by excellent examples in the studies of Scythian royal mounds [Alekseev 1991; Mozolevsky, Polin 2005]. Of relevance is also the method of spatial analysis developed by the present author; this has proved to be quite effective in establishing social hierarchies, when the depth of graves and their location, with respect to each other and the space organization inside the mounds, are taken into special consideration [Ochir-Goryaeva, 2018].

Keywords

genetic methods, planigraphy of the kurgan groups, archaeological research

Note/comment

KIN AND POWER IN EARLY CELTIC COMMUNITIES OF SOUTHWESTERN GERMANY

Joscha Gretzinger¹, Angela Mötsch¹, Felicitas Schmitt², Michael Francken², Hannes Rathmann^{3,4}, Günther Wieland², Katerina Harvati^{3,4,5}, Wolfram Schier⁶, Dirk Krausse^{2,7}, Johannes Krause & Stephan Schiffels^{1,8}

¹ *Max Planck Institute for the Science of Human History*

² *State Office for Cultural Heritage Baden-Wuerttemberg*

³ *Institute for Archaeological Sciences, Eberhard Karls University, Tübingen*

⁴ *Senckenberg Centre for Human Evolution and Palaeoenvironment, Tübingen*

⁵ *DFG Centre for Advanced Studies 'Words, Bones, Genes, Tools: Tracking Linguistic, Cultural and Biological Trajectories of the Human Past', Tübingen*

⁶ *Institute for Prehistoric Archaeology, Free University Berlin*

⁷ *Institute of Prehistory, Early History and Medieval Archaeology, Eberhard Karls University, Tübingen*

⁸ *Max Planck Institute for Evolutionary Anthropology*

The European Iron Age is characterised by the two key archaeological cultures Hallstatt and La Tène in a large region to the north of the Alps, which are broadly associated with 'Celts'. While this term does not serve as an accurate description or grouping of a homogenous people or ethnic group, it highlights the close connection between a specific archaeological horizon, hypothesised linguistic affiliations (Celtic languages), and historical sources. The pan-European patterns and linguistic evidence for cultural connections during this time are complex and encompass a huge region from the Iberian Peninsula throughout Central Europe and as far east as Anatolia (during the 3rd century BC). However, during the earlier phase of the Iron Age (800 – 450 BC, Hallstatt C and D), a core region in Southwestern Germany and Eastern France, the 'West-Hallstattkreis', stands out in its archaeological importance, as highlighted by the emergence of rich and unprecedented 'princely burials', typically associated with the early Celts. Up to the present-day, the identity of these buried elites and the political power they represented remain controversial, with suggestions including chieftains, spiritual leaders, or even kings. Here, we describe and analyse the first genome-wide data from Southwest Germany dating to the late Hallstatt period. By reconstructing the genetic profiles of more than 20 individuals from this early Celtic population in Germany, we gain insights into familial relationships, transregional connections, system of rule, and the substantial population movements postdating the Iron Age in the region.

Keywords

Celts, Hallstatt, Kinship, Population Genetics, ancient DNA, Iron Age

Note/comment

Missing email address (schiffels@shh.mpg.de) and affiliation (Department of Archaeogenetics, Max Planck Institute for the Science of Human History, Jena & Department of Archaeogenetics, Max Planck Institute for Evolutionary Anthropology, Leipzig) for last author Stephan Schiffels. Reformatting of the Abstract author(s) section is necessary.

ANCIENT GENOMES REVEAL SOCIAL AND GEOGRAPHIC STRUCTURING OF THE POPULATION IN CARPATHIAN BASIN AT THE TIME OF THE AVAR EMPIRE

Guido Alberto Gneccchi Ruscone¹, Anna Szécsényi-Nagy², István Koncz³, Gergely Csiky², Zsófia Rácz³, David Reich^{4,5,6,7}, Tivadar Vida^{2,3}, Zuzana Hofmanová^{1,8}, Choongwon Jeong⁹, Johannes Krause¹

¹ *Department of Archaeogenetics, Max Planck Institute for Evolutionary Anthropology, 04103, Leipzig, Germany*

