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THE GENETIC CHALLENGE TO MEDIEVAL HISTORY AND ARCHAEOLOGY

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The Genetic Challenge
to Medieval History
and Archaeology

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Editor's Introduction: The Genetic Challenge to Medieval History and Archaeology

Walter Pohl

This issue deals with a topic that may at first surprise a reader of a journal of global medieval history: the use of genetics in the study of the past. Genome analysis has hardly yet been addressed in the context of global history, although it certainly is a matter of global interest. The genomes of Richard III, of the descendants of Genghis Khan, or of the indigenous populations of North America and Australia have been the object of genetic study. Geneticists have addressed Bantu migrations (see Eggert in this issue) and Viking raids (see Hofmann here too). Methodological problems and, sometimes, public misconceptions are very similar across the globe. Still, ›genetic history‹ has not yet raised much interest among historians; if at all, profound skepticism has prevailed. In medieval history, Patrick Geary is one of the pioneers who have critically monitored the use of genetics for historical questions (see his contribution in this issue).

Genetic methods are well established as tools in prehistoric archaeology, and geneticists have often taken the lead in recent debates about migrations and cultural flows in the deep past. Neanderthal admixture, the settlement of the Americas or the expansion of Neolithic culture are well-known cases in point. In historical archaeology, lively debates have begun about the way in which genetic and archaeological evidence can be synthesized. As several contributions (Feuchter and Samida, Brather, Burmeister) in the present issue show, the critique is certainly not directed against the use of genetic analyses and other methods of scientific archaeology to supplement more traditional modes of archaeological interpretation. There is, however, a concern about geneticists' claims that these ›scientific‹ data could supersede the more intricate forms of cultural interpretation by archaeologists. Yet the interpretation of genomic data is an art in itself. They allow calculating relative distance between individuals, and constructing clusters of more or less genetically related samples. As historians and archaeologists we have to insist that defining populations or even peoples does not directly emerge from the genetic evidence – it requires a historical interpretation, which needs to conform to historical methodology. Many geneticists have taken this requirement rather lightly so far, to say the least.

It is thus no coincidence that many contributions in this issue address problems of ›genetic history‹ rather than its impressive potential. If we want to profit from the extraordinary possibilities that the breathtaking progress of genetic methods offers – and all the contributors agree that we should – we need to calibrate our interdisciplinary methodology. This is a scientific as well as a political issue. The emergence of genetics has spurred high hopes in the general public that there can finally be a scientific answer to the fundamental questions of identity: who am I?, and, who are ›we‹? In the course of history, the last word in this matter has mostly passed from one humanities discipline to another: theology, philosophy, history, physical anthropology, psychology; now it is the turn of genetics. Being a Viking, a German,

an American Indian or a descendant of Genghis Khan suddenly seems to matter much to many people; the genes, rather than one's cultural baggage or a neurosis developed in infancy now seems to decide who one ›really‹ is. The media (including scientific journals such as *Science* and *Nature*) exploit and popularize such notions (see the examples in Feuchter and Samida in this issue).

Among humanities scholars, this raises a double concern: first, the historical experience with the race theories promoted by physical anthropologists in the later nineteenth and earlier twentieth centuries shows that a scientific method that inescapably classifies humans by their bodily ›essence‹ is bound to prompt political misuse, from exclusion to extermination. It needs to be acknowledged that geneticists, starting with Cavalli-Sforza, have openly condemned racism and refuted ›race‹ as a scientific category, but that may not be enough. Second, the short-cut identification of genetically defined populations with historical peoples falls far behind the state of the art in the humanities and social sciences. We have made significant progress since the mid-twentieth century in deconstructing collectives. For historians of the nationalist era, nations and peoples were naturally constituted and clearly delineated collective agents – the nation, not the individual was the true subject of history. Since that time, we have learnt much about the ways in which peoples, states and ethnic groups emerge from a constant process of cultural construction, social negotiation and political competition. Methodologically, this means that we cannot take for granted to which degree there is an overlap between the people who believe or are believed to belong to a named (ethnic) grouping, the speakers of a certain language, those who can be distinguished by a recognizable cultural habitus (for instance, in the archaeological evidence), and of course those who share a certain biological or territorial origin. These four types of ›population‹ (in the sense of a group of humans defined by a criterion that we choose for scientific purposes) do not naturally converge in a ›people‹. They may overlap to very differing degrees, and some of these criteria may fade at the margins in broad and dynamic grey zones. As Sebastian Brather argues in this issue, even single cultural criteria may circumscribe rather different groupings. In this complex situation, there is no way in which genetic results can help to define a clear distinction between those who should be included in a people and those who must be excluded – trying to do so would be both methodologically incorrect and politically hazardous.

Again, there seems to be consensus among the authors of this issue that these methodological principles can provide a sound basis for the future collaboration between geneticists, archaeologists and historians. They are as yet not uncontested, but there is growing awareness in the disciplines involved that simplistic models in which genetic evidence could be neatly accommodated are not much help. Much progress has been made in genetic research in the last 20 years or so (for an overview, see Geary and Veeramah in this issue). Cavalli-Sforza and his contemporaries still had to work exclusively with modern DNA, and with data-sets that in practice only allowed to distinguish collectively between modern nations. They thus worked (and had to work) with statistical averages of populations constituted by modern peoples or ethnic groups. It took some time to realize the methodological problems of this type of data analysis. Scientific progress helped to arrive at more complex models. The ability to use the whole genome and not just Y-Chromosome and mt-DNA allows going beyond a few haplotypes as defining features of certain populations. The increased availability of ancient DNA means that precarious inferences across many centuries or even millennia

ceased to be the only way to assess the genomes of people living in a distant past. Bayesian mathematics and advanced computer modelling (the field in which Krishna Veeramah excels) can lead to more complex interpretations of the genetic data – although a historian who is used to balancing many factors and variables in his interpretations of the past might wish that one day computer models will accommodate more than two or three variables.

Most of all, many geneticists have come to realize that their complex evidence would be wasted if it was just fed into very simple historical models, and that large migrant groups usually do not travel with a quasi-identical genome and cultural baggage. One conclusion that emerges from all of the contributions to the present volume therefore is that we need more interdisciplinarity – research groups that unite geneticists (and other scientists), archaeologists, where relevant, linguists, and, for the historical periods, historians. Patrick Geary and Krishna Veeramah present a model project on the Longobard migration to Italy in the sixth century CE in this issue, which involves a large interdisciplinary team. It deals with a case very well attested in written sources and in well-dated graves, which can yield extensive data for scientific analyses. If successful, this project may provide exceptional clues as to how a historical migration is reflected in all the different types of evidence, how to deal with this multiplicity, and to what extent a synthesis of all the results is possible.

Finally, the editors of ›Medieval Worlds‹ are grateful to Jörg Feuchter and Stefanie Samida who organized the Conference ›Genetic History: A Challenge to Historical and Archaeological Studies‹ in Berlin in October 2015. Some of the contributions of the present issue are based on papers presented at this conference, and the article by the two organisers offers important elements of a synthesis. This is a debate that should be continued, and might also be pursued further in future issues of this journal.

Why Archaeologists, Historians and Geneticists Should Work Together – and How*

Stefanie Samida and Jörg Feuchter**

In recent years, molecular genetics has opened up an entirely new approach to human history. DNA evidence is now being used not only in studies of early human evolution (molecular anthropology), but is increasingly helping to solve the puzzles of history. This emergent research field has become known as »genetic history«.

The paper gives an overview on this new field of research. The aim is both to discuss in what ways the ascendant discipline of genetic history is relevant, and to pinpoint both the potentials and the pitfalls of the field. At the same time, we would like to raise the profile of the field within the humanities and cultural studies. We hope that the opportunity for communication between representatives of different disciplines will contribute to loosening up the widespread monodisciplinary method of working and, in particular, bring together the relevant scientific and cultural streams of research.

Keywords: genetic history; history; archaeology; genetics; interdisciplinarity.

History in an age of genetics

In recent years, the media have repeatedly seized on the findings of genetic research to make headlines such as the following: »Finding the Iceman's 19 living relatives«;¹ »A million Vikings still live among us: One in 33 men can claim direct descent from the Norse warriors«;² »How Germanic are we?«;³ »Britain is more Germanic than it thinks«;⁴ and »We Europeans are Asians«.⁵ Articles such as these already attest to the increasing attention the field of »genetic history« is receiving in public discourse. They also clearly evoke a major fascination of this new discipline: the promise of a new link between history and modern identities, a connection between past and present established biologically, via the genes people have inherited from historical ancestors. Unlike other scientific methods applied to the study of history and archaeology (e.g. carbon dating or isotope analysis), genetics is immediately con-

* This paper presents remarks made among the conveners of the conference »Genetic History: A Challenge to Historical and Archaeological Studies« (Humboldt University Berlin, 1-2 October 2015). Some paragraphs have been translated by E.-R. Jaksch.

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- 1 Langemak, So wurden Ötzis 19 lebende Verwandte aufgespürt.
- 2 Anonymous, A Million Vikings.
- 3 P.M. Magazin, Wieviel Germane steckt in uns?
- 4 Schulz, The Anglo-Saxon Invasion.
- 5 Bild der Wissenschaft, Wir Europäer sind Asiaten.

cerned with issues of identity, since the modern mind perceives DNA as a carrier of identity. Thus problems of the past are often conflated with the question of the ethnic identity of modern populations.

One of the most famous examples of genetic history in recent times are the DNA tests performed on the bones of the last Plantagenet king, Richard III, reburied in Leicester in late March 2015. Excavations, surrounded by much media hype, had begun in 2012. Archaeologists had suspected for some time that the king's remains would be found beneath a Leicester parking lot on the site of the former Greyfriars Church, where Richard is said to have been buried. Many pieces of classical archaeological and bio-anthropological evidence already pointed with overwhelming probability to the fact that the skeletal remains found there were really those of the Machiavellian figure portrayed by William Shakespeare in his play of the same name. In addition, a DNA analysis was performed. It resulted in a close match with living relatives on the female line of descendance of Richard III. But there was no match with those on the male line. Therefore DNA analysis on its own did not give conclusive proof of identity. Yet the mismatch was explained by the plausible hypothesis that there had been »illegitimate« children descending from Richard. And the DNA analysis did not stop at mere efforts of identification. It was also used to reconstruct, with some probability, the hair and eye colour of the individual from Leicester, namely blond hair and blue eyes; thus, the researchers came to the conclusion that the earliest extant portrait of Richard III gives an accurate representation of his physical appearance, while all the later ones do not.⁶ Thus the case of the king beneath the parking lot highlights a second quality that is so appealing in DNA-based history, namely the potential to oppose biological evidence that is perceived as objective and therefore as superior, to traditional documentary or pictorial historical evidence considered subjective and possibly flawed.

Genetic evidence was first used in studies of early human evolution and migration, a field often labelled »molecular anthropology«.⁷ Yet today it is increasingly applied in attempts to try to help solve the puzzles belonging to the field of history »proper«, i.e. those traditionally falling into the academic discipline of that name. Consequently, the emergence of a new, »genetic« history was noted both by participants in the field and by outside observers towards the end of the first decade of the new millennium. Already in 2008 geneticist David B. Goldstein stated: »[...] genetics is slowly earning a place in the historical sciences. Our narratives describing the histories of peoples and events, from the Aryan invaders of India to the Viking attacks on the British Isles, are all being augmented and refined by genetic analyses in a field now often called genetic history.«⁸ In 2010, another geneticist, Chris Tyler-Smith, commented: »[...] genetics is now starting to get at real details of history.«⁹ Anthropologist Yulia Egorova wrote: »The assumption that ›DNA evidence‹ may help in historical research appears to have informed a whole new field in population genetics, which is sometimes described as genetic anthropology or genetic history.«¹⁰ One year later, in 2011, historian of science Veronika Lipp-

6 Buckley *et al.*, ›The King in the Car Park‹; King *et al.*, Identification of the Remains.

7 Sommer, *Evolutionäre Anthropologie*, 135 sqq. gives a comprehensive overview on molecular anthropology and outlines its early phase.

8 Goldstein, *Jacob's Legacy*, 3.

9 Quoted in Callaway, *Spanish Inquisition*.

10 Egorova, *DNA Evidence*, 349.

hardt stated: »[...] now, the last 2000 years are being taken to the laboratory, and history may soon not belong anymore to historians alone.«¹¹ In 2012 anthropologist Nadia Abu-El Haj defined genetic history as a »subset« of »anthropological genetics.«¹² There can be no doubt that history, like anthropology before, today finds itself in an »age of genetics«.¹³ This age is marked by the fact that genetics is understood as »the dominant discourse describing the human condition.«¹⁴ Already a quarter of a century ago a »geneticization«¹⁵ touching upon many fields of knowledge was described, and that claim has only gained in validity since the complete deciphering of the human genome in 2001. Today the prosperity of genetic history is such that we can safely say that it has passed beyond any period of emergence and that historical research that includes DNA evidence is coming now into its own, alongside the study of the traditional sources of archaeology (material evidence) and of history (written sources). The establishment of the field can also be measured by its institutionalisation and public funding. In the last few years, large research laboratories and institutes exclusively devoted to it have been created in several countries, perhaps most prominent among them the Max Planck Institute for the Science of Human History in Jena (Germany).¹⁶

Genetic history studies are finding great attention in the media and the public, as the headlines cited above prove. Academic historians however have been slow to recognise the challenge. With the exception of a very few scholars, namely US medieval historians Patrick Geary (Institute for Advanced Study, Princeton) and Michael McCormick (Harvard University), until recently they have failed to realise both the potential and the provocation genetic history represents.¹⁷ Archaeologists, traditionally more open to scientific methods due to the fact that they have always worked with material sources, have been faster to acknowledge the new field.¹⁸ However, among archaeologists there is an alarming tendency to take the results of genetic history – and indeed of other scientific methods – for granted, a tendency that contributes to an understanding of archaeology as a matter of quantitative science instead of an interpretative cultural studies discipline.¹⁹ It is safe to say that genetic history is not only here to stay, but will grow in importance in the foreseeable future, especially if we consider recent progress in sequencing technology methods and the disposability of DNA material both modern and ancient. It is thus urgent that historians and archaeologists face the chal-

11 Lipphardt, *Der Körper als Substrat*, 109 (translation of original German quote by Jörg Feuchter).

12 Abu El-Haj, *Genealogical Science*, 3.

13 See title of Lindee et al., *Anthropology in an Age of Genetics*.

14 Lippman, *Prenatal*, 18.

15 The concept of »geneticization« was introduced by Abby Lippman in a medical context, see *ibid.*, 19, »Geneticization refers to an ongoing process by which differences between individuals are reduced to their DNA codes, with most disorders, behaviors and physiological variations defined, at least in part, as genetic in origin. It refers as well to the process by which interventions employing genetic technologies are adopted to manage problems of health.« The concept has then been generalised and transferred to non-medical disciplines like the production of knowledge about individual genealogies; see Palmié, *Genomics, Divination, »Racecraft«*, 207. Against employing the term: Abu El-Haj, *Genealogical Science*, 25.

16 For a detailed overview on facilities and on public funding of aDNA research, and the most promising field in genetic history today, see Gibbons, *Ancient DNA Divide*. On the founding of the Jena Institute see also Feuchter, *DNA der Geschichte*.

17 See for example Geary, *Using Genetic Data*; Geary, »Völkerwanderung«; McCormick, *Molecular Middle Ages*.

18 See for example Renfrew and Boyle, *Archaeogenetics*; Renfrew, *Archaeogenetics*; Alt, *Grenzüberschreitungen*.

19 See Samida and Eggert, *Archäologie als Naturwissenschaft?*; Samida, *Archaeology in Times of Scientific Omnipresence*.

lenge of this new discipline of the past. Instead of ignoring the competition from the biology department or accepting it without any deeper understanding, an active engagement with genetic history has to take place in history and archaeology.

The 2015 Berlin conference on genetic history

This is the background against which we – an archaeologist and a medieval historian – organised the first interdisciplinary international meeting on the subject.²⁰ Financed by a grant from the Fritz Thyssen Foundation, »Genetic History: A Challenge to Historical and Archaeological Studies« took place at Berlin's Humboldt University in October 2015 and brought together geneticists, archaeologists and historians, as well as anthropologists and historians of science.²¹ Our first general aim was to discuss among different disciplines in what ways the ascendant discipline of genetic history is relevant, and to pinpoint the potentials and pitfalls of this new field of research, which until now has usually been shaped by geneticists alone. Another aim of the meeting was to raise the profile of the field within the humanities and cultural sciences. As already mentioned, unlike prehistoric and proto-historic archaeology, the historical disciplines, especially medieval history with which we are primarily concerned, have paid very little attention to genetic history to date, even though the discipline is engaged in research on highly controversial topics of medieval history, such as the ethnogenesis of early medieval groups like the Lombards and the Anglo-Saxons. By creating an opportunity for communication between representatives of different disciplines, and creating awareness of genetic history within the historical disciplines, we wanted to contribute to a loosening up of the widespread disciplinary method of working and, in particular, bring together relevant scientific and cultural streams of research.²² More than ever before, a discourse between the natural and the cultural scientists is urgently needed today.²³

The conference also aimed at discussing different methods of research and to confront our invited participants with divergent or new approaches. Our concern here was not to delineate the boundaries between disciplines, but rather to encourage dialogue across these boundaries – dialogue from which all the participating disciplines will ultimately benefit. The conference deviated from the usual structure by scheduling papers to be given in tandem. Two speakers discussed every topic, each from the perspective of his or her discipline or field of research. This approach was meant to help sharpen argumentation from both sides and to elucidate developments within each discipline. This did not, however, mean that we were aiming to polarise the arguments. On the contrary, we were interested in joint discussions and an in-

20 Other conferences held before have concerned themselves with genetics and the past from the viewpoint of anthropology. See Sommer and Krüger, *Biohistorische Anthropologie*.