² *Institute of Archaeology, Research Centre for the Humanities, Eötvös Loránd Research Network, 1097, Budapest, Hungary*

³ *Institute of Archaeological Sciences, Eötvös Loránd University, 1053, Budapest, Hungary*

⁴ *Department of Genetics, Harvard Medical School, Boston, MA 02115, USA*

⁵ *Department of Human Evolutionary Biology, Cambridge, MA 02138, USA*

⁶ *Broad Institute of Harvard and MIT, Cambridge, MA 02142, USA*

⁷ *Howard Hughes Medical Institute, Harvard Medical School, Boston, MA 02115, USA*

⁸ *Department of Archaeology and Museology, Faculty of Arts, Masaryk University, 60200, Brno, Czechia*

⁹ *School of Biological Sciences, Seoul National University, 08826, Seoul, Republic of Korea*

According to historical records, the Avars settled the Carpathian Basin in 568 CE, where they established the Avar “Qaganate” that lasted over 250 years, exerting a major influence in shaping the history Early Medieval Europe. Archaeological records of their material culture testify Inner or Central Asian origin of certain elements, but intensive contacts with the Byzantine Empire and the Eastern European steppe are also detected. Despite the rich archeological record and various historical sources, the genesis of the Avars and the social and political composition of their nomadic empire is still highly controversial and debated among scholars. The Qaganate unified people of different origin, and incorporated them to the empire on various levels. Local elites emerged that kept distinct traditions, but autochthon people probably also admixed with the newcomers.

Here we analyze new genome-wide data of 66 Early Medieval period individuals from present-day Hungary. Part of them were uncovered from Avar period elite burials located in the Danube-Tisza region, the primary power center of the Avar empire. The remaining were retrieved from different archeological contexts in the immediate surrounding areas from the IV-VIII. centuries. Our results reveal striking patterns of genetic structuring, mirroring geography and social stratification of the both culturally and genetically heterogeneous population of the Avar empire.

Keywords

Ancient DNA, Avar, Early Medieval, Carpathian Basin, Ancient genomes

Note/comment

MATERNAL LINEAGES FROM 10-11TH CENTURY COMMONER CEMETERIES OF THE CARPATHIAN BASIN

Kitti Maár¹, Gergely Varga², Bence Kovács², Oszkár Schütz¹, Balázs Tihanyi^{2,3}, Zoltán Maróti^{4,2}, István Nagy^{5,6}, István Raskó⁷, Endre Neparáczki^{2,1}, Tibor Török^{1,2}

¹ Department of Genetics; University of Szeged, Szeged, Hungary

² Department of Archaeogenetics; Institute of Hungarian Research, Budapest, Hungary

³ Department of Biological Anthropology; University of Szeged, Szeged, Hungary

⁴ Department of Pediatrics and Pediatric Health Center; University of Szeged, Szeged, Hungary

⁵ SeqOmics Biotechnology Ltd., Mórahalom, Hungary

⁶ Institute of Biochemistry; Biological Research Centre, Szeged, Hungary

⁷ Institute of Genetics; Biological Research Centre, Szeged, Hungary

The conquer of the Carpathian Basin by the Hungarian tribes in the 9th century played a fundamental role in the history of Hungary, but the origin of the 10-11th century Hungarian people is still poorly understood. Based on the burial characteristics an elite social stratum can be discriminated from the major, commoner layer of the Conquer Period, but nothing is known about the genealogical relationship of these two groups. Genetic studies so far mostly concentrated on the investigation of the elite, therefore we set out to examine the genetic structure of the commoners, in order to be able to compare the two groups. We determined the complete mitochondrial genome sequences of 202 remains, most of them belonged to the plebeian people of the 10-11th century Carpathian Basin. We detected considerable (12%) Asian phylogeographic ancestry among the investigated individuals, which was considerably smaller than that in the elite (30%). Population genetic analyses revealed significant differences between the two groups, and mapped the commoners to ancient European populations, while the elite was mapped much closer to Asian groups. However shared sub-haplogroups between the elite and commoner layers indicated admixture between them, which happened in both directions, but by the 11th century this was not yet enough for genetic equalization.