21 The speakers were: Kurt W. Alt (Danube Private University, Krems), Sebastian Brather (Albert-Ludwigs-Universität Freiburg), Stefan Burmeister (Museum und Park Kalkriese), Manfred K. H. Eggert (Eberhard-Karls-Universität Tübingen), Yulia Egorova (University of Durham), Jörg Feuchter (Humboldt Universität zu Berlin), Kerstin P. Hofmann (Freie Universität Berlin), Mark Jobling (University of Leicester), Johannes Krause (Max Planck Institute for the Science of Human History, Jena), Veronika Lipphardt (University College Freiburg), Brigitte Pakendorf (Centre National de la Recherche Scientifique and Université Lyon Lumière 2), Walter Pohl (Universität Wien), Stefanie Samida (Zentrum für Zeithistorische Forschung, Potsdam), Frank Siegmund (Universität Düsseldorf) and Krishna Veeramah (Stony Brook University). For further information see conference website: www.genetic-history.com (retrieved on 14 September 2016).

22 For intriguing examples of non-collaborating research see Pluciennik, *Clash of Cultures?*; Egorova, *DNA Evidence?*

23 See Egorova, *DNA Evidence?*

terdisciplinary exchange of ideas in which each side respects the other; in other words, what we tried to make possible was a debate that was unprejudiced and open, but also critical. We did not seek to establish interpretational sovereignty, but to engender constructive dialogue. At the end of the conference we were satisfied that these aims were, on the large, achieved.

Among the general questions raised at the conference were the following: How do geneticists work together with historians and archaeologists? What are the advantages and disadvantages of such cooperation? What new knowledge can the results of DNA analysis yield for historical and archaeological research? Does genetic history raise new issues or does it return to old questions of history that were believed obsolete? What is the significance of genetic history in public discourse? How do its findings affect identity and the discourse of remembrance? And, finally, how does genetic history change other disciplines? The conference was organised into seven thematic blocks: »Genetics and History«; »Genetic History: Past and Future of a Discipline«; »Genetic History and Migration«; »Genetic History and Kinship«; and two case studies: »The Vikings« and »The Bantu«. The focus of the conference was thus genetic history's concern with the migratory movements of peoples²⁴ and languages²⁵, and its relevance for kinship studies. Genetic epidemiology, research on the historical origins and development of diseases, was left out.²⁶ The 2015 Berlin meeting could only be a first step. It is much too early to expect elaborate answers on the general questions and specific topics enunciated at the conference. But we are very happy that some of the participants have transformed their lectures into papers and have published them in this issue of *Medieval Worlds*. As the conveners of the conference we want to contribute to the issue by writing up some of our thoughts on why archaeologists, historians and geneticists should work together – and how. We do this in three steps: First we want to highlight again the potentials and limits of genetic history; then we present a short overview of genetic history research on a special topic, the Anglo Saxon migration to Great Britain; and lastly, we highlight different methods by which different disciplines might work together.

Potentials and pitfalls of genetic history

The geneticist Bryan Sykes from Oxford University – author of several books including *The Seven Daughters of Eve* and *Blood of the Isles: Exploring the Genetic Roots of our Tribal History*, and also creator of a commercial DNA ancestry testing company – has done more than almost any scientist before him to popularise molecular genetics as a tool for researching the past, both individual and collective.²⁷ Again, more than almost any other scientist, he extols the possibilities which he believes this research could unlock. The prologue to *The Seven*

24 On historical migrations as one of the main focal issues of genetic history see Feuchter, *Mittelalterliche Migrationen*.

25 E.g. by correlating recent and ancient DNA evidence with the spread of Indo-European languages. The works of Colin Renfrew (Renfrew, *Archaeology*; Renfrew, *At the Edge*; Renfrew, *Archaeogenetics*; Renfrew and Boyle, *Archaeogenetics*) are of particular interest in this context. Favourably disposed towards archaeogenetics from the very beginning, he seeks to link archaeology, genetics, and linguistics. For a critical view see, among others, Eggert, *Bantu und Indogermanen*. On current results claiming new insights into the dispersal of Indo-European languages see review article Novembre, *Human Evolution*, and strong criticism by Heggarty, *Ancient DNA and the Indo-European question*.

26 On this important field see Green, *Genetics as a Historicist Discipline*.

27 Sykes, *Seven Daughters*; Sykes, *Blood of the Isles*; the company is *Oxford Ancestors*, see www.oxfordancestors.com (retrieved on 14 September 2016).

Daughters of Eve amounts to a hymn in praise of genetics: »Where do I come from? How often have you asked yourself that question? We may know our parents, even our grandparents; not far beyond that, for most of us the trail begins to disappear into the mist. But each of us carries a message from our ancestors in every cell of our body. It is our DNA, the genetic material that is handed from generation to generation. Within the DNA is written not only our histories as individuals, but the whole history of the human race. With the aid of recent advances in genetic technology, this history is now being revealed. We are at last able to begin to decipher the messages from the past. Our DNA does not fade like an ancient parchment; it does not rust in the ground like the sword of a warrior long dead. It is not eroded by wind or rain, nor reduced to ruin by fire and earthquake.«²⁸ To be fair, it has to be mentioned that Sykes's efforts at popularisation and linking these with his own commercial enterprise have been heavily criticised by other geneticists.²⁹ Yet Sykes's basic claims – that DNA is a document containing »messages from the past« revealing descent and therefore identity, and that this document is superior, because more objective and stable than the usual historical (»ancient parchment«) or archaeological sources (»swords«, ruins) – are echoed by many genetic historians.³⁰ Human DNA is considered a biological »history book«.³¹ Its promise is that it »offers to unlock the past«,³² or, in the words of Alan H. Goodman, the era of genetics comes with a »supersaturated belief in the power of genetic knowledge to tell pasts and predict futures.«³³ Genetic Historians are undoubtedly correct in so far that genetics offers several advantages for historical research and may be used to answer some questions which could not have been resolved in the past using only traditional sources. From an archaeological perspective, for example, it might be possible to determine whether and how individuals in a burial site were related to one another, and to use this data together with archaeological findings and any available historical sources to develop new interpretations of the kinship structure of prehistoric and proto-historic societies. Additionally, genetic analysis of individuals can offer insights into their »physical biography«.³⁴ In other words, ge-

28 Sykes, *Seven Daughters*, 1. See analysis of Sykes approach to individual DNA genealogy in Sommer, »It's a Living History«.

29 E.g.: Bandelt *et al.*, *The Brave New Era of Human Genetic Testing*. For strong criticism of the claims made by individual DNA ancestry researchers see also Thomas, *To Claim Someone has ›Viking Ancestors‹*.

30 See for example the quotes by geneticists in Wolinsky, *Our History, our Genes*, esp. Rene Herrera: »[h]istory can get contaminated over time. But DNA does not lie« (ibid., 129).

31 »Every one of us is carrying his or her personal history book around inside us – we simply need to learn how to read it.« (Wells, *Journey of Man*, XVI, quoted after Abu-El Haj, *Genealogical Science*, 228). See also the observation by Abu-El Haj, *Genealogical Science*, 225: »We are witnessing the emergence of a new kind of ›source within: the genome as an empirical and legible record of our authentic, cultural, and historical selves.«

32 Wailoo *et al.*, *Introduction*, 5

33 Goodman, *Towards Genetics*, 227. Kristiansen, *Towards a New Paradigm?*, 17 sqq., recently spoke of a »third science revolution« in prehistoric archaeology, predicting a paradigm shift connected with the increase in »big data«, »quantification and modelling«, and the »theoretical power of new knowledge«; the increase in and integration of scientific methods (especially those of genetics) are central to his argument. Critical reactions were not long in coming; Niklasson, *Shutting the Stable Door*, 62, countered as follows: »Big Data does not mean better data; after all it is often just the same data linked up. It makes ›bigger‹ interpretations possible, which is great, but this does not equal ›better‹ interpretations, and importantly, just because it is true, it does not mean it is right.«

34 The media and the public sphere are eager for details of genetic analysis such as the colours of our ancestors' eyes and hair, which are believed to permit a »more authentic« reconstruction of their appearance, as in the case of Richard III mentioned above. However, the claim that the Iceman, the Hauslabjoch mummy, also known as »Ötzi«, had brown hair, is largely worthless from the perspective of cultural history.

netic analysis may be able to provide a variety of additional information for historians and archaeologists which would be inaccessible using conventional anthropological analysis (in particular, osteological analysis). Sometimes it may also correct or more precisely describe facts suggested by traditional historical and archaeological evidence that is flawed or vague.

However, hymns of praise like the one by Sykes quoted above somewhat obscure the fact that genetic history is itself beset with a number of problems that tend to circumscribe its capacity to deliver conclusive results. For instance, analyses of ancient human DNA have frequently involved contaminated samples. As a result, proper procedures for sample collection have become an issue of growing importance.³⁵ Indeed recently developed new techniques and methods are promising to resolve contamination problems and even to make it possible to extract DNA from human fossils found in conditions unfavourable to preservation. Yet even in a revolutionary »golden era« of ancient DNA research that has been proclaimed in recent years,³⁶ there is still the problem of uneven sample distribution. Earth burials were not allocated to everyone in past societies, and in many societies most or all bodies were burned. Questions of how representative buried individuals are for a whole population will therefore prevail, no matter how good geneticists are becoming at extracting DNA.³⁷ Another potential problem arises in the use of analyses of recent (»modern«) DNA to extrapolate from people living today to earlier populations. This method is potentially risky when applied to events such as the movements of large numbers of people during the Migration Period, »because it assumes extremely stable communities both before and after the events one hopes to study.«³⁸ In such cases, the models are dependent on hypotheses that are underpinned by statistical methods.

But the problems are not limited to technical issues. They also extend to the way research is organised and conceived. Until now, the new field has been dominated by scientists and geneticists claiming to do historical and cultural research. Archaeologists or historians are seldom among the authors, and even more rare are instances where they have contributed to the initial research design. The way many genetic historians work with history has been aptly described by Mark Jobling, himself a geneticist, as »cherry-picking« those facts from history that fit the hypothesis built from the DNA findings (while other facts are left out).³⁹ Thus the seemingly hard facts of genetics are often arbitrarily inserted into historical contexts.⁴⁰

35 See for example the advice of Brandt *et al.*, Beprobungsstrategien.

36 See for example Knapp *et al.*, Re-Inventing Ancient Human DNA; Gibbons, Revolution in Human Evolution; Cullotta, New life Life for Old Bones; Slatkin and Racimo, Ancient DNA and Human History.

37 On this see Deguilloux and Mendisco, Ancient DNA, esp. 127.

38 Geary, Using Genetic Data, 5.

39 »An additional problem is that geneticists who observe a pattern in their data and seek an explanation for it tend to visit a library, take out a history book and read about a past event that seems to explain the pattern they see. This kind of historical cherry-picking leads to a lack of objectivity in asking what kinds of past events could have given rise to modern genetic diversity« (Jobling, The Impact of Recent Events on Human Genetic Diversity, 794).

40 See also Egorova, Authentizität und historisches Gedächtnis, 53. There is always a certain subliminal biological essentialism at play in such cases; Schmidt, *Was sind Gene nicht?*, 318, calls for a change of thinking »from essentialist readings of genetic entities to an open, pluralistic concept« which, while not abandoning the genome as a crucial component of inherited patterns, nevertheless leaves open the question of which »factors and processes are essential for ontogenesis and which are accidental« (*ibid.*, 319; translation of original German quote by E.-R. Jaksch). This aspect has not featured in the discourse to date.

How important a close collaboration between scientists on the one hand and archaeologists and historians on the other might be is highlighted by a dating error pointed out by Eszter Bánffy, Guido Brandt, and Kurt W. Alt. They showed that a study involving DNA sequencing had incorrectly dated medieval individuals to the Neolithic period – which, of course, led to completely erroneous conclusions.⁴¹ Bánffy, Brandt, and Alt rightly concluded that »all efforts to produce authentic ancient DNA data are worthless if the archaeological background to a genetic project is missing or insufficiently explored.«⁴² While such glaring errors are admittedly rare, it is regularly the case that scientific results in general are not subjected to sufficient critical scrutiny by people working outside of the respective discipline but only competent in the historical era in question.⁴³ Rather, results are often accepted at face value by other disciplines and by the media. As genetic history widens its focus to include more and more »recent« eras (»recent« as opposed to pre-historical), and population genetics is now being used, for instance, to determine the extent to which England was colonised by the Anglo-Saxons and the Vikings, we must keep in mind that biological groups and archaeological groups are two different systems that cannot be regarded as necessarily equivalent, and that genetics cannot determine the membership of a given individual in a given social group.⁴⁴ Thus, a certain degree of restraint seems advisable, especially in view of the terrible consequences of linking race, language, and culture that occurred during the Nazi era, a dark chapter in the annals of disciplines such as prehistoric archaeology,⁴⁵ history⁴⁶ and genetics alike.⁴⁷ This is all the more necessary when references to blood ties with ancestors from thousands of years ago are increasingly becoming a dominant factor in discussions of the culture of remembrance and of social and cultural identity formation, and are leading not infrequently to attempts at instrumentalisation – especially when political and religious interests are involved.⁴⁸ Indeed, Keith Wailoo, Alondra Nelson, and Catherine Lee maintain that modern genetics does not only influence our thinking about the past or about a shared past, but rather, that it has »real effects in the present, for example, by impinging concretely upon the rights of groups within a nation-state or redefining the very boundaries of kinship and nationality.«⁴⁹ Some of these aspects are reflected in our following case study of genetic history research on Anglo-Saxon migration to Great Britain.

41 Bánffy *et al.*, »Early Neolithic« Graves.

42 Bánffy *et al.*, »Early Neolithic« Graves, 468.

43 See also the case of a mathematical error reported in Zimmer, DNA Study.

44 Siegmund, *Kulturen, Technokomplexe*, 53-54.

45 See Steuer, *Eine hervorragend nationale Wissenschaft*.

46 See Schulze and Oexle, *Deutsche Historiker im Nationalsozialismus*.

47 Weiss, *Nazi Symbiosis*.

48 See, e.g., the papers in Sommer and Krüger, *Biohistorische Anthropologie*; Reardon and TallBear, »Your DNA is Our History«; Scully *et al.*, Remediating Viking Origins; Abu-El Haj, *Genealogical Science*; Sommer, History in the Gene; Sommer, »It's a Living History«.

49 Wailoo *et al.*, Introduction, 2. Similar Lindee *et al.*, Introduction, 16: »Blood rewritten as genes provides powerful frames for kinship and identity, race and culture, history and the human future. What stories do genes tell? And what stories do we tell about genes and, in so doing, about others and ourselves, science and society, and nature and culture?« For this reason Goodman, *Towards Genetics*, 229 suggests: »Genetics knowledges, discourses, and practices are too important, too determinative, to escape critical study. What is needed is not an age of genetics, but an age of anthropology to think through the localness, partiality, instability, and context of genetic information. Genetics need anthropology to help fashion its questions and to make sense of its results.«

*Genetic history on the Anglo-Saxons, 2001-2016*⁵⁰

In June 2011 *Spiegel Online*, Germany's leading online news website, featured the article with the headline already quoted above: »Britain is more Germanic than it thinks.«⁵¹ The German author of the piece unequivocally told his readers: »It is now clear that the nation which most dislikes the Germans were once Krauts themselves. A number of studies reinforce the intimacy of the German-English relationship.« The studies in question were mostly genetic analyses of Anglo-Saxon migration from northern Germany to England. The Angles, Saxons, and Britons were proto-historic late antique and early medieval North-Western European populations whose names have come down to us in ancient written sources. However, these sources generally do not tell us conclusively whether these peoples were ethnic groups who believed they had a common ancestry, perceived themselves as a group distinct from other ethnicities, spoke a common language, acknowledged political leaders, or had developed a degree of cultural uniformity. Nor do the written sources reveal the extent to which any of these factors may have existed, the time that they emerged, or for how long they had endured. These questions are constantly being re-examined by historians from various different perspectives.⁵² Thus for historians or archaeologists attempting to study the field of ethnicities in proto-history, the point of departure is anything but straightforward. At issue thus is whether, and how, putative ethnic groups are reflected in archaeological finds and analyses. This question has been the subject to intense and, overall, controversial debate for decades.⁵³ In the case of the Anglo-Saxons and Britain, the discussion goes back more than a century.⁵⁴ Given this difficult state of historical and archaeological research, it is easy to understand the desire for a patent remedy – and this is where the methods of molecular genetics and palaeogenetics are brought into play.

The current state of Anglo-Saxon studies was concisely summarised by archaeologist Heinrich Härke, who noted in 2012 that efforts over the last decade had focused mainly on using palaeogenetics and isotope chemistry to distinguish the Angles and the Saxons from the autochthonous Britons.⁵⁵ Härke stressed that there were certain difficulties with trying to reconcile the new scientific findings with the findings of archaeology. For one thing, as we have noted, assigning ethnicities to archaeological discoveries is a fundamentally controversial issue. In this specific example, the task is to distinguish archaeologically between the Angles and Saxons on the one hand and the Britons on the other. He also pointed out that the extent to which a biologically defined population is normatively connected with a historical group of persons united by an ethnic and cultural identity remains an open question.⁵⁶ In the last fifteen years, various analyses of recent and ancient DNA have been published in connection with this topic. A start was made with a study in 2002. It first gave a summary of changing opinions in archaeology and history stating that the »use of migration as an

50 See also Samida and Eggert, *Archäologie als Naturwissenschaft?*, 42 sqq.

51 Schulz, *The Anglo-Saxon Invasion*.

52 See, e.g., the extensive treatment of the question in Kleinschmidt, *Migration und Identität*.

53 See for example Brather, *Ethnische Interpretationen*.

54 See overview in Lucy, *From Pots to People*.

55 Härke, *Entstehung der Angelsachsen*, 432 sqq.

56 Härke, *Entstehung der Angelsachsen*, 434.

explanation for cultural transitions has varied greatly over the past 100 years and remains controversial.⁵⁷ The authors then presented DNA evidence as an »obvious« contribution to the solution of this problem: »Genetic data comprise an obvious source of information to help resolve these issues.«⁵⁸ In its results, the study claimed to have proven that there was »Y chromosome evidence for Anglo-Saxon mass migration« (the title of the publication). Several other studies followed.⁵⁹ They presented differing results but had this in common: they each demonstrated the existence of genetic continuity – although varying from place to place – since the early Middle Ages. This is certainly an interesting finding, but from the perspective of archaeology and the study of the written sources of Anglo-Saxon history, the conclusions of population genetics do not amount to very much more than a general confirmation of the migration theory, which archaeologists and historians had good reason to favour all along. Thus the findings of DNA analysis have ultimately done no more than confirm a hypothesis that had long been on the table.⁶⁰ However, they are not particularly helpful when it comes to finding out *who* came into the country and *when* they arrived, or how the migrant Angles and Saxons were able to prevail against and impose their language and culture on the indigenous population. In this context, the theory, based on studies of population genetics, that early Anglo-Saxon England was characterised by an apartheid-like social structure between immigrants and autochthonous Britons, is favoured by Härke and others,⁶¹ but is the subject of heated debate.⁶² For example, John E. Pattison has stressed that the data used by Härke and others do not necessarily indicate the existence of an apartheid-like model.⁶³ The most recent analyses appear to confirm this objection. Genetic research of ancient DNA from individuals in the Oakington cemetery dating from the early Anglo-Saxon period have led Stephan Schiffels and his co-authors in a recent paper to come to the following conclusion: »we see evidence even in the early Anglo-Saxon period for a genetically mixed but culturally Anglo-Saxon community, in contrast to claims for strong segregation between newcomers and indigenous peoples«. ⁶⁴ These latest results show that early medieval migration patterns can take a large variety of different forms and that the integration of migrants was achieved in a number of different ways. Thus we will have to dismiss the notion of one-dimensional migration and mixing models. How England became Anglo-Saxon remains largely a problem of cultural studies, not of biology.⁶⁵

57 Weale *et al.*, *Y Chromosome Evidence*, 1008.

58 Weale *et al.*, *Y Chromosome Evidence*, 1009.

59 Most important: Capelli *et al.*, *A Y Chromosome Census*; Töpf *et al.*, *Tracing the Phylogeography*; Leslie *et al.*, *The Fine-Scale Genetic Structure*; Schiffels *et al.*, *Iron Age and Anglo-Saxon Genomes*.

60 »What all the studies do suggest is that Germanic people in their thousands did cross the North Sea after the end of Roman rule and that they did not all exterminate all the natives.« Grigg, *Genetics and the Anglo-Saxon Invasion* (no page numbers).

61 Thomas *et al.*, *Evidence for an Apartheid-Like Social Structure*; Thomas *et al.*, *Integration versus Apartheid*; Härke, *Die Entstehung der Angelsachsen*, 449-450.

62 Geary, »Völkerwanderung«, 50 put it as follows: »Such conclusions are then certainly plausible, but so much depends on the sampling technique, assumptions about ancient and modern migration, and assumptions about reproductive advantage that this theory remains hotly contested by many British historians.«

63 Pattison, *Is it Necessary*; Pattison, *Integration versus Apartheid*.

64 Schiffels *et al.*, *Iron Age and Anglo-Saxon*.

65 See Kleinschmidt, *Migration und Identität*, 24.

To sum up, it can be argued that the DNA analyses that have been conducted in connection with the Anglo-Saxon question have brought to light a number of new problems rather than providing answers to existing questions.⁶⁶ Thus it seems all the more necessary to strive for more, and closer, interdisciplinary cooperation in the future.⁶⁷

*On interdisciplinarity*⁶⁸

Some terminological clarification appears appropriate here. Four different modes of doing research are generally agreed upon: monodisciplinarity, multidisciplinarity, interdisciplinarity and transdisciplinarity. They are differentiated (1) on the involvement of one or more disciplines; (2) on the manner of input toward solving a given problem; and (3) on the degree of integration achieved in the process of cooperation. While monodisciplinary research need not be considered and transdisciplinary will not be described here due to its application-oriented nature, some remarks are necessary as far as multidisciplinarity is concerned. Commonly understood, it refers to a situation in which two or more disciplines engage in tackling a given task. The important point here is that each of these disciplines is largely self-centred in that it proceeds on the basis of its own methods and perceives the task from its proper perspective. In doing so, cooperation within the disciplines is minimal: they work side by side rather than starting from a common definition of the problem at hand, continually interacting as research progresses. Although each discipline profits to some degree from this kind of investigation, its overall outcome is essentially limited. Currently, this is, to our mind, the state of the art when we talk about collaboration between archaeology, history and genetics.

In contrast, interdisciplinarity is based on quite another perception of successful research. In this case two or more disciplines – each following its specific methods – practice a high degree of cooperation from the very beginning. This implies that the problem to be solved is analysed and defined jointly, each discipline bringing in its particular perception of the task and possible ways of solving it. This leads to a discussion of the conceptual frame of reference as well as of procedure, and the discussion continues whenever necessary as a (more or less) institutionalised structure throughout the entire research process. In other words, this mode of collaborative research hinges on a continuous exchange of ideas, insights and results while the investigation proceeds, or as Mark Pollard and Peter Bray put it some years ago: »It has to be an equal partnership, with a mutually intelligible language of communication, agreed objectives, and equal inputs.«⁶⁹ To put it briefly, there can be no interdisciplinarity without a genuine reflection on theories and methods in each of the participating disciplines. This, however, is the most basic prerequisite. Interdisciplinary research gets much more deman-

66 For an overall critical evaluation, see Grigg, *Genetics and the Anglo-Saxon Invasion*. Hedges, *Anglo-Saxon Migration*, 89 is sceptical that molecular genetics will be able to provide solutions at all in the foreseeable future: »It is more a matter of time, rather than of luck, for the molecular genetic methods to reach more definitive conclusions – though given the resources and knowledge needed, this may not be very soon.«

67 See Hofmann, *What Have Genetics Ever Done For Us?*, for similar conclusions for her field, Neolithic studies.

68 Some aspects outlined in this chapter are already published in Samida and Eggert, *Über Interdisziplinarität*.

69 Pollard and Bray, *A Bicycle Made for Two?*, 246. Quite similarly a few pages further on: »There are three fundamental keys to successfully riding the bicycle. One is a common goal [...], secondly a shared language, and the third, mutual respect – not simply personal respect, which is a sine qua non, but mutual academic respect. [...] Communication over a carefully defined question is the key. Integration cannot be defined just by the quantity of joint papers: It comprises discussion, meetings, conferences, and negotiation.« (*ibid.*, 255 sq.)

ding when it comes to collaboration with the sciences. This is due to the fact that the methodology of both is not only fundamentally different but, in addition, only rarely understood by the partners. Additionally, the problems are often linked to differences of epistemology of the participating disciplines, to differences in data acquisition and analysis, to difficulties in the project's organisation and management, and finally, to difficulties concerning the institutional frame (e.g., introduction of interdisciplinary approaches into university teaching, creation of new funding lines, training of referees).⁷⁰ The difficulties with regard to interdisciplinarity practice are manifold, and they are not only of an epistemological nature but are also located on a structural, institutional and actor-centred level. Cooperative research of the mode we are discussing here demands mutual knowledge exchange as well as a considerable measure of openness toward the participating disciplines, e.g., their theories and methods. Interdisciplinarity is not a kind of natural consequence of combined efforts to solve specific questions with a common project: »slipping into another discipline is not necessarily something that can just be ›done‹.«⁷¹ Rather, it has to be an ongoing process of interaction on all levels of the research involved.

Conclusion

We would like to end this introduction with an anecdote, which we gathered from Mark Pollard and Peter Bray who described the following, quite amusing scene: »At a meeting on scientific dating among the British some time ago, the technical difficulties associated with obtaining high-quality radiocarbon dates for archaeological research were being discussed at length, largely by radiocarbon specialists. After some hours of intricate technical discussion, a patient but obviously irritated senior archaeologist stood up and said, ›Archaeology is difficult, too!‹ Stunned silence descended. Clearly this was an aspect that had been lost sight of in the welter of technical details. This attitude is not the basis for an equal partnership«⁷² – and of course, one might add, this applies to both sides. Interdisciplinarity and integration comprises fruitful scientific controversies at all levels. This also applies for the emerging field of research described here.

70 See Fuest, »Alle reden von Interdisziplinarität aber keiner tut es«, 6.

71 Garrow and Shove, *Artefacts between Disciplines*, 130.

72 Pollard and Bray, *A Bicycle Made for Two?*, 255.

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New Questions instead of Old Answers: Archaeological Expectations of aDNA Analysis

Sebastian Brather*

Traditional views and ›master narratives‹ have long been outdated by recent research. Identity has become a keyword in social research. It means the self-consciousness of groups. Ethnic identity therefore characterises the perceptions of a people and their particularity, and varies among every other nation. Nevertheless, this is a social and cultural construct depending on each group's specific situation. Ethnic identity has to be flexible and appropriate to the necessities and interests of each group. Genes are a matter of biology. Ancient DNA is preserved in smaller fragments which mainly allow approximations of population development. Modern DNA reflects actual distribution and the complex, but overlapping historical information at the population level. Expecting any direct accord between population history and social history would be a fall-back into nineteenth century conceptions of the ideal nation state: homogeneous in space, race, culture, language and people. This could only be a rare historical exception. The complex relations between both research fields provide promising perspectives, which can be followed only by a narrow exchange between biological and historical disciplines. Together, new and adequate questions should be developed.

Keywords: chronology; typology; spatial analysis; contextual analysis; isotope analysis; aDNA analysis; early middle ages; methodology.

Recent interpretations of scientific isotope and aDNA analysis tend to reconstruct ›peoples' migrations‹ which can be demonstrated by archaeological as well by scientific publications. This view follows ›master narratives‹ created by ancient ethnographers – refreshed by nineteenth century researchers and general public, which presents a simple but suggestive world view, considering the congruence of space, culture, people, race and language – giving ›old‹ answers by new methods (section 1). In contrast, modern humanities disproved such concepts and demonstrated that – instead of culturally homogenous ›people‹ – the self-consciousness of groups is decisive. Groups at different levels are bound together by their identities, which means by concepts of themselves defining differences to others (section 2). For archaeological research this shift means that traditional ›ethnic interpretations‹ of material culture have come to be challenged. Instead of interpreting regional ›cultures‹ as ›peoples‹, new insights have been achieved, mainly within local societies or by characterising supra-regional elites (section 3). Exemplifying these fundamental methodological problems

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of ›old questions‹ seen against the actual state of the art in Roman and medieval archaeology, some historical interpretations of scientific data need further discussion and some revision.

Genetic analysis in archaeology looks for kinship in local societies as well as for population history. In the first case, only biological descent is detected, while social alliances are established by marriage. For population development (not that of ›people‹), the second case, the number of aDNA samples seems to be quite small yet, and the comparison with recent distributions lead to a-historic results (section 4). The Lombards have been the subject of recent studies which demonstrate that the outcome of isotope analysis reflects much more local mobility than ›migration‹ – which is very interesting for the reconstruction of marriage patterns. aDNA analysis will probably achieve similar results if we take into consideration the cultural and political heterogeneity of the Lombards according to the written record (section 5). Summarising these observations, it has to be emphasised that the identity of social groups cannot be reflected in the genes – or at least that identity will be demonstrated by genetic diversity. In general the archaeological as well as the scientific record rather complement than confirm each other (section 6). In this view ›old‹ answers have become doubted, and should be tested in detail and replaced by more balanced interpretations.

Therefore archaeologists as well as scientists are being challenged to develop together new research questions instead of trying to verify old answers in reconstructing once again ›peoples' migrations‹ in antiquity and the middle ages, especially given today's global political situation. A precondition will be a sufficient mutual understanding of methods and research agendas – laying the ground for a promising interdisciplinary cooperation and research (section 7).¹

1. *Traditional views and ›master narratives‹*

›Master narratives‹ do not only guide the public perception of history, but sometimes research too. They usually present simple, general explanations for very complex developments, and they appear to be very influential. At the present time, ›peoples' migrations‹ are very frequently mentioned in the news, often also simultaneously referring to late antiquity and the collapse of the Roman Empire. But are the ideas of the nineteenth century in fact a solid basis for our understanding of history and politics?

It is obviously the idea of the modern national state which constitutes the basis for such suggestions. Implicitly, inward homogeneity and outward distinctiveness represent the starting points for several considerations. But even in modern states, with their extensive administrations and bureaucracies, far-reaching similarity or even ›equality‹ has not yet been achieved; instead ›nations‹ and populations today are characterized by many social, cultural and religious differences – and they can successfully handle them. We should therefore doubt that early societies were homogeneous in any substantial way – the larger they were the more complex their differences must have appeared.

Albeit at first hand ›archaeological cultures‹ seem to represent homogeneous regional societies, they remain classifications of research and nothing more. By definition, both the term and the concept look for similarities and marginalize differences. That ›cultures‹ of this kind do not represent past societies or ›peoples‹ can be demonstrated by simple cases: for Central Europe several culture groups have been described for the first to fourth centuries

1 For biomolecular analysis in archaeology see Brown and Brown, *Biomolecular Archaeology*.

AD, but they do not fit at all to names which appear in written sources of that time. Apparently different aspects are concerned – on one hand the perception from outside, reflecting the search for order within the barbarian world (possibly indirectly reflecting the political situation), and on the other hand, structural relations and communications over larger distances reflected in the archaeological record.²

The traditional ›ethnic interpretation‹ in archaeology (or its ethnic focus) apparently depends on several circles of data and their interpretations; but this is impossible without a written record which localizes a specific group. Starting from the reconstructed territory, comparisons to selected archaeological distribution maps are made, leading to the suggestion of ›ethnic symbols‹ and the identification of ›foreigners‹ somewhere else. The circles become more numerous and puzzling when further data are included. Relations between material culture and languages cannot be reconstructed, because we do not have any dating and localization of dialects and languages (Indogermanic, Celtic or Germanic) in European prehistory. Considering images, antique topoi of barbarians obscure the interpretation, and one should be aware of the transformation of meanings and media. Bones have led to some misinterpretations too which could easily be exemplified by the suggested plan-occipital skull of the bell-beaker ›people‹³, or the postulated long skull of ancient Germans (both still relevant in research literature).⁴ Recently, aDNA and isotopes have also been included (*Fig. 1*). This traditional view has been challenged and changed fundamentally. Archaeology, influenced by historiography as well as by ethnology and the social sciences, has developed new concepts. ›Peoples‹ no longer represent the main object of research, but the players and their agencies are the focus now. Social groups are another focus, and their cohesion by interests and identities.

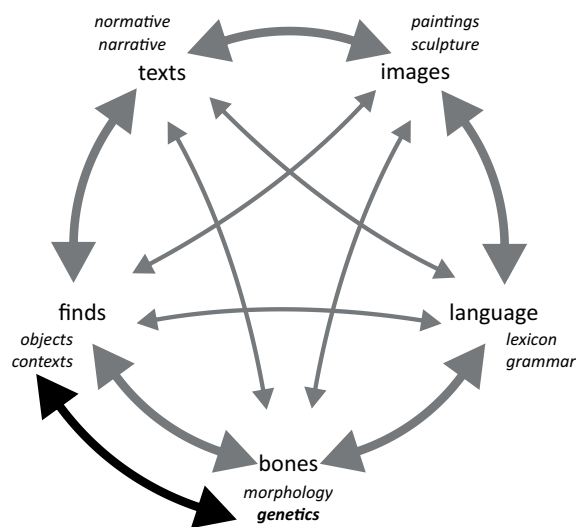


Fig. 1: Circles of misleading ›mixed‹ interpretations. The archaeological record, texts, images, and scientific samples are often combined, but instead of mutual confirmation the sources and their interpretation represent different perspectives which complement each other. Therefore no direct conclusion can be made from one record to the other

2 Cf. Brather, In *stammeskundlichen Fragen*, 57, fig. 3.

3 Gerhardt, *Glockenbecherleute*.

4 Ecker, *Crania* (›Reihengräbertypus‹).

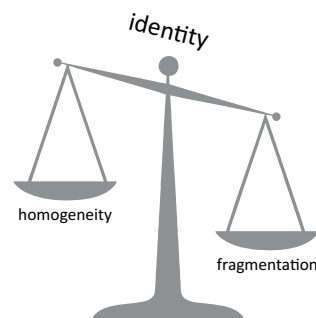
2. Identities and ethnic groups

During the last decades ›identity‹ has become a keyword in social research. One gets the impression that everyone has to have an identity, and identity can explain everything. Common sense suggests that a sense of identity characterises every group, and that it is just this consciousness that is necessary for the existence of social groups and their characteristics. While on one hand this perception has been established by research, on the other, politics and politicians as well as specific interest groups claim certain identities (and for the right to make that claim). Both perspectives underline that identity is more a political statement than a social reality.⁵ It is the earmarked enhancement of existing characteristics and differences.

Identity is not a given, but constantly evolves. Its general function is to establish the impression of a definite and stable group. Therefore, identity is primarily a suggestion; furthermore, it can be used to hide important differences within groups and to emphasise their characteristics in comparison to other groups. Because groups, interests and situations change, identities change too. For this reason it would be an unfounded expectation to presuppose that continuous identities would exist over long periods of time without modification. Quite the contrary: steady change reflects a ›normal‹ social and cultural situation and its perception.