Keywords

ancient DNA, population genetics, mitochondrial DNA, Hungarian conquest period

Note/comment

**THE LATE-ANTIQUE FUNERARY COMPLEX OF ITTENHEIM (ALSACE, BAS-RHIN).
RE-READING OF ARCHAEO-ANTHROPOLOGICAL DATA AT THE DAWN OF
GENOMICS**

Melanie Pruvost¹, Fanny Mendisco¹, Hélène Barrand-Emam², Fanny Chenal³

¹ *Université de Bordeaux, CNRS, UMR5199 PACEA, Allée Geoffroy Saint-Hilaire, 33600 Pessac*

² *ANTEA-Archéologie, UMR 7044, 11 rue de Zurich, 68440 Habsheim*

³ *Inrap Grand Est, UMR 7044, 10 Rue d'Altkirch, 67100 Strasbourg*

The Ittenheim site "Lotissement du stade" (Bas-Rhin, France) delivered a small Late Antiquity community burial complex consisting of 23 burials, occupied over a short period of time from AD 350 to 430-450. Confined within a small space of 225 m², the funerary ensemble seems to be organised in small groups of tombs separated by empty areas and a few loosely arranged graves. A study of the age and sex composition of the population showed that the mortality profile was compatible with that of natural mortality, with the exception of the total absence of individuals under one year of age. The way in which burials are laid out in small groups of graves raises questions about the type of recruitment with possible kinship ties (biological or social) between these different individuals.

In order to verify these working hypotheses, a palaeogenomic study was carried out over the entire necropolis. Thanks to the excellent preservation of DNA on this site, it was possible to obtain the complete genome of more than 90% of the individuals. These results enabled us to find family links between individuals within the different groups and partially confirm the hypotheses of family regroupings established by the archaeological studies. However, these analyses also raised new questions, particularly about the origin of these individuals.

The relatively small number of burials on the Ittenheim site and the favourable taphonomic conditions have enabled an almost exhaustive palaeogenetic analysis of this site, making it an exemplary site for comparing genomic and archaeological data at different levels : management of the burial space, geographical origin of the individuals and also the variability of funeral practices within the same family group, chronology of the site...

Keywords

paleogenomic, Late Antiquity, Kinship analysis, funeral practices

Note/comment

INVESTIGATING KINSHIP PRACTICES THROUGH DENSE SPATIAL AND TEMPORAL SAMPLING OF 5-6TH CENTURY CEMETERIES IN PANNONIA

István Koncz¹, Deven Vyas², Tivadar Vida^{3,4}, Balázs Mende⁴, Johannes Krause^{5,6}, Janet Kay⁷, Walter Pohl⁸, Krishna Veeramah², Patrick Geary⁹

¹ *Eötvös Loránd University, Institute of Archaeological Sciences*

² *Department of Ecology and Evolution, Stony Brook University*

³ *Institute of Archaeological Sciences, Eötvös Loránd University*

⁴ *Institute of Archaeology, Research Centre for the Humanities, Eötvös Loránd Research Network*

⁵ *Department of Archaeogenetics, Max Planck Institute for the Science of Human History*

⁶ *Institute for Archaeological Sciences Archaeo- and Palaeogenetics, University of Tübingen*