The American sociologist Rogers Brubaker wrote recently: »What cognitive perspectives suggest, in short, is that race, ethnicity, and nation are not entities in the world but ways of seeing the world. They are ways of understanding and identifying oneself, making sense of one's problems and predicaments, identifying one's interests, and orienting one's action. They are ways of recognizing, identifying, and classifying other people, of constructing sameness and difference, and of ›coding‹ and making sense of their actions. They are templates for representing and organizing social knowledge, frames for articulating social comparisons and explanations, and filters that shape what is noticed or unnoticed, relevant or irrelevant, remembered or forgotten.«⁶

In principle, identity has to establish a balance which allows a group to exist. Complete homogeneity is practically impossible as is extensive fragmentation (*Fig. 2*). In theory (and in theory only), both situations represent the two ends of a continuous scale. The necessary



*Fig. 2: Social identity as a specific balance between homogeneity and fragmentation. Depending on the actual situation and on the function, the ›place‹ of identity may be closer to homogeneity or nearer to fragmentation – in order to hold a group together (arranged after Straub, *Identität*)*

5 Niethammer, *Kollektive Identität*.

6 Brubaker, *Ethnicity*, 81 (my emphasis).

balance has to mediate between too much fragmentation in order to keep the group together, and at the same time too much homogeneity because then the group would be too small (and at the end limited to a single individual only). Which aspects shall be used and how, and how a group should be characterised, depends on the situation as well as on perception and function.⁷ Generally, identity provides integration and separation and is of fundamental importance. Separation can range from alterity (which can be retranslated) to alienity (radical strangeness).

Groups as well as individuals possess identity, yet groups possess their own relevance through the actions of their members. Because every individual belongs to different groups everybody has a complex identity, each with some aspects different from those of others – or, if you will, some identities. Many groupings and identifications compete with each other, depending on the specific circumstances of relevance and effectiveness. Various aspects overlap each other, and their emphasis depends on each situation and the necessity of demonstrating specific characteristics. As such, all ›identities‹ exist at the same time, but only one is stressed in a specific circumstance, while others are of secondary or tertiary importance.

Because of this flexibility of identity, it cannot be named in one situation and analytically transferred to another. Analysis has to acknowledge the contexts and processes of identification when it tries to understand its function and contents. Research is open to changes and to flexible use, instead of expecting a hard ›traditional‹ kernel of identity from every group. According to Brubaker, relevant studies should concentrate on »identification and categorization, self-understanding and social location, commonality and connectedness«⁸ – i.e., the ways in which people and groups perceive their reality.

Ethnic identities represent a specific case. Contrary to suggestions made in the wider public, for most individuals, ethnic identity is not the most important aspect of one's identity. But because it is the context in which a certain identity becomes important, ethnicity is emphasised in confrontation with other ethnic groups. For Patrick Geary, ethnic identity should be characterised as »a situational construct« and does not fundamentally determine one's consciousness.⁹ In every-day life it is of secondary relevance at most. To look only at ethnicity over-estimates its relevance in terms of the national lenses of the twentieth century in Europe as well as globally.

Ethnic names which appear in written sources during antiquity and the middle ages do not necessarily meet modern expectations. Of course they have been understood as labelling specific groups in certain regions, sometimes ›migrating‹. In several cases this entails a misunderstanding because often the names are regional descriptions referring to populations in certain areas (e. g. Celts, ancient Germans or Slavs as well as Franks and Alemans). In other cases, such names mainly reflect political situations and relations, such as those which can be argued for the early medieval Frankish kingdom(s). In all of these situations ›ethnic‹ names do not signify a culturally and socially homogeneous reign but its political claims, labelling and belongings. The engaged search for these names by historical and archaeological research often meant a misunderstanding of the context which the names described and explained a long time ago – as can be shown by recent concepts of identity.

7 Straub, *Identität*.

8 Brubaker, *Ethnicity*, 4.

9 Geary, *Ethnic Identity*.

3. *Past identities in archaeology*

As in other disciplines ›identity‹ has become an important topic in archaeology over the last few decades. In many studies, it has developed into a term often used, but too often not combined with any specific concept. There, it is simply applied to certain observations of similarities in space and time, but whether there was any consciousness beyond that is not reflected. The advantage of using ›identity‹ as an analytical tool lies in the research perspective. Instead of reconstructing ›real‹ conditions directly as is reflected in the archaeological record, they are filtered through the ideas and perceptions of past groups and societies. So, burials do not directly inform us about social structures of local societies, but mainly about the way the dead were buried and which concepts may have been behind that.

Archaeology has to make a principal assumption when it is asked about identity: if groups had a consciousness and identity, then they had to express these by signs of material culture that can be reconstructed. There are several ways to act according to one's group identity; these can be described by Pierre Bourdieu's concept of habitus. People can use different elements of cultural practice – from language and behaviour through religion and up to burying the dead. But the material representation is of fundamental importance, as otherwise any archaeological attempt will fail. If so, the material expression might be seen as placing special emphasis on these elements – according to Jan Assmann's hypothesis that identity has to be a clear enhancement of reality and its perception.¹⁰

Apparently material symbols were not the usual expression of ethnic identity. When we look in antique and early medieval texts then there are indeed some descriptions of such material markers. The most famous is Tacitus' mention of the Suebic hair knot. But in the following sentence the author explains that other tribes (we do not know who the Suebi were really) were imitating this prestigious symbol, and moreover it had been a sign of an elite. Similarly the typical Frankish axe called therefore francisca (Isidor of Sevilla), the seaxe of the Saxons (Widukind of Corvey), or the long beards of the Lombards (Paul the Deacon). All of these material symbols represent interesting stories and were obviously recorded later than when they happened, but provide no starting point for any historical research.¹¹ People in antiquity and the middle ages referred to relevant characteristics in a more flexible way.

To come closer to past identities additional and independent information is necessary. Only when skeletons have been biologically sexed, can archaeology identify gender specific grave furnishings that reflect gender roles. Similarly, age determination helps us see whether there were social positions dependent upon the age of the deceased. Further information comes from religious symbols (known for Christianity, but unknown for pagan beliefs), as well as from instruments (indicating smithies and other craftsmen). Groups of graves may indicate families but have to be checked further. What can be analysed by this approach is focussed on the individual, local level, but is not valid for larger populations. Instead of regional identities, groups within local societies can be reconstructed and assumed to have had specific identities.¹² Any ethnic labelling in archaeology refers to the so-called ›geographic argument‹.¹³

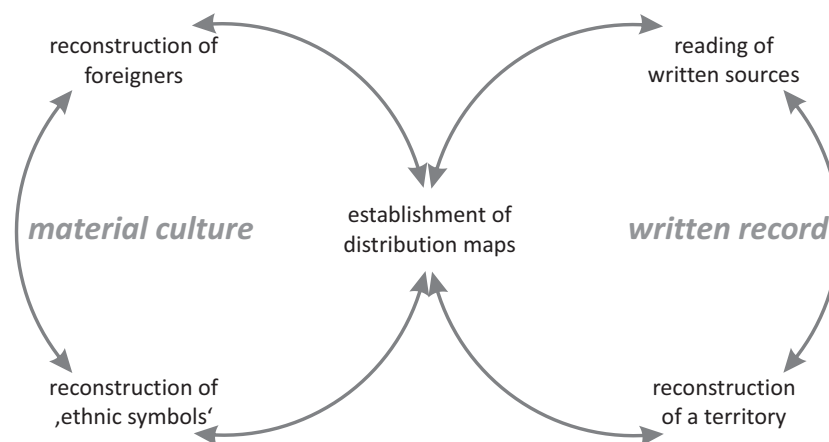
10 Brather, Identity.

11 Brather, *Ethnische Interpretationen*, 310-317.

12 Brather, Alteritäten.

13 Martin, Ethnic Identities.

Elements of material culture which seem to be regionally concentrated and typical are very often archaeologically interpreted as specific to a people or tribe. The information given simply becomes a distribution map. What is effectively reflected by mapping is hardly ever asked. One would expect greater communication. Eventually everything in archaeology has its localisation and space, but not everything can be called ›ethnic-specific‹ (as additional and specific information would be needed). There are two opposing opinions: one argues that only when the names of certain tribes in specific regions are known can an ethnic interpretation become possible for archaeologists.¹⁴ The other is satisfied with the geographic argument and calls the cultural grouping the reflection of an ›archaeological ethnos.‹¹⁵ The former hypothesis is the most common (*Fig. 3*) but does not escape from fundamental methodological problems. It is often combined with the hypothesis of far-reaching ›peoples' migrations‹, but we mainly observe the mobility of individuals.



*Fig. 3: Two circles of ethnic interpretation in archaeology, mixing the reading of written sources with the archaeological record. The geographic distribution remains the central and only argument – showing that the search for ›people‹ is not an archaeological question, but induced by the written record (rearranged after Hakenbeck, *Roman or Barbarian?*, 39 fig. 1)*

When we look at the written record then the meaning of suggested ›ethnic‹ names becomes questionable. Celts, ancient Germans and Slavs had been terms to describe the ›others‹ outside the Mediterranean world. They have been turned into a modern linguistic nomenclature but reflect nothing less than the identities of the people described. But too, names like Franks and Alemans were not the self-descriptions of two Germanic tribes, but, at least at the beginnings of the Roman administration, inventions used in order to regulate the opposite side of two provinces along the river Rhine. Such descriptions much more reflect the view and identity of the authors than that of the people concerned (and sometimes, the expectations and identities of the wider public, including some archaeologists). Self-perception possessed a much more political rather than cultural meaning; the Franks were the elite

14 Bierbrauer, *Ethnos*, 5.

15 Siegmund, *Alemannen*.

of the Merovingian and Carolingian kingdom(s) and their people. The name thus refers to the actual political framework, and does not imply that the whole population was culturally homogenous and saw themselves as being of Frankish ›origin‹. For ethnicity in its strict sense these groups are much too large; cultural anthropology has extensively shown that only smaller face-to-face societies of some thousand members develop an identity in this way.¹⁶ Ethnicity is therefore situated at a much smaller spatial scale than all of the archaeological observations made so far.¹⁷

Material culture too does not primarily nor only reflect an identity.¹⁸ It may have – beyond its practical function – many and manifold meanings depending on the context in which it is situated. But not always and not every object or decoration has much or any cultural meaning, and even that may not have been stable over a longer period of time. Therefore no direct link can be made per se from an element of material culture to some socially or culturally important meaning or identity.¹⁹ What is needed is both information on material identity markers and the existence of such markers that represent identity: »Representation is the process by which members of a culture use language (broadly defined as any system which deploys signs, any signifying system) to produce meaning. Already, this definition carries the important premise that things – objects, people, events, in the world – do not have in themselves any fixed, final or true meaning. [...] Meanings, consequently, will always change, from one culture or period to another. [...] So one important idea about representation is the acceptance of a degree of cultural relativism between one culture and another [...], and hence the need for translation«, as Stuart Hall has expressed it.²⁰

If this balanced view, referring to the complexity of ancient and medieval history, is challenged and falsified by modern scientific analysis, it would be a big surprise for both archaeologists and historians. It would not only contradict the results of decades of research, but also provide history with a decisive biological basis. Can this be possible? A cursory view may suggest direct relations between genes and culture, but every careful study will show that the past was much more complex. In the following, a few arbitrary examples will be shown in order to present methodological problems of some arguments based on biological information – and not the scientific method itself, which would not fit to my expertise and is much better explained by other studies.²¹

4. *Genetic analysis in archaeology*

In recent years, not only has the analysis of ancient DNA undergone fundamental improvements, it also has been applied in a number of archaeological studies.²² Research on cemeteries is particularly interested in individual relationships, as earlier epigenetic studies have been. In most cases so far possible kinship can be established, and even a genome-wide

16 Müller, *Magisches Universum*.

17 Wotzka, Maßstabsprobleme.

18 Cf. Jones, *Archaeology*; Brather, *Ethnische Interpretationen*.

19 Hahn, Eigensinn.

20 Hall, *Work of Representation*, 61.

21 As a helpful introduction see Brown and Brown, *Biomolecular Archaeology*.

22 Cf. Brown and Brown, *Biomolecular Archaeology*, 9-37, 173-189.

analysis would identify just two degrees of relationship.²³ The results concern and illustrate biological kinship among local societies (if we may expect a reasonable sample of a local society to be buried at a cemetery).²⁴ This is just one half of kinship – biological descent. The other half is represented by affiliation, mainly by marriage patterns which establish alliances between families and social groups (in the Middle Ages, there would also be cases of spiritual relationship). Archaeology argues on the basis of grave groups within cemeteries (though there might be other reasons too for their being together), or with similar grave furnishing (which may have been a matter of chronological background). Only both aspects seen together may lead to a complex understanding of kinship in past societies – both perspectives complement each other.²⁵

On a population level – beyond the micro-regional scale – it becomes difficult to reconstruct patterns of kinship in this historical sense. There are two main reasons: (1) the aDNA is so fragmented that the results so far present only indications instead of certainty – but this is to be improved now by genome-wide analysis, (2) Beyond very close relationships of just a few (perhaps up to three) grades of relationship we only acquire general information about relationships. In most cases the analysis detects mitochondrial DNA, which reflects descent along the mother's line. This may be interesting for the general genetic composition of a population, but from a historical perspective we come no closer to looking at kinship and marriage patterns because there are too many possibilities of explaining the genes historically. DNA from the cell nucleus provides much more detailed information, but again often in a broader statistical sense. Additionally, social reality makes the situation more complex: family structures could have included patchwork families, and cultural norms competed with deviations and violations.

Studies of DNA in modern populations appear completely different. They use the distribution of genes today and want to reconstruct their ›history‹, and alongside that the ›history‹ of the populations. The main methodological problem is that the ›historical‹ information is mixed and can hardly be separated and dated.²⁶ The supposed sensation, e.g. that ›the British are more Germanic than thought before‹ – dating back the similarities between the British Isles and the continent to ›the Germanic invasion‹ of the fifth century – is problematic.²⁷ 1500 years would have heavily influenced and changed the distribution of genes, and there might also have been earlier connections. Furthermore, the size of the samples is not yet very large and their reliability is disputed – as well as the establishment of the population samples themselves, suggesting relatively homogeneous groups at the beginning in order to detect admixtures. Therefore the actual situation is not very appropriate if one wants to reconstruct and explain certain historical events by them or to reconstruct the development of cultures.

23 Personal communication Johannes Krause, Jena. For interpretive implications see Brown and Brown, *Biomolecular Archaeology*, 168-189.

24 In the seventh century there have been ›complementary‹ burial places which only together represented the local societies; cf. Theuvs, *Changing settlement Patterns*.

25 Brather, *Verwandtschaft*; Alt and Röder, *Biologisches Geschlecht*.

26 Cf. Harding *et al.*, *Viking DNA*.

27 Devlin, *Genetic Study*.

The approach resembles the analysis of blood groups made decades ago. Blood types apparently vary in their geographic distribution today (Fig. 4). How old these patterns are and how they can be interpreted, remains a disputed matter although geographic distance and intensity of interactions are apparent. Sometimes the frequencies have been used for the ›reconstruction‹ of the spread of languages and migrations. As Luigi Luca Cavalli-Sforza and others have argued, blood types would reflect the spread of Neolithic agriculture and also that of the ›Indo-Europeans‹, but this is only plausible when an accordance is principally expected and assumed – a self-fulfilling prophecy.²⁸ The assumptions remained disputable, probably because many reasons lay behind the modern (!) distributions of blood characteristics, and they can hardly be arranged chronologically.

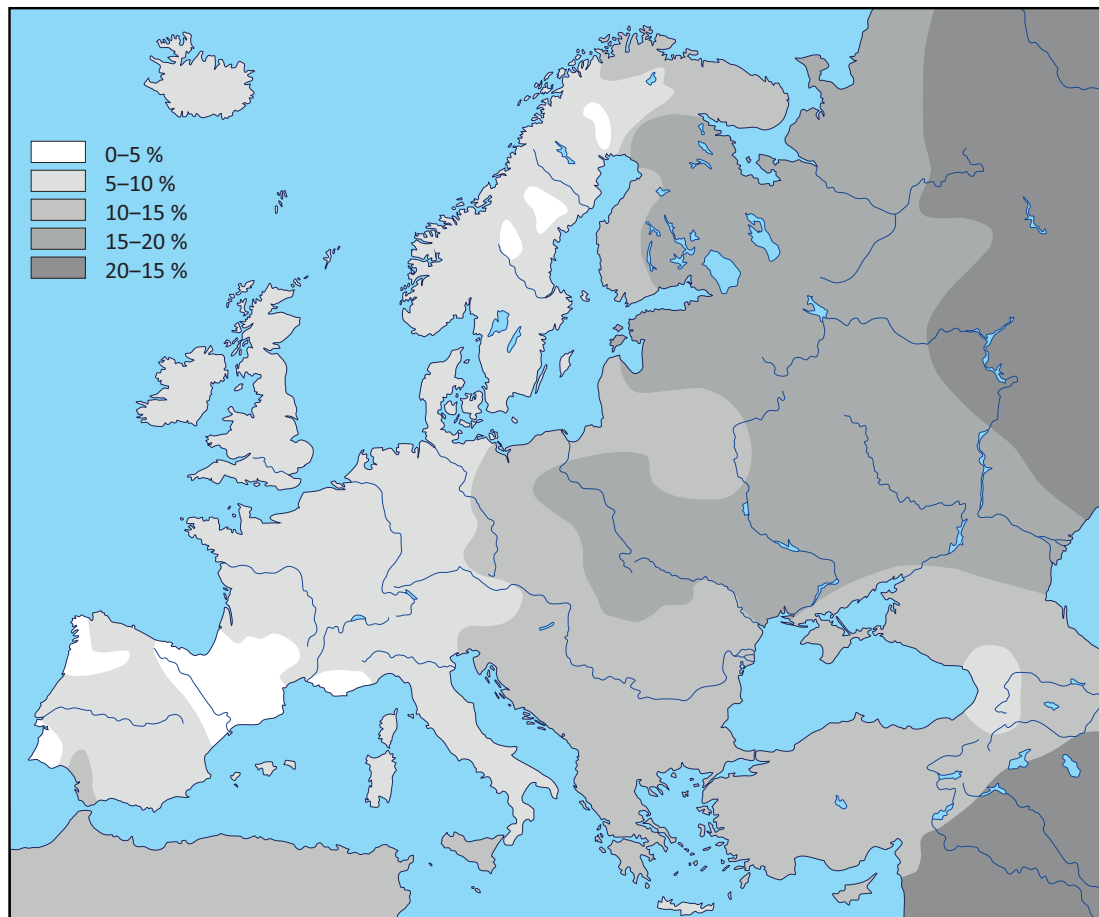


Fig. 4: Frequency of blood group B in Europe, simplified twentieth century distribution. How this map can be interpreted is an interesting, but complex challenge because of several factors lying behind it: space as the most important factor and individual mobility as another (though social) factor; different time spans during which the actual distribution may have developed in different regions; and genetic drift as a biological cause. Therefore no simple explanation is possible (e.g., only immigration from the east or Asia) (draft: www.nap.edu/openbook/0309045878/xhtml/images/img00013.jpg)

28 Cavalli-Sforza, *Genes*.

Modern national states are hardly a solid frame when historical developments in populations are addressed. Differences between modern nations are assumed, but really there is much differentiation within them, regionally as well as chronologically. Modern countries developed in the course of the nineteenth century, and they included very different regions, cultures and populations, even though homogeneity was theoretically and politically intended. Populations and cultures, languages and societies show many similarities crossing modern boundaries, and sometimes the differences within a state are larger (on average) than between states (a well-known statement for the comparison of populations).