⁷ *Department of Art & Archaeology, Princeton University*

⁸ *Institute for Medieval Research, Austrian Academy of Sciences*

⁹ *School of Historical Studies, Institute for Advanced Study, Princeton*

When used in conjunction with archaeology, paleogenomics can be a powerful tool to better understand human history, demography and with the sampling of whole sites it could also provide insights to the processes involved in the formation of communities and social structures. This is especially interesting in the Middle Danube Region as very few parts of Europe witnessed so many population shifts in a few centuries as this area during the early Medieval period. After the decline of the Roman rule in Pannonia (433 AD) came a time of political instability. From the last decades of the 4th century onward until the arrival of the Avars in the late 6th century, population groups arrived continuously into the Carpathian Basin. This political instability led to the emergence of a mosaic-like cultural landscape with small burial sites consisting of around 20-50 graves. In our study, we analyze three cemeteries near the southern shore of Lake Balaton (in present-day Hungary) from the 5th and 6th centuries. We present new findings from two nearby late-5th-century cemeteries named Hács and Balatonszemes and compare them to the mid-6th-century cemetery of Szólád published by Amorim et al. (2018). We use principal component analyses and genetic clustering analyses to characterize the genetic ancestry of the 25 individuals and estimate levels of kinship between them. We analyze these results alongside the archaeological record of the sites to investigate how differences in ancestry and kinship are reflected within the layouts of the cemeteries and whether these are similar from cemetery to cemetery. Furthermore, we also use analyses of identity-by-descent (IBD) tracts in the genomes to test whether there is population continuity between the late fifth century Hács and Balatonszemes with sixth century Szólád or whether there is evidence of the continuous immigration attested by the written sources.

Keywords

ancient DNA, kinship, Carpathian Basin, social organisation, early medieval Europe

Note/comment

INVESTIGATING KINDREDS AND WAVES OF MIGRATION IN 6-8TH CENTURY NORTHERN ITALY THROUGH ARCHAEOLOGICAL AND PALEOGENOMIC ANALYSES

István Koncz¹, Yijie Tian², Alessandra Modi³, Caterina Giostra⁴, Janet Kay⁵, Elena Bedini⁴, Walter Pohl⁶, David Caramelli³, Johannes Krause^{7,8}, Patrick Geary⁹

¹ *Institute of Archaeological Sciences, Eötvös Loránd University*

² *Department of Ecology and Evolution, Stony Brook University*

³ *Dipartimento di Biologia, Università degli Studi di Firenze*

⁴ *Dipartimento di Storia, Archeologia e Storia dell'Arte, Università cattolica del Sacro Cuore*

⁵ *Department of Art & Archaeology, Princeton University*

⁶ *Institute for Medieval Research, Austrian Academy of Sciences*

⁷ *Department of Archaeogenetics, Max Planck Institute for the Science of Human History*

⁸ *Institute for Archaeological Sciences Archaeo- and Palaeogenetics, University of Tübingen*

⁹ *School of Historical Studies, Institute for Advanced Study*

The Langobard conquest of Italy is one of the most well documented migrations in early medieval Europe. Collegno, near Turin – founded around the turn of the 6th-7th centuries and remained in use till the 8th century – is among the most important burials sites dated to the beginning of the Langobard occupation. Previous study from the Veeramah Lab showed that the community was organized around biological kinship with multiple kindreds. The former study focused on the first phase of the site, but additional sampling from its later phases allows us a more comprehensive study of this cemetery. While a large part of the earliest period individuals had more ancestry associated with contemporary northern Europeans, the later period is marked by the arrival of a new genetic ancestry. This pattern suggested that there might have been multiple different groups of people that arrived and settled in this region gradually within a period of time. We were able to find new kindreds and complement the old ones with individuals from the later phases. Integrating paleogenomic results with archaeological data we found correlation between burial customs and kindred groups and we identified patterns that suggest the community was indeed organised around biological relatedness, but rather than around the wider kinship, the focus was on the core families.

Keywords

ancient DNA, kinship, migration, early medieval Europe, Italy

Note/comment

USING ADNA AS PART OF A MULTI-PROXY APPROACH TO UNDERSTAND BIOLOGICAL AND SOCIAL KINSHIP OF UNUSUAL BURIALS FROM PORTMAHOMACK (SCOTLAND)

Claire-Elise FISCHER¹, Iñigo Olalde^{2,3}, David Reich^{4,5,6,7}, Ian Armit¹, Martin Carver¹, Cecily Spall⁸

¹ *Department of Archaeology, University of York, York YO1 7EP, UK*

² *Institute of Evolutionary Biology, CSIC - Universitat Pompeu Fabra, 08003 Barcelona, Spain*

³ *Department of Genetics, Harvard Medical School, Boston, MA 02115, USA*

⁴ *Department of Human Evolutionary 46 Biology, Harvard University, Cambridge, MA 02138*