But ethnic identities in pre-modern societies were spatially much more restricted than in modern states of the twentieth century. New modes of communication and larger political units enable identity constructions (›invented traditions‹) which connect people not just over long distances, but also people who have never met or even seen each other, but now constitute the population of a nation. Before, consciousness could be established only in face-to-face societies where members at least potentially met and interacted. Elite identities could reach much further, reflecting political interests and alliances. Genetic relations could be analytically detected when marriage interlinked elite families of different regions; but this is true for individual cases and not for larger populations.

For the general public, the bio-sciences are very attractive. They seem to present ›objective‹ data which leave no room for discussion. But this is not true for several reasons. Data range from the fragmented preservation of aDNA to the many possibilities of explaining certain results: e.g., a common descent along the mother's line may have meant several very different individual variants of kinship. Furthermore the ›scientific‹ interpretation depends on the model of historic and cultural development which derives from historic and archaeological research. Therefore even the suggested ›objective‹ data remain a matter of interpretation. They are no more reliable than any other information from historiography and archaeology – nor are they superior to other arguments and models. The interrelations and dependencies of written, archaeological and biologicals record can be exemplified by the case of the Lombards during the sixth century – a ›people‹ thought to present a famous example of large scale migrations.

5. The Lombards as a recent case study

The Lombards have recently become the object of some scientific projects, and I will comment on two of them because of their suggestive agendas. Both projects promise and provide new and unexpected insights. The first focuses on isotope analyses at different places in Bohemia and Hungary and wants to reconstruct the Lombard migration from the lower Elbe up to northern Italy.²⁹ The central interest of the project follows thus a traditional ›master narrative‹ which has already been challenged; a recent exhibition catalogue on the Lombards doubts the migration theory and suggests the re-appearance of the name only in the fifth century, probably as a link to old traditions.³⁰

Until now only the data of one graveyard have been published: Szólád in Hungary, where about 45 people were buried during the sixth century. According to the grave furnishings, such burial sites are called ›Lombard‹, but we do not know how the dead saw themselves and whether they were immigrants or not. Beyond this fundamental historical question the

29 That two Thuringian gravefields are included too, is not justified in any relation to the Lombards.

30 Pohl, *Die Langobarden*, 25–26.

Strontium isotope ratios do not reflect ›migration‹ or mobility directly as has often been suggested; instead they point to nutrition. Mobility could be established if information regarding nutrition was local. But when cereals were exchanged between the regions or the cattle was fed in the mountains, then the isotopes would reflect the origin of the food instead that of the people. The supply of the Roman troops would also be revealed in the isotopes, not the regional ›origin‹ of the soldiers.³¹ Interpretation has to consider this carefully. The results of the study are surprising at first sight. Nearly no indication of long-distance mobility could be detected although this was the aim of the project. Instead, much small/regional mobility was observed; this referred to the relations between neighboring places and settlements.³² This result is very interesting for archaeology because it offers new insights which, moreover, fit on actual concepts. It focuses on local societies represented by graveyards and settlements, which are a primary source for archaeologists. Much mobility between neighbouring communities should be the normal case – and probably reflects marriage patterns and kinship.³³ Every settlement, depending on residential rules, exchanges brides and grooms with surrounding places. The interesting question would be what percentage of non-locals represents stable populations, and what minimum number of non-locals has to be exceeded when we look for immigration? Above all, how graveyards were related to settlements remains an open question in general (*Fig. 5*).

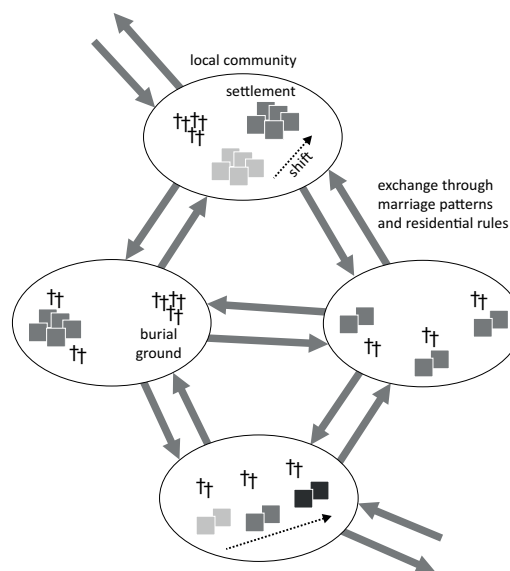


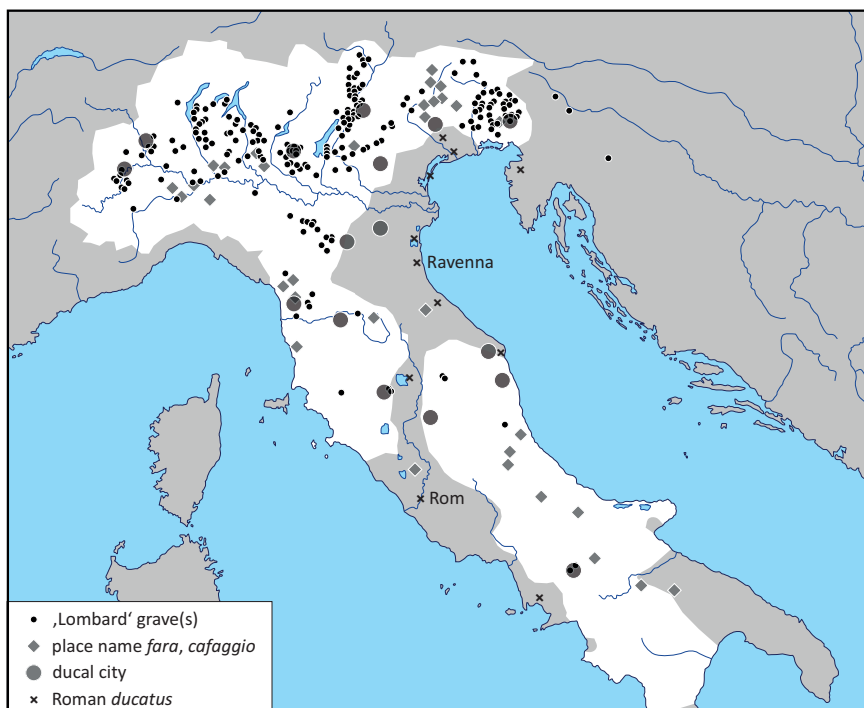
Fig. 5: Schematised interactions between neighboring settlements within local societies. They exchange individuals following specific marriage patterns and residential rules. The archaeological reconstruction according to graveyards only may become complicated because it remains unclear how they were related to settlements as shown here. There could have been more than one burial ground per settlement and vice versa; the situation becomes more complex when settlements shifted. Not shown here is the location of fields and meadows

31 Cf. Pollard, *Isotopes*; Gruppe and McGlynn, *Isotopic Landscapes*; Brown and Brown, *Biomolecular Archaeology*, 79–88, 190–209.

32 Alt *et al.*, *Lombards*.

33 But cf. in a different context Gehlen, *Nahrungstabus*.

The second project is coordinated by Patrick Geary at Princeton University and uses genetic data for the reconstruction of the ›Lombards' migration‹ between Hungary and Italy in 568.³⁴ So far no detailed results have been published, but the general approach deals with a situation which at first sight seems to be clear.³⁵ Following the passage by Paul the Deacon, the migrants from Pannonia were a very heterogeneous mixture consisting of Gepids, Bulgars, Sarmatians, Pannonians, Suebi, Norici and others.³⁶ Furthermore, the archaeological ascription of burials with grave goods to the Lombards remains problematic; following actual research it is more the periphery that is characterized by grave furnishing (in Northern Italy as well as in Northern Gaul or Pannonia as well as Spain). This fits the observation that the ›Lombard‹ finds are concentrated mainly north of the river Po while specific place names referring to mobile groups appear mainly in Central Italy, and the political centers (ducal seats) were established throughout the Lombard Kingdom (*Fig. 6*).³⁷



*Fig. 6: The early medieval Apennine peninsula with ›Lombard‹ graves (defined by specific grave furnishing), specific place names (of unsecure chronology), and the political centers of the Lombard reign (ducal cities). The different records do not fit well together, and the grave furnishing in the north seems to be a peripheral phenomenon rather than specifically ›Lombard‹. The Lombard territories of the early seventh century are highlighted (according mainly to Menghin, *Langobarden*, 105 fig. 88; Scardigli, *Cultura orale*, 157)*

34 See Geary and Veeramah in this issue; and Brown and Brown, *Biomolecular Archaeology*, 9-37.

35 Geary, Genetic data; Vai *et al.*, *Genealogical Relationships*.

36 Paul the Deacon, *Historia Longobardorum* II, 26, ed. Waitz, 87: *Certum est autem, tunc Alboin multos secum ex diversis, quas vel alii reges vel ipse ceperat, gentibus ad Italiam adduxisse. Unde usque hodie eorum in quibus habitant vicos Gepidos, Vulgares, Sarmatas, Pannonios, Suavos, Noricos, sive aliis huiuscemodi nominibus appellamus.*

37 Cf. Scardigli, *Cultura orale*, 157; Menghin, *Die Langobarden*, 105 fig. 88.

Not all Lombards are therefore represented in so-called ›Lombard‹ graves (which apparently differ from their Pannonian counterparts, and both represent heterogeneous situations too), and not all individuals buried in them had been (immigrated) Lombards.³⁸ What is to be expected is complex genetic data (due also to the small distances in space and time between them), carefully interpreted through intensive discussions by archaeologists, historians and geneticists – a real challenge for the project according to its presentation. What we should expect is again much data on local populations and their small-scale descent and affiliation.

Despite the Lombards and similar case studies, languages are sometimes looked for in certain studies, but in general they have no correlation in the material record because they leave no traces. Furthermore (Indo-European) language stages cannot be dated before their first appearance in inscriptions or texts. And the reconstruction of a ›proto-language‹, based on similarities with later languages, represents just one single possibility of interpretation: relations could have been established by overlapping dialects as well as by mutual influences between languages too. Therefore language reconstructions are more complicated than often thought, and they do not have any ties to material culture nor to biology. Therefore genes cannot be linked directly to culture and identity.

6. Identities ≠ genes

Identities and genes are two very different things. Identities reflect the consciousness of social groups and societies under specific circumstances. They are developed in certain situations when social cohesion on one side and distinction on the other become important; these lead to flexible emphasis and response, and change with such situations and in time. Genes are exchanged through marriage and they reflect biological descent. Behind them lies a biological population history which again differs depending on the situation: when we look at the local level family relations should become visible, while at the regional level general trends and differences can be recognised apart from the people themselves. A good example of this fundamental difference in disciplinary perspectives is seen in kinship.

Genes reflect descent and therefore the biological line of ancestors. This is perceived by people over just a few generations. Beyond the communicative memory a rather mythological series of ancestors can be constructed.³⁹ The social aspect of kinship is marriage alliances – this means regulations as to who can marry or not marry whom. Families' relationships are therefore defined as being culturally-specific. How alliances between families shall be arranged is then a matter of social actions. During the early middle ages there was a long debate as to how to count the nearest relatives; two methods competed – ›Roman counting‹ and ›canonist counting‹. The latter dominated since the eighth century and doubled impossible marriage partners – including spiritual relationships.⁴⁰

38 Barbiera, *Changing lands*. Cf. Possenti, *Necropoli Longobarde*; Paziienza, *Identity*.

39 Cf. Assmann, *Kulturelles Gedächtnis*, 48-56.

40 Ubl, *Inzestverbot*.

The central point of many recent debates seems to be to avoid the methodological misunderstandings so often made in the nineteenth and twentieth centuries. The national idea – referring to the perceptions of modern national states – is responsible for a wide-spread but mistaken notion (*Fig. 7*): that the accordance of space, race⁴¹, language, culture and people (and identity?!) inspires national fantasies. But this is not a historical fact. Even modern states with bureaucracies and administrations, including protected borders, could not homogenise their inhabitants to such an extent. The notion is true if one wants humankind and its history to have a biological basis; but history is made by economy, culture and politics – its social formations are determined by economic conditions, social interests and cultural practices. Therefore identity is not a matter of genes but of social circumstances.

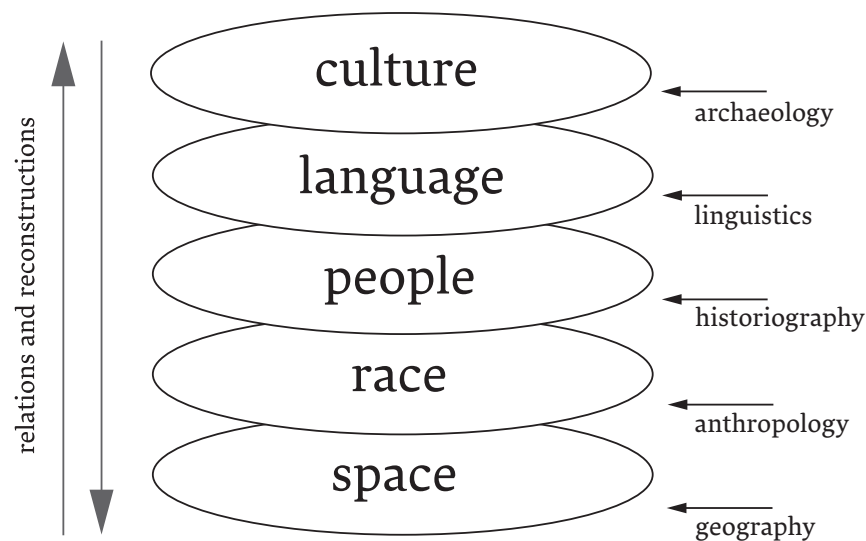


Fig. 7: Suggested accordance of space, race, language, culture and people. It is based on the idea of homogeneous and distinct modern national states developing during the nineteenth century – and a misleading starting point for any historical analysis. In fact, these aspects are far from being directly linked and explaining each other

The other way round, genetics and history (including archaeology) represent each other very well by complementary perspectives. Both disciplines possess their own sources, methods and views – and neither confirms each other directly. Seen from the archaeological point of view, analysis is focused on the local level simply because individual data from a neighbourhood population is collected there. Identities within local societies can be reconstructed because differences between social groups were shown during burial – when they were demonstrated at all. At the regional and supra-regional levels, identities remain more than vague because the ›geographic argument‹ is very weak and reflects nothing more than communication. But biological trends can be analysed at the population level to, reflecting

41 Cf. Caspari, *Deconstructing Race*.

gene drift rather than any perception by the people themselves. It is important to differentiate between ancient and modern DNA: both provide us with specific, but different information.

Because both perspectives – the historical and the biological – are complementary, intense research cooperation is necessary and welcome. It has to be combined with a careful discussion of methodological approaches and interpretive models; this would be the essential precondition in order to prevent fundamental misunderstandings by either side, funding institutions and the wider public. There needs to be opportunities for the discussion of problems concerning research, methodology and other questions. On such a basis the combination of a biological and a historical approach should be very successful. The historical and biological results will not (directly) confirm each other (as with other disciplines like philology) but will together draw a much more complex and therefore ›realistic‹ image of the past. Archaeologists have to have an idea of the principal methodological aspects of genetics today, and biologists have to develop a fundamental understanding of recent archaeological interpretations. Together we have to develop adequate questions which will remain historical questions. What we can achieve together is to find new answers to newly developed questions.

When, for example, we do not expect homogeneous ›tribes‹ but political interest groups in the early middle ages – what this would mean for the genetic record and its interpretation? Is there any realistic biological approach possible at the regional population level, or should we concentrate much more on local societies and their marriage patterns? Locally, the methodological approach can be much more precise and comprehensive because it captures individuals in their social setting. Culturally expressed roles of sex and gender can only be reconstructed archaeologically when we have the biological determination of sex, and can combine it with their possible expression in grave furnishings. When we study past societies, the biological perspective seems to be vertical (by descent), while the archaeological is rather horizontal (by alliance). Bringing both perspectives together offers really new insights – much more than explaining one by the other.

7. Preconditions and Perspectives

To recapitulate, I am pleading for an intense cooperation between bioscience and archaeology which promises many new insights instead of old answers, new perspectives instead of traditional narratives. It may be useful to repeat some of the ideas mentioned above concerning medieval archaeology. To be successful, our auspicious interdisciplinary cooperation has to consider a few principles in order to avoid any misunderstanding of data and interpretations delivered by the other side:

- orientation of archaeologists as well as of biologists as to the actual status of knowledge, and discussion by each side – and a willingness to understand each other⁴²;
- methodological transparency and strong debates, even if it is very laborious and extensive;
- avoiding biological explanations for cultural history – otherwise facing the danger of obsolete and outdated biologism;
- both perspectives tend to complement each other rather than to confirm the other, which is the legitimization of every research perspective.

42 Cf. Müldner, Diet, 342.

Instead of asking ›old‹ questions, which in many cases seem to be outdated by actual later research, now many interesting new insights should become possible because of new scientific analytical methods. To develop the ›right‹ questions – those adequate to the sources available – will be a promising challenge for future research. These may include:

- nutrition and social status in the biographical change of individuals in their setting;
- heterogeneity and stability of local populations incompletely represented in graveyards;
- long-term and long-distance relations between populations beyond cultural history;
- local as well as global studies (without direct connections between different spatial ranges);
- complex instead of simple explanations in a careful and well-discussed interdisciplinary analysis.

Together we should avoid simplistic answers. When the biological record is complicated in itself and also in its understanding, then the archaeological and written record possesses no less complexity. Therefore different disciplines have developed and established their own methodologies. Together we will make further progress when we agree that »biology and culture are dialectically intertwined« rather than being directly linked.⁴³ Some interpretations of scientific data may be possible but historically implausible because of new archaeological research and theory. Furthermore, »the reporting and interpretation of biological information is unavoidably a political act«, which underlines the necessity of truly interdisciplinary research.⁴⁴ My critique does not question scientific methods, which I appreciate very much, but simplistic interpretations of complex information. The problem is especially apparent for Roman and medieval times with their dense written records, while for prehistoric times research is focused on long-time and wide-ranging population developments.

43 Goodman, *Traversing the Chasm*; Leatherman, *Chasm*, 5.

44 Leatherman, *Chasm*, 24.

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Archaeological Research on Migration as a Multidisciplinary Challenge

Stefan Burmeister*

Migration is a key concept in archaeology. It is a common explanation for the distribution and diffusion of cultural traits. However, it is more often an axiomatic postulate than the result of sound methodological analysis. The weaknesses of this approach have become apparent and have brought migration-as-explanation into disrepute. For archaeological investigation of the Migration Period the problem is further aggravated. Ancient written sources report an abundance of migrations associated with particular peoples. These sources often provide the coordinate system of archaeological investigations with fatal consequences as archaeology runs the risk of losing its independent methodological basis. Recently, new methods derived from the life sciences have joined in and have created new approaches to migration analysis. These methods sometimes provide a corrective that can compensate for the weaknesses of archaeology's own methodology. Archaeology now faces new challenges. Archaeological sources are often neither compatible with written sources, nor with the findings of the diverse life science methods. It is becoming apparent that archaeology has lost its previous methodological command for investigating migration. As a scientific discipline archaeology has to find its place in migration research anew.

Keywords: archaeology; migration; genetics; Anglo-Saxons; Indo-Europeans.

Migration is a key concept in continental European archaeology. According to the discipline's tradition, migration was – and still is – reckoned as a major cause of cultural change. In retrospect, however, it must be said that migration itself was largely absent as a subject of research in its own right. Mobility is in continental European archaeology a common explanation for the spatial distribution of archaeological finds – but this only as an axiomatic assumption of observed phenomena.¹ Neither is migration in itself seen in need of explanation – and thus seen as a genuine research topic – nor has the explanatory potential of the phenomena of culture change been reflected. Above all, we have to assert an obvious methodological lack of clarity in differentiating between migration and other potential causes of culture change. A clear theoretical distinction between different cultural mechanisms which lead to culture change has for long been neither systematically drawn nor reflected. The unclear distinction between independent development, diffusion – e. g. by trade and other forms of knowledge and culture transfer – and migration is a significant shortcoming of archaeological analysis. All three phenomena causally affect the spatial distribution of certain cultural features, but only migration is necessarily linked to the mobility of groups.

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1 Cf. Burmeister, Migration und Ethnizität.

Bruce Trigger already complained about this methodological deficit in archaeology in the 1960s;² systematic approaches to solving the problem have not been developed since: a missing theoretical comprehension of prehistoric migrations and their study is still criticized today.³ In the Anglo-American world, with the ›New Archaeology‹, migration as an explanatory model for culture change was abandoned and banished from the gaze of archaeological research. However, archaeology's rejection of migration is not primarily rooted in the methodological shortcomings of migration-as-proof, but more so in the rejection of the discipline's cultural and historical tradition, as well as in a shift to an evolutionistic paradigm.⁴ Lewis Binford, one of the protagonists of the ›New Archaeology‹, saw migration as an exclusively historical explication that affects a mechanism of cultural processes, but »add[s] nothing to the explanation of the processes of culture change and evolution«.⁵ Because migrations are specific events and not the result of evolutionary processes, they offer no general explanation to the reference frame of the structural and functional characteristics of cultural systems – and thus would have no explanatory power in the matter of processes of culture change.⁶ This is remarkable insofar as Binford made White's dictum of culture as an »extra-somatic means of adaptation for the human organism« the basis of his disciplinary re-adjustment. Migration could fit easily into this cultural concept, however it lacked a basic understanding of the processual character of migration. The vast number of historical and present migrations reveals mobility as an adaptive strategy in dealing with changing ecological, economical and political conditions. Only later did the multifaceted processual character of migration find its way into the archaeological discourse.⁷ This lack of methodological and theoretical comprehension should not lead to letting the field of research lie fallow in general. In fact, David Anthony later remarked that here was a case of the baby being thrown out with the bathwater.⁸

The history of mankind is a history of migrations. Migration is considered to be a part of the human condition⁹ – the human being as a *homo migrans*.¹⁰ The historical potency of migration especially in late antiquity has been discussed; whether the so-called barbarian migrations really caused the end of the Roman Empire will remain undecided here. In any case, migrations changed the political map of Europe as well as the social structures of societies to a large extent. In this sense, Walter Pohl spoke of »migration as the cradle of Europe«.¹¹ To eliminate migration as a research topic would be culpable, as that would be to

2 Trigger, *Beyond History*, 26-47.

3 Cabana, *Problematic Relationship*, 25; van Dommelen, *Moving On*, 479.

4 E. g. Adams, *Invasion, Diffusion, Evolution*; Adams *et al.*, *Retreat from Migrationism*; Myhre and Myhre, *Concept ›Immigration‹*.

5 Binford, *Archaeology as Anthropology*, 218.

6 The *New Archaeology* strongly aimed at generalisations of cultural processes, which is opposed to a study of historical events disqualified as particularism. For a critical review of *New Archaeology/Processual Archaeology* see Eggert, *Prähistorische Archäologie und Ethnologie*; Trigger, *History of Archaeological Thought*, 294-303.

7 Seminal: Anthony, *Migration in Archeology*; in later variations: Burmeister, *Archaeology and Migration*; Prien, *Archäologie und Migration*; Tsuda *et al.*, *Unifying Themes*.

8 Anthony, *Migration in Archaeology*.

9 Bade *et al.*, *Enzyklopädie*, 19; Fassmann, *Migration*.

10 Bade *et al.*, *Enzyklopädie*, 19; Burmeister, *Homo migrans*.

11 Pohl, *Entstehung des Europäischen Weges*.

make an important aspect of cultural processes invisible. Above all, migration is part of the research agenda of the archaeological disciplines. For about two decades methodological development in the natural sciences has made isotope analysis and genetics available methods that can overcome the methodological problems of archaeological research on migration and provide the first reliable proof of prehistoric migrations. Thus, archaeology seems to have a repertoire of methods at hand that should convince even notorious sceptics of archaeological migration studies. The fact that the results obtained here are now observed with great public interest may also have led to the veritable research boom that has arisen. The abundance of research projects and publications can hardly be overlooked. Although the projects are interdisciplinary and all involve close cooperation between the natural sciences and humanities, it is obvious that archaeology plays only a subordinate role in knowledge production. Despite the euphoria about these new opportunities, it makes sense to step aside for a moment and reflect upon the methodological foundations of migration archaeology and its evidence, and also to determine the relationship of the disciplines involved. In the following, the main focus will be on the German archaeological discourse, which has been very lively and controversial in recent decades. The methodological and theoretical problems of migration archaeology clearly come to light here.

Material culture as methodological tool

Migration, culture transfer and acculturation have long been studied by archaeology. The necessary methodological lever provided by material culture is tangible in the archaeological record. The spatial distribution of specific cultural features – including both things and knowledge – with subsequent expansion or relocation mirrors mobility processes; as these features did not spread by themselves, we seize here upon the mobility of the people who distributed them. Mapping is a heuristic device for further investigation, but provides no explanation in itself for the processes underlying the distribution. Although earlier voices may have warned against postulating migration solely on the basis of individual cultural features,¹² this often was – and still is – the usual practice. In particular, in the archaeology of migration periods the spread of individual types of costume elements is seen as evidence of a people's migration.¹³ This is certainly seen in the context of historical background knowledge; but in this way archaeology at best illustrates ancient textual evidence: an independent interpretation is not given. Costume elements – mostly made of metal – are not only numerous in the archaeological record – and thus represent a quantitatively significant source – they also touch on the common assumption that costumes reflect the self-concept of their wearers. It may be marked here only in passing that metallic jewellery constitutes only a very small facet of costume and perhaps reveals more about craft traditions and the distribution circuits of metalsmiths than about the representational needs of costume wearers. It is undisputed that costume is an important medium of social communication and interaction. It allows individuals to express their social affiliation and thus has great significance for forming one's identity. The problem, however, is the common understanding of costume, which has its origins in the movements of the nineteenth and early twentieth centuries that aimed at producing and preserving tradition.

12 Hachmann, *Ostgermanische Funde der Spätlatènezeit*; Werner, *Verbreitung frühgeschichtlicher Metallarbeiten*, 78.

13 E.g. Böhme, *Ende der Römerherrschaft in Britannien*.

It is based on a very static concept of costume and misunderstands what many ethnographic studies demonstrate: that is, that costumes in many cases originate in specific historical situations and transform over the course of social processes. They are by no means permanently tied to a specific group.¹⁴ This ethnographic perspective on costume is also supported by historical studies.¹⁵

The ambivalence concerning the interpretation of the archaeological record becomes evident in the case of the Visigoths' immigration into Spain. As a result of the downfall of the so-called Visigothic Kingdom of Toulouse in Gaul, there was an immigration of Visigothic groups and the foundation of a new empire at the beginning of the sixth century in Spain. Here an influx of Gothic or Gothic-inspired objects and new burial customs becomes apparent. Essentially two contradictory approaches compete for interpretation of the archaeological evidence, and both are situated within the context of the historical record.¹⁶ (1) The Spanish burial finds indicate a specific costume that can be traced back to the costume of the Černjachow-Sîntana de Mures culture in southern Ukraine and Romania. This particular culture is historically identified with the Goths. For two centuries Goths had preserved their traditional costume. This costume would permit, in combination with the textual evidence, the identification of the Spanish burials with the Visigoths. (2) In contrast to this view is Michel Kazanski's concept of a »mode danubienne«. ¹⁷ What the first approach takes to be a Gothic costume, is in the latter a common Danubian fashion that originated in the amalgam of different cultural influences, especially equestrian/nomadic. The high social prestige that the Huns particularly enjoyed at the time ensured that this style was adopted by a cosmopolitan aristocracy often of Germanic descent. The sudden appearance of the Danubian fashion in Spain can indeed be seen in connection with external cultural influences, but not necessarily with migration, and certainly not with one that could be identified ethnically by costume. Barbara Sasse even goes so far as to say that after decades of migration the Visigoths had no longer a genuine material culture that could be distinguished archaeologically from that of the late Roman population.¹⁸ Both sides then bring forward their arguments, without a solution to the interpretive dilemma in sight.

This raises the fundamental question of how culture is bound to specific groups and specific situations. Units of production, distribution and consumption are seen as significant bases for the local reproduction of culture.¹⁹ Inspired by the work of Michel Foucault and Pierre Bourdieu this understanding has fundamentally changed cultural studies. Material culture is increasingly seen less as a reflection of social norms and social practices, but as a means of social communication, as a strategy for shaping social relations. It structures social actions and, as Tilmann Habermas points out, does it very effectively.²⁰ Material culture is in a constant process of negotiation of meaning and practice. Foreign objects, especially, can experience a complete redefinition of their meaning and function in a new context.²¹ In par-

14 Cf. Burmeister, *Zum sozialen Gebrauch von Tracht*, 179-188, with further references.

15 Pohl, *Telling the Difference*; Rummel, *Germanisch, gotisch oder barbarisch*; Rummel, *Habitus barbarus*.

16 For an overview see Eger, *Westgotische Gräberfelder*.

17 Kazanski, *Diffusion de la mode danubienne*.

18 Sasse, *Westgoten in Südfrankreich und Spanien*, 42.

19 Cf. Hahn, *Diffusionism, Appropriation, and Globalization*.

20 Habermas, *Geliebte Objekte*, 193.

21 See e. g. Hahn and Weiss, *Mobility, Meaning and Transformation of Things*.

ticular, immigrant societies reveal such flexibility in their cultural practices that any attempt to identify migrations archaeologically can easily be lead astray.²² In confrontation with a new ecological and social environment as well as changed economic conditions immigrants often adjust their cultural habits. The same applies to indigenous groups that respond to immigrants and new social constellations.²³ All these processes cannot be depicted by a simple mapping of cultural features.

Ethnic interpretation as methodological tool

One would think that this problem does not arise in protohistoric archaeology. The abundance of ancient accounts of contemporary migrations cannot be overlooked nor ignored. The records link historical events with tribal names and geographical entries. Thus they offer a historical coordinate system to archaeological interpretation. It is therefore hardly surprising that such diverse information has a large impact on archaeological interpretations. It is hardly surprising then that under the influence of these records, migrations become an obvious model for the interpretation of foreign features on archaeological distribution maps. Interpretation seems to be easier in combination with the additional information of the ancient texts, which should be more a benefit than a burden. Furthermore, alternative interpretations are always confronted with the ›diktat‹ of the historical evidence and may have to be reasoned more soundly than those interpretations that are close to the written sources. A link between the textual evidence and the archaeological record is made by ethnic interpretation. Archaeological distribution patterns are set in relationship with regionalised demonyms and should allow an ethnic interpretation of archaeologically identified cultural features. Cultures can be traced in their temporal displacement and can be identified by historical interpretation as migrating *gentes* or peoples. As easy as this procedure seems, so too does it hold as many problems. The archaeological analysis is centred on the so-called culture model. In a landmark study, Rolf Hachmann presented this concept in the 1950s as an archaeological proof of migration.²⁴ In his argumentation he explicitly did not refer to individual cultural elements, since these are too open to diverse interpretations. According to him, the essence of a culture will not be captured by the sum of its cultural elements, and cannot be represented by a limited number of isolated cultural traits. His thought followed a functionalist culture model that aims at the nexus between cultural features. That those specific cultural elements chosen in his study reflect this context, however, remained a postulate. Hachmann understood culture as a social organism, a unique and unrepeatable historical fact; culture in this sense would lose its integrity by transferring only individual elements. By assuming its historical uniqueness, direct connections can be established between the same culture at different locations.

22 Burmeister, *Archaeology and Migration*, 541-542; *Migration – Innovation – Kulturwandel*, 39-44.

23 In archaeology, the change of perspective was initiated by Hodder, *Symbols in Action*. In his ethno-archaeological studies, he not only showed how social behaviour was actively shaped by material culture, but also how this behaviour was adapted to specific group constellations, e. g. in interethnic contact. With it, he rejected to explain cultural behaviour with general, universal models as propagated by *New Archaeology/Processual Archaeology*, thus opening up the view again for particular historical contexts (*ibid.*, 216 f.). However, this did not lead to putting migration back onto the agenda of *Post-Processual Archaeology*.

24 Hachmann, *Ostgermanische Funde der Spätlatènezeit*.

In German archaeology this culture model, following Hachmann, is the fulcrum of ethnic interpretation. In a region in which a specific *gens* is attested historically, cultural patterns are inferred from the archaeological record; in an ideal case, these should be limited to the *gens* and can thus be considered intrinsic to this group of people. Elements of burial rites, costume and weapons, are identified as ethnic markers and used to identify migrations. The choice of these elements has on the one hand pragmatic reasons: since settlement finds for the respective groups are hardly known and then usually elude an ethnic approach, the focus is necessarily on funeral culture and grave goods. On the other hand, costume and burial customs are regarded as a strong expression of the self-understanding of a population. This usually remains unspoken and can only be considered as a postulate without thorough cultural reasoning.²⁵

This approach is based on a classificatory concept of culture,²⁶ which is made up of a static, primordial concept of ethnicity. According to this understanding ethnicity is determined by birth; this makes it possible to empirically distinguish ethnic affiliation. First of all, designated cultures are scientifically classified by archaeology with the aim of systematically structuring the archaeological record. But it is unclear here how these classifications reflect former life contexts and historical reality. The transfer of archaeological systems of order to real life contexts is in fact produced by the classifying concept of culture – but beyond its implicit assumptions, this is not sufficiently justified.

Another aspect of ethnic interpretation deals with the parallelism generated between textual and archaeological evidence and problems that are thus far unresolved. Since the historical record is the methodological starting point of archaeological ethnic interpretation, Volker Bierbrauer explicitly states that *gentes* names can only be used by archaeologists in the sense given to them by historians according to the current state of research.²⁷ Recall, however, that for historians *gens* is not a simple concept, and one with which ›Barbarian‹ social orders cannot adequately be represented. In no case does current historical science understand it as denoting a primordial, self-contained community of lineal descent. The term designates more accurately an open, continuously changing group of political actors, who are moreover united by a common ideology of descent.²⁸ The use of gentile names by archaeologists therefore is hardly compatible with the historians' concept of *gens*.