⁵ *Broad Institute of MIT and Harvard, Cambridge, MA 02142, USA*

⁶ *Department of Genetics, Harvard Medical School, Boston, Massachusetts 02115, USA*

⁷ *Howard Hughes Medical Institute, Boston, MA 02115, USA*

⁸ *FAS HERITAGE*

The Tarbat Discovery Programme is best known for the excavation of an 8th-century Pictish monastic settlement which lay around and beneath the Church of St Colman, Portmahomack, Easter Ross, Scotland. The results of the 20-year research programme also identified exceptional archaeology belong to a later medieval settlement of the 13th to 16th centuries. Evidence for housing and craft-working was excavated, as well as over 80 medieval burials from the nave (Carver et al. 2016)

This paper presents the results of a recent scientific enquiry into a group of highly unusual burials, including a grave that contained six skulls. It was located in the central part of the nave of the church to accommodate an oak coffin containing the body of an adult male, bearing signs of perimortem sharp force injuries. This individual was buried with a group of four skulls around his head. Sometime later, the grave was reopened for the burial of a second man, an event accompanied by the rearrangement of the skull of the grave's earlier occupant. These highly unusual burials have been the subject of a multi-proxy approach, combining detailed osteological study, radiocarbon dating including Bayesian analysis, multi-isotope analysis, facial reconstruction and ancient DNA analysis. For the aDNA, nine samples were targeted from which eight yielded genome-wide data.

Results highlight that seven of the individuals are males, with only one female was identified. They also show a high diversity of mitochondrial DNA and a relatively low diversity of the Y chromosome. Kinship analysis performed on these samples indicates a family composed of five individuals, including a woman.

Altogether, the data allows different scenarios for this family to be constructed and provides insight into Scottish clan organisation.

Keywords

aDNA, Kinship, Late Medieval, Clan organisation

Note/comment

SURVIVAL OF ADNA IN TOOTH AND BONE SAMPLES FROM IRON AGE (7TH - 12TH CENTURIES AD) BURIALS IN LATVIA

Renate Ranka¹, Jānis Ķimsis¹, Alise Pokšāne¹, Elīna Pētersone-Gordina², Antonija Vilcāne², Alisa Kazarina¹, Guntis Gerhards²

¹ *Latvian Biomedical Research and Study Centre*

² *Institute of Latvian History, University of Latvia*

Ancient DNA (aDNA) studies offer new possibilities for the in-depth investigation of ancient social structures at local and regional scales. Human aDNA studies have helped to decode the human history on the Eurasian continent. Present-day Latvia is situated in north-eastern Europe with a coastline along the Baltic Sea. During the Iron Age the local inhabitants began to form distinct ethnic and regional identities. The productive farms continued to develop, and crafts and trade became increasingly important. Studies of historical genomes and metagenomes may help to explore many different perspectives, in particular kinship, female/male mobility, funeral ritual practice, and life experiences. However, endogenous DNA preservation in human skeletons is crucial for aDNA studies. Here, we examined DNA preservation within tooth and bone samples from two Iron Age cemeteries in Latvia: Lejasbiteni (Vidzeme region), and Cunkani-Drengeri (Zemgale region) (7th – 11th centuries AD). The DNA extraction was performed according to a modified version of the protocol of Keyser-Tracqui and Ludes, 2005. Metagenomics shotgun libraries were sequenced using Illumina technologies. Raw-read sequencing data were processed using the EAGER pipeline for aDNA sequencing data. For microbial DNA analysis, read files were analyzed using MALT 0.5.0. The results indicated that human DNA proportion in bone samples was less than 10%. Higher proportion of human DNA was recovered from the petrous pyramid and well-preserved tooth samples, while mitochondrial DNA yields varied greatly between individual specimens. The presence of oral microbiome signature was detected in archaeological tooth samples indicating the preservation of ancient microbial DNA. Overall, we were able to access the endogenous aDNA in archaeological tooth and bone samples. The availability of aDNA data will be highly useful for investigation of the demographic history and social structures in Iron Age Latvia.

Acknowledgements. This study was supported by the Latvian Council of Science project No lzp-2018/1-0395.

Keywords

aDNA, Iron Age, Latvia

Note/comment