This is an understanding of ethnicity that is currently favored in the social sciences and puts more emphasis on the process character of ethnicity. Following Stuart Hall, we must think of the construction of identity as being »produced in specific historical and institutional sites within specific discursive formations and practices, by specific enunciative strategies.«²⁹ Identity construction is therefore not a direct reflection of social conditions, but the field where social claims are negotiated. Identity discourse is thus always a means of defining

25 For further details and literature see Burmeister, *Migration und Ethnizität*, 237-240. For the general problem see Eggert, *Prähistorische Archäologie*, 273-296.

26 See Brather, *Ethnische Interpretationen in der frühgeschichtlichen Archäologie*, 51.

27 Bierbrauer, *Zur ethnischen Interpretation*, 49. – He states »daß dem Gebrauch von *gentes*-Namen durch den Archäologen nur jene Sinnhaftigkeit beigemessen werden kann, die der Historiker in Interpretation der Schriftquellen diesen nach dem derzeitigen Forschungsstand beimißt.«

28 E.g. Pohl, *Gentilismus*; Steinacher, *Wiener Anmerkungen zu ethnischen Bezeichnungen*; Wolfram, *Germanen*, 91-92.

29 Hall, *Introduction*, 4.

social participation and power relations anew. One does not possess an ethnic identity, but creates one. This insight is the starting point for Walter Pohl in his methodological reflections on the analysis of strategies of identification.³⁰ Ethnicity is not given, but is the result of historical and social processes. As he points out in numerous examples, ethnic markers lose their function as proof of origin in migration research. Although they can express discursive efforts for identity in specific cases, they say nothing about a person's origin. Historically attested demonyms are in a similar field of discourse: migrating groups merged, joined together; their gentile name could be transferred to other groups or they could adopt a new one that was more prestigious or which was assigned to them by foreign appellation.³¹

In the sense described here for the construction of identity, archaeological cultural models can also be thought of as strategic expressions of cultural participation. But through the processes outlined here, demonyms and material culture lose, on the one hand, their assumed bond, and on the other, their suitability as proof of migration. The determination of ethnic identity does not provide any methodological levers for an archaeological proof of migration. In a provisional appraisal, it can be attested that archaeology is lacking suitable methods to adequately study migration issues.

Ideology as guideline for migration research

The archaeological debate on migration is not only a disciplinary, but also always a social discourse. How migration is discussed often reflects a society's self-image in terms of its self-positioning in both history and in the present. Just think of the German archaeological technical term for migration period: ›Völkerwanderungszeit‹ – »the period of the migration of people«. This definition is well established in both technical as well as popular terminology. Although it has its firm place in the archaeological system of chronology, it has been defined historically: the Migration Period began with the arrival of the Huns on the eastern border of the Roman Empire and the crossing of the Danube by the Goths in 375 AD, and ended 568 AD with the founding of the Lombard Kingdom in Italy. As historical cornerstones these dates are largely arbitrary. The Migration Period thus defined had no historical significance for either those people invading the Empire or for the Romans; but it did have significance for German historians who not only saw the decline of the Roman Empire but especially saw Germanic groups claiming the Roman heritage during this period. The term can be traced back to the eighteenth century, when it takes on a national perspective, and is less rooted in the historical events of the so designated ›Völkerwanderungszeit‹ than in the process of German nation-building in the eighteenth and nineteenth centuries. Friedrich Schiller, for example, envisioned these migrations as the beginning of a historical process which culminated in European nation building and the Enlightenment. He wrote in 1790: »The sword of the Vandals and Huns that reaped without mercy through the Occident, and the powerful race which occupied the cleaned scene, and from a millennial war came un-

30 Pohl, Introduction.

31 Pohl, Entstehung des Europäischen Weges, 34. – The historian Ulrich Kahrstedt stated already in 1934: »Bei allen Stammeswanderungen gilt es, sich klarzumachen, daß der Personenstand eines solchen Volkes sich ständig verschiebt, einzelne Gruppen, Familien und Personen zurückbleiben, andere sich anschließen und der Name des betr. Stammes bald einen ganz anderen Bestand von Individuen bezeichnet als vor Beginn der Wanderung« (Kahrstedt, Politische Geschichte Niedersachsens, 4).

conquered – these are the creators of our present felicity.«³² In contrast, in the destination areas of Germanic migration, one does not usually speak today of a »period of migration of people,« but rather of »the barbarian invasions«, »les invasions barbares«, »le invasionsi barbariche« or »las invasiones bárbaras«, which, of course, are also modern technical terms. Whether »migration of people« or »invasion of barbarians«, the ideological subtext of these different denominations can hardly be denied.

The debate on the immigration of Anglo-Saxons in England is also a very illustrative example of how those scenarios developed by historians and archaeologists are strongly influenced by ideological assumptions. From the German side, there is no doubt that, according to written records, numerous peoples from northern Germany migrated in the fifth and sixth centuries AD to Britain and formed there the nucleus of the modern English nation. For long, even in England, the idea of a mass immigration of Germanic groups and the expulsion of the indigenous British population was accepted.³³ In British archaeology a seminal article by Grahame Clark in 1966 launched a general rethinking in which the importance of immigration to England was widely denied for British prehistory.³⁴ However, the paper finds its parallels in two other paradigm shifts at that time: one academic, in the Anglo-American turn to *New Archaeology*, which took a more evolutionary perspective and in which historical events such as migrations were attributed no explanatory power;³⁵ and a contemporary historical context in which the public debate in England was marked by the Commonwealth Immigrants Act of 1962 and its racist-motivated policies against immigrants from the former colonies.³⁶ This shift in British archaeology – referred to by critics ironically as »immobilism« – also reached Anglo-Saxon archaeology. The pendulum now swung in the opposite direction: no longer was mass immigration the favoured model, but instead the influx of small groups of warriors, who managed to establish themselves as an elite and ultimately imposed their language and culture on the British majority population. Mass immigration versus small group migration or: Where are we rooted? In the humus of Romanized Britons or with the Germanic barbarians?

It need not be emphasized that the archaeological research – here, migration archaeology – is situated in the context of its contemporary political discourse and is strongly influenced by it.³⁷ This ideological bias is not dependent on the methodological weaknesses of migration archaeology, but it does affect the orientation of the research and thus its results. The issue

32 Schiller, *Allgemeine Sammlung historischer Memoires*, XXIX: »Das Schwert der Vandalen und Hunnen, das ohne Schonung durch den Occident mähte, und das kraftvolle Völkergeschlecht, das den gereinigten Schauplatz besetzte und aus einem tausendjährigen Kriege unüberwunden kam – diese sind die Schöpfer unsers jetzigen Glücks.«

33 For a review of the debate in English archaeology see Härke, Entstehung der Angelsachsen, 429-434.

34 Clark attributed to British archaeology a downright invasion neurosis (Clark, Invasion Hypothesis in British Archaeology, 173). For the debate, his final sentence should have deserved more attention: »Invasions and minor intrusions have undoubtedly occurred, even if far less often than other forms of culture contact, *but their existence has to be demonstrated, not assumed*« (ibid., 188 – my italics).

35 Marciniak and Coles, Preface, name Clark as one of the founders of the *New Archaeology*, but it can be doubted that he himself would have agreed. In any case, his concept of archaeology, one that he had already developed in earlier works, clearly parallels the new disciplinary paradigm. Clark's studies had a strong focus on environmental and economic issues; he was interested primarily in adaptation strategies to natural and social environments, and in these he saw the essential motor for culture change. See Fagan, *Grahame Clark*.

36 Miles and Cleary, Britain, 165.

37 Härke, Archaeologists and Migrations; Härke, Wanderungsthematik, Archäologen und politisches Umfeld.

of migration obviously touches upon questions of national self-image. The question of the continuity or discontinuity of certain groups, the historical fate of migration winners or losers – these touch upon conceptions of man and history that are the guiding themes of our scientific path to knowledge.

Solutions to inherent methodological problems

Solutions to the numerous problems and controversies shown here could be offered by scientific methods such as genetics and isotopic analysis. They provide a repertoire of methods, which focuses on the study of migration on a sounder basis. The debate on Neolithic transition has benefited considerably from these in recent years and, with respect to our understanding of these processes, constituted a significant leap.³⁸ Also, as to the question of Anglo-Saxon migration, scientific methods are thinning out the jumble of controversial opinions.³⁹ The picture that emerges now is complex and varied. It shows that there were regions where complete family groups immigrated; here the indigenous population and the immigrants lived together in an apartheid society. In other regions, both groups lived in separate village communities, but had marital relationships. At the northern periphery of the Anglo-Saxon settlement probably only a small group of immigrants replaced the native elites. Although this multi-layered model is not new – similar scenarios have previously been formulated and it has also been emphasized that the Anglo-Saxon migration is not to be represented in a single, monothetic model of a uniform process⁴⁰ – genetics seem now to validate this comprehensive, polythetic model.

Scientific methods provide a corrective to compensate not only the weaknesses of archaeology's own methodological basis, they are also a corrective when it comes to the intellectual proliferation of controversial, sometimes ideologically motivated representations of history. With the new scientific methods, new possibilities open up. The Mainz research project of bio-archaeometric identification of mobility in the fourth and third centuries BC shows that in Celtic Central Europe only a few people migrated in the course of their lives; most were stationary⁴¹ – and this in a time where we have been informed by textual evidence of large migratory movements. La Tène material culture also points to far-reaching inter-regional contacts and cultural transfers. As indicated above by the Anglo-Saxon example, migration is becoming a more complex process. The models identified here put the universal model – ethnic group migrates from A to B – on the academic dump heap. The now numerous and promising results also point to a new level of understanding: migration is no longer an axiomatic explanation, but is studied as a social process in its own right. Demographic and social processes solidify and enhance our understanding of the societies under investigation.

So far everything seems to be progressing well. Looking at the pending issues too, we can be confident when we know that the natural sciences are on our side. In an interview in 2009, nine German archaeologists unanimously stated that the greatest advancements of

38 For a review of the archaeological debate see Kienlin, *Von Jägern und Bauern*; Bollongino and Burger, *Palaeogenetische Studien zum Neolithikum*; Bramanti *et al.*, *Genetic Discontinuity*; Brandt *et al.*, *Human Paleogenetics of Europe*.

39 Härke, *Entstehung der Angelsachsen*; Anglo-Saxon Immigration and Ethnogenesis.

40 E. g. Burmeister, *Archaeology and Migration*, 552; Hills, *Origins of the English*, 114.

41 Hauschild *et al.*, *Nebringen, Münsingen und Monte Biele*.

knowledge were achieved in archaeology in recent decades by scientific methods.⁴² With regard to the funding of research projects, it seems likewise obvious: currently, archaeological migration research is hardly eligible without cooperation from the relevant sciences.⁴³

New problems for archaeology

But I am still reluctant to draw a positive balance. I see archaeology being encountered by new, major challenges and academic problems. Recently, the results of a large-scale study on the colonization of the North American Arctic were presented.⁴⁴ Based on genetic studies of the palaeo-Eskimos and modern Inuit the authors were able to show that the ancient processes are not fully apparent in the archaeological record. The material culture of the palaeo-Eskimos seems to mirror migration processes that are not evidenced by genetic data. According to the study, the archaeologically comprehensible processes of cultural diffusion and acculturation were based on the transfer of ideas, not on the spreading and mixing of populations.

Migration Period case studies have produced similar results. A preliminary report of the analysis of samples from the Thuringian cemeteries of Obermöllern and Rathewitz is as interesting as it is disillusioning. These early medieval cemeteries were examined in the context of a European project to gain more insight into the Langobard's migration. Individuals who can be identified as immigrants because of their isotopies, fit completely into the cultural habits of the regional population. However, those individuals who, by their burial objects, show external influences, do not provide any proof of mobility by isotope analysis.⁴⁵

All of these diverse examples clearly demonstrate that the scientific data are not in alignment with the archaeological record. This is of course not a general statement but one that is derived from individual case studies and applies only to – and is only valid for – these cases. This observation, however, gives food for thought and leaves such strong statements as those given by Alexander Koch even more questionable. He postulated: »The ethnic ties of many Merovingian brooches ... cannot be dismissed« – and – »No Frank woman will have worn Ostrogothic, Thuringian or Lombard bow fibula, unless she was forced to by particular circumstances«. ⁴⁶ A striking example is given by Doris Gutschmiedl showing the discrepancy between the origin of a certain brooch type and the origin of a person equipped with one according to isotope analysis.⁴⁷ Though we are here faced again with the problem of ethnic interpretation, this also affects migration issues. First of all, Koch's quotes reveal a problematic understanding of scientific logic: the statements made are postulates which form the starting point of the investigation, not its results. What should be a result of scientific analysis only comes as a prerequisite of investigation – with the expected output. If Merovingian fibulae were ethnically bound, then the scientific results described show that individuals could change their ethnic identity entirely. Though this may correspond very well to current discourse in the social sciences, it is certainly not what Alexander Koch meant.

42 AiD-Redaktion, AiD-Jubiläum, 38-39.

43 This becomes even more important when one considers that many of the respondents in the interview today occupy key positions in the peer review process of the national funding programs.

44 Raghavan *et al.*, Genetic Prehistory of the New World Arctic.

45 Knipper *et al.*, Mobility in Thuringia or Mobile Thuringians.

46 Koch, *Bügelfibeln der Merowingerzeit*, 537: »Die ethnische Gebundenheit vieler merowingerzeitlicher Fibeln ... ist u. E. nicht von der Hand zu weisen« – and – »Keine Fränkin wird ostgotische, thüringische oder langobardische Bügelfibeln getragen haben, sofern sie nicht durch besondere Umstände dazu gezwungen wurde«.

47 Gutschmiedl, Justinianische Pest nördlich der Alpen.

Anyhow, these observations are provocative as they clearly show us archaeology's epistemological limits. It becomes obvious that archaeology has lost its previous methodological hold on investigating migration. Maybe we are just in the same situation as archaeology was after the advent of radiocarbon dating. At that time the results of archaeological dating were not compatible with the new data of the radiocarbon method. This resulted in fierce defensive battles on the part of archaeology. That alone should warn us about fighting an unstoppable movement in the face of the loss of interpretive authority. Joseph Maran has clearly pointed at the errors of the conservative Miložić group: the lack of reflection on their own methods.⁴⁸ We shouldn't make this mistake again. For archaeology, this demands a more open debate about the cultural and historical processes that basically structure the archaeological record. This is simply to say that we still need more open-minded reflection of current discourses in the cultural and social sciences.

Genetics in archaeology

It is undisputed that genetics has not only given archaeology new impetus, but also has great potential for the investigation of topics traditionally settled by archaeology. The results of such large-scale projects as the study of Lombard migration can therefore be expected with great anticipation.⁴⁹ The project outline by Patrick Geary gives hope for the solution of many previously unsolved problems of migrations in Late Antiquity. Solely to open new perspectives for research is reason enough to understand the question asked by Daniela Hofmann »What have genetics ever done for us?« as merely rhetorical.⁵⁰ But are expectations immediately a promise that gives rise to euphoria? Here it is worth taking a closer look, so I would like in the following to focus briefly on two case studies.

Genetics of Anglo-Saxon migration

Let us return to the Anglo-Saxon migration. The results delineated by Heinrich Härke reveal, as shown, a complex model of Anglo-Saxon immigration in post-Roman Britain, which seems to dissolve the academic controversies about the nature and extent of this migration.⁵¹ The immigration was neither a displacement nor even a genocide of the Romano-British population; their fate seems to have been social marginalization in an apartheid society. This appears to be supported by a number of genetic studies. The soft – albeit hard-fought – discourse of the human sciences could have come to an end by the hard facts of natural science. But this is not so; scepticism and criticism remain.⁵² This raises the question of how

48 Maran, *Mit den Methoden der Gegenwart*, 341-342. – For Vladimir Miložić the method of stylistic comparison provided more reliable information on the temporality of cultures. His criticism was fostered by problems of the radiocarbon method that occur unavoidably at any first application of a new scientific method. Miložić's postulate of interpretive authority over the archaeological record and his massive statement »Indessen haben wir unwiderlegbare archäologische Tatsachen, die die Gleichzeitigkeit der Gumelnita- mit der Vinča-Kultur über jeden Zweifel erheben« (Miložić, *Absolute Chronologie der Jungsteinzeit*, 10) nevertheless reveal a conspicuous overassessment of archaeological methods.

49 Geary, *Rethinking Barbarian Invasions through Genomic History*; Knipper *et al.*, *Mobility in Thuringia or Mobile Thuringians*. See also Geary and Veeramah, this volume.

50 Hofmann, *What Have Genetics Ever Done for Us?* – She herself sees the strong impulses and new insights achieved through genetics in the debate of Neolithic transition and promotes a strong interdisciplinary cooperation.

51 Härke, *Entstehung der Angelsachsen; Anglo-Saxon Immigration and Ethnogenesis*.

52 See e. g. Hills, *Anglo-Saxon DNA*; Hills, *Anglo-Saxon Migration*.

›hard‹ and resilient the results obtained by genetics really are. It is worth noting that the results were not based on genetic analysis of ancient DNA, but on exclusively modern DNA.⁵³ There were no statements made about individuals from Anglo-Saxon times, but only general statements about the ancestry of modern English people. DNA is an archive in which the individual genealogical history is inscribed – and where even distant, past migrations become apparent. Comparing modern British DNA with the DNA of other modern Europeans can indeed reveal past migrations, but it allows neither clear statements about the date of migration nor about the origin of the migrants.

The date of a migration is basically determined by probability calculations based on specific demographic parameters. The demographic composition of the migrants affects the outcome of migration in terms of the number of migrants in relation to the indigenous population. Further decisive factors are the duration of the migration and the socio-economic relationship between natives and immigrants; and also the length of a generation and the resulting reproduction rate have an impact on the genetic make-up. In addition to the Anglo-Saxon migration there were further waves of immigration to Britain in earlier and later centuries that might have had an influence on today's genetic map. Assuming other parameters, John Pattison comes to a different estimation regarding the genetic impact of Anglo-Saxon immigration. He rejects the results of those studies that argue for a massive immigration and sees the data in accordance with an elite immigration.⁵⁴ A decision as to which of the underlying parameters best match the historical situation cannot be arrived at from the data itself. One can further speculate as to whether the statements made so far on the basis of modern DNA about an Anglo-Saxon mass immigration would have been so unambiguous without knowledge of the overwhelming textual evidence. Thus, the ball lies again in the field of the historical sciences. Only the analysis of aDNA permits *de facto* statements concerning historical subjects.

Another point is the geographical origin of immigrants estimated by today's genetic maps. The common ancestry of different populations can certainly be identified by the Y-chromosome haplotypes. If Weale *et al.* determine a strong genetic similarity between the present inhabitants of central England and Friesland,⁵⁵ Friesland is however not yet to be designated as the home country of the immigrants to Britain. What is today Friesland has in its history also experienced a number of demographic changes, so that the gene map here can be the result of various migration processes. It would be naive to think that those regions at the moment not in the focus of immigration analysis have been historically at a standstill.

One last point should be noted here. Special attention of course is called by the postulate of an Anglo-Saxon apartheid society.⁵⁶ Due to their calculations – based on modern DNA – the authors come to the conclusion that during the first two centuries after conquest there occurred no significant marital relationships between Anglo-Saxons and native Britons.

53 Capelli *et al.*, Y Chromosome Census; Thomas *et al.*, Evidence for an Apartheid-like Social Structure; Weale *et al.*, Y Chromosome Evidence.

54 Pattison, Is it Necessary? – For a reply see Thomas *et al.*, Integration versus Apartheid.

55 Weale *et al.*, Y Chromosome Evidence.

56 Thomas *et al.*, Evidence for an Apartheid-like Social Structure.

They assume that, for the maintenance of long-term segregation, specific social mechanisms are needed in apartheid societies. This explanation of the occurrence of modern DNA patterns is based on probability calculations of various demographic models, and was also previously formulated by historians⁵⁷ and archaeologists⁵⁸. The argumentative basis for the model of an apartheid society ultimately is not rooted in scientific data based on DNA analysis, but is based on general sociological considerations and legal texts of the seventh century. Apartheid is today seen as a discriminatory form of racial segregation; it can also be generally extended to ethnic groups. Segregation is accompanied by the denial of equal rights and is enforced through a series of laws. Apartheid is a legal system that cannot be reduced to closed marriage relations. For this, however, genetics cannot contribute any statement. The model of reproductive segregation along ethnic lines may be due to different social mechanisms. Even in today's western immigration societies, there are class barriers between the various population groups that socially proactively shape society and counteract mixing even after generations. Apartheid consequently cannot be determined from genetic analysis, but through studies of legal and social history only. A deficiency of the current debate is that the genetic analysis has so far mainly been carried out using modern DNA. I know of only two studies that are based on the analysis of aDNA.⁵⁹ While Töpf *et al.* remain indifferent to the problem of Anglo-Saxon immigration, Schiffels *et al.* come to at least partially deviating results. According to them, 38 % of the modern population of eastern England can be traced back to Anglo-Saxon immigration. The Anglo-Saxon population, however, was genetically mixed, and there were no signs of strong segregation. It could even be observed that natives had a richer grave furnishings than did immigrants in the same burial ground. The model of an Anglo-Saxon apartheid society has to be rejected on this basis.

Genetics cannot yet provide a genuine contribution that solves the problems of the study of Anglo-Saxon migration.⁶⁰ Its findings allow demographic processes to be modelled for at least a part of the immigration area. This provides important evidence, but cannot so far resolve the contentious issues satisfactorily. To date, genetic analysis touches only one segment of the multi-stage immigration model: those regions for which there is a mass immigration in discussion. The regions that experienced an elite immigration are not covered there. The model, which assumes various, differently structured immigrations, is not based on genetic analyses, but on archaeological and historical studies, and was formulated previously.⁶¹ Despite all the attention that genetics has received here, the natural sciences have not yet reinvented Anglo-Saxon research.

57 Higham, *Rome, Britain and the Anglo-Saxons*, 193; Woolf, *Apartheid and Economics in Anglo-Saxon England*.

58 Härke, *Population Replacement or Acculturation?*

59 For their study, Töpf *et al.*, *Tracing the Phylogeny of Human Populations*, analyzed the DNA of 156 individuals from Romano-British and Anglo-Saxon cemeteries. The study by Schiffels *et al.* 2016 is based on ten individuals from Eastern England (Schiffels *et al.*, *Iron Age and Anglo-Saxon Genomes*). I am grateful to the reviewer for this reference.

60 For an overview see also Hedges, *Anglo-Saxon Migration and the Molecular Evidence*.

61 Härke, *Briten und Angelsachsen im nachrömischen England*; Härke, *Sächsische Ethnizität und archäologische Deutung*.

Genetics of Indo-European migration

I now come to my final case study: outgoing migration from the North Pontic and Caspian steppe in the third millennium BC. In this region the so-called Yamnaya culture originated in the 4th millennium, and then spread westward about 3,000 BC into the steppe belt and to the Carpathian Basin. In central and northern Europe the so-called Corded Ware culture developed in the early centuries of the third millennium BC. It was one of the first archaeologically-identified cultures in the nineteenth century and since then there has been an ongoing controversy as to whether it was created by mass immigration or small group infiltration and acculturation.⁶² Already early, Corded Ware culture was associated with the spread of the Indo-European language.⁶³

In recent years, two large-scale genetic studies have been presented that seem to bring clarification to this controversy. The basis of both studies is the use of ancient DNA. In one case, gene samples from 94 individuals were analysed,⁶⁴ and in the other of 101 individuals;⁶⁵ the sample material derived from both female and male individuals and could each be 14C-dated and assigned to an archaeological culture. Both studies conclude that Yamnaya culture was the starting point of a large and comprehensive migration that ultimately led to the displacement of large parts of the native populations in the immigration areas. While the results of the study of Allentoft *et al.* are barely exposed in detail, Haak *et al.* make an effort to quantify the changes in the genetic make-up caused by migration. They conclude that about 75 % of the Central European genetic make-up was replaced by immigrant Yamnaya groups. This high percentage can be established for individuals of Corded Ware culture; younger samples – for instance from the Bell Beaker Culture – again showed a lower percentage: the authors explain this by another, though less profound displacement process that was triggered by Western and Central European groups.

The two studies provide strong evidence that cannot be ignored in view of the notorious controversy on the issue of migration. The results they achieve, particularly with aDNA – and thus based on historical subjects – will be, at least for archaeologists and historians, more reliable than extrapolations based on modern genetic maps. With aDNA the date of migration can be identified on firmer ground. However, with regard to the demographic processes the studies remain indifferent. The data is interpreted as a result of mass immigration, but for such an explication, demographic simulations are needed to determine the extent of genetic displacement. The controversy of Anglo-Saxon migration shows the impact that population models have on the evaluation of the genetic make-up. Thus, in a society with an immigrant group of 20 % of the total population, the genetic make-up has been replaced after 15 generations by a ratio of more than 50%.⁶⁶

The result of the 75 % ratio of ›Yamnaya-genotype‹ in the Corded Ware population is based on the analysis of four individuals from Esperstedt in Saxony-Anhalt. In the Middle Elbe-Saale region the Corded Ware culture began around 2750 BC,⁶⁷ the sampled individuals

62 Pro mass immigration see e. g. Harrison and Heyd, Transformation of Europe; Frînculeasa *et al.*, Pit-Graves, Yamnaya and Kurgans; – pro acculturation e. g. Furholt, Entstehungsprozesse der Schnurkeramik, 493.

63 See Suhrbier, Und bewegten sie sich doch.

64 Haak *et al.*, Massive Migration from the Steppe.

65 Allentoft *et al.*, Population Genomics of Bronze Age Eurasia.

66 Weale *et al.*, Y Chromosome Evidence, 2653.

67 Furholt, Entstehungsprozesse der Schnurkeramik, 484.

date around 200-400 years later⁶⁸ and, therefore, certainly do not belong to the generation of immigrants, but to a significantly later population. Again, without comprehensive analysis, the question remains as to when immigration exactly took place: with the first appearance of the Corded Ware culture in a later period. In the latter case, the Corded Ware phenomenon would be the result of an acculturation process in the context of impending social change. In addition, it cannot be determined how representative the genetic data of Esperstedt is here for the Corded Ware culture in the Middle Elbe-Saale region. Against this background the postulate of comprehensive population displacements in the third millennium BC is to be regarded with caution.

Both studies link the migrations of the third millennium BC with the spread of the Indo-European language, with Haak *et al.*, for example, prominently in the title of their publication. They take up an old argument that has again been strongly propagated in recent years.⁶⁹ Since language is not reflected in DNA, the arguments are necessarily weak. The link between the emigration of the Yamnaya population and the spread of Indo-European is primarily based on two assumptions: (1) Language spreads through the migration of larger populations; (2) the spread of Indo-European must have occurred after the invention of the wagon, mid-fourth millennium BC.⁷⁰ These assumptions have been formulated before by Indo-European studies,⁷¹ and are thus not originally connected to genetic studies. However, these assumptions cannot necessarily warrant the far-reaching implications of the studies presented. There are a number of examples which clearly show that language changes do not have to be caused by population changes or extensive migration.⁷² And the purely linguistic argument that the spread of Indo-European must have occurred between the end of the 4th and the close of the 3rd millennium also presents problems. The fact that a number of technical wagon terms are represented in all Indo-European languages, but the word for ›spoke‹ is not, dates the spread and splitting of the Indo-European proto-language to the period between the development of the wagon, mid-fourth millennium BC, and the development of spoked wheels, c. 2,000 BC. This would give us a chronological anchor point for migration that coincides well with the date determined by genetic analysis.

A serious problem remains disregarded in the postulated scenario of Yamnaya culture as the starting point of the Indo-European language expansion. Various terms from the semantic fields of farming and ploughing as well as settledness are also among the words that were already present in the Indo-European proto-language.⁷³ The nomadic, pastoral way of life of Yamnaya culture is however in clear contrast to this linguistic evidence. From a linguistic point of view we would not see this steppe culture as a nucleus of the Indo-European language family. And finally, it must also here be emphasized that genetics has provided an important proof of migration processes in the third millennium BC. These have to be considered in view of the recent controversies. Nevertheless, it cannot ultimately support several of the additional interpretations.

68 Haak *et al.*, Massive Migration from the Steppe, Supplementary Information 3, 31.

69 E. g. Anthony, *The Horse, the Wheel, and Language*.

70 Haak *et al.*, Massive Migration from the Steppe, Supplementary Information 11.

71 See e. g. Hettrich, Expansion des Indogermanischen. – I thank Heinrich Hettrich and Sabine Ziegler warmly for access to the unpublished book manuscript.

72 Balanovsky *et al.*, Genetics of Indo-European Populations, 24; Gippert, Sprachwandel und Rekonstruktion.

73 For an overview see Hettrich, Expansion des Indogermanischen, 53-54.

What remains?

It is obvious that genetics provides important results and impulses, and opens up entirely new perspectives for the historical sciences. Kristian Kristiansen sees archaeology here on the threshold of the third scientific revolution after its establishment as an independent scientific discipline and the development of the radiocarbon method.⁷⁴ But we are only at the beginning here. Interdisciplinary cooperation between the sciences involved has yet to become attuned. Serious mistakes in the selection of samples have been made by genetics,⁷⁵ and the quality of cooperation has often been criticized, with archaeology as a subordinate partner.⁷⁶ That is all grist to the mill of the notorious sceptics among archaeologists. However, the strength of genetic analysis is highly visible. It offers – under certain conditions – methodologically sound evidence that people have migrated. The scientific approach also provides a test instrument as to what extent migrations are manifest in the material culture, and thus make an important contribution to basic archaeological research. The opening of archaeology to genetics is, therefore, not a question of ›if‹, but rather of ›how‹. It is not desirable that one side only supplies the samples, the other only the data. The entire discussion process must be a joint one. On this process both sides have to come to an agreement. Robert Hedges stressed that scientific data are free from cultural and social assumptions; in principle, he says, they are objective.⁷⁷ This is, in my opinion, not really the case. In the various case studies shown here, it became obvious that the genetic data are, for our research questions, in need of interpretation, and that interpretation is laden with a series of cultural and social assumptions. The scientific methods provide data that only make a statement about the genetic code or isotopic compositions in skeletal material. Human behavior is not their subject of analysis. Scientific results alone provide no historical knowledge, but have to be interpreted within the context of cultural studies. The disciplines involved must agree on the rationality of data and the logic of their interpretation. Future archaeological migration research will only develop further in conjunction with the natural sciences; but the explanations that have to be given lie mainly in the field of the humanities.

74 Kristiansen, *Towards a New Paradigm?*

75 See Bánffy *et al.*, ›Early Neolithic‹ Graves of the Carpathian Basin.

76 Lidén and Eriksson, *Archaeology vs. Archaeological Science*, 13-14; Egorova, *DNA Evidence?*

77 Hedges, *Anglo-Saxon Migration and the Molecular Evidence*, 80.

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Mapping European Population Movement through Genomic Research

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This article reviews scientific publications that have attempted to use genetic and genomic data in order to investigate European migrations between the fourth and ninth centuries. It considers early single-locus studies that used mtDNA and y-chromosome data. These studies were successful in formulating hypotheses concerning migration and heterogeneity, primarily between the Continent and the British Isles and Iceland, but could only examine a small portion of the entire genetic inheritance. The article continues with a presentation of more recent genome-wide studies. In particular, it evaluates the problems of using modern genomic data to understand past migratory processes, arguing that modern DNA is a problematic source for understanding population histories of the past fifteen hundred years and urges the sequencing and analysis of ancient DNA. It also presents some of the problems of research teams that did not include archaeologists and historians as integral participants in the planning, collection, and evaluation of data. It concludes with a brief outline of the authors' current project that examines migration between Pannonia and Italy in the sixth century.

Keywords: genomics; migration; ancient DNA; population genetics; Langobards.

In 2008 Novembre *et al.* published an extraordinary map of the genetic diversity of Europe in the journal *Nature*.¹ Utilizing data from the Population Reference Sample (POPRES) project, the authors examined 1,387 European individuals genotyped at ca. 500,000 single-nucleotide polymorphisms (SNPs) from across the genome. They then used principal components analysis (PCA) to summarize the observed genetic variation. Though levels of genetic variation amongst Europeans are generally very low, when plotting the two main components explaining most variation in the data on a simple xy-axis, it becomes immediately apparent that the result bears a remarkable similarity to a geographic map of Europe, even though knowledge of the geographic origins of the samples was not included in the original PCA. The continental regions of Europe are clearly visible, as are the British Isles and the Iberian and Italian peninsulas.

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1 Novembre *et al.*, Genes Mirror Geography within Europe.

Novembre *et al.* concluded that »we find a close correspondence between genetic and geographic distances; indeed, a geographical map of Europe arises naturally as an efficient two-dimensional summary of genetic variation in Europeans.«² One might trivialize these conclusions as stating simply that people have sex with people who are geographically proximate to them (in population genetics parlance this pattern would be summarized as »isolation-by-distance«). However, at a more serious level, it suggests that the population of Europe, while containing meaningful and recognizable differences, has been largely static: while some individuals in the study appear »out of place« (for example, the one Slovakian individual appears within the »southern Italian« cluster), one sees no evidence of major population movements, isolated populations, migrations, or other abnormalities that might put one population genetically closer to another, more geographically distant population. One does not observe, for example, a closer relationship between South and North Slavs than between North Slavs and North Germans and South Slavs and Italians or Hungarians. The latter, while speaking a language that is clearly an isolate, have a genetic profile that fits exactly where it should between Slavic, Germanic, and Romance speakers.

What are the implications of Novembre *et al.*'s research for understanding the history of Europe's population across centuries and even millennia? First, we need to account for certain limitations of the underlying data: since the individuals are identified only by nationality and language, it is not possible to know if a German was from Passau or Hamburg, or if an Italian was from Alto Adige or Naples, and thus the geographical coordinates of the individuals lack resolution. Second, this is a database collected largely from people who happened to pass through clinics in London or Lausanne and who agreed to be genotyped. Thus it is unlikely to be representative of local populations, and particularly from regions of Europe from which few individuals travel to major cities.

Nevertheless, such a map poses a fundamental challenge to the history of European demographics. We know that since first being colonized by Paleolithic hunter-gatherers around 40,000 years ago, Europe underwent various periods of major population movement and replacement during the Neolithic and Bronze Age. Recent paleogenomic studies have demonstrated that these prehistorical events left major signatures of admixture in modern European genomes, with Lazaridis *et al.* identifying the contribution of at least three ancestral populations that entered the continent at slightly differing times and that formed the basis of contemporary European genetic variation.³

Yet, nowhere in Novembre *et al.*'s map can one find clear evidence of the migrations, the population exchanges, or the diffusions of more recent centuries, particularly those of the so-called »migration age« (fourth to ninth centuries of the Common Era) that we are accustomed to encountering in our historical texts as well as in our archaeological work.

However, it is important to recognize that this map represents only one way of summarizing a particular type of modern genomic data, and to appreciate that signals of more recent demographic events involve migrations amongst populations that are genetically quite similar, since even northwestern and southeastern Europeans demonstrate only very subtle

2 Novembre *et al.*, *Genes Mirror Geography within Europe*, 98.

3 Lazaridis *et al.*, *Ancient Human Genomes*.

genetic differences. Such recent events would be expected to leave very small genomic signatures in modern genomes than the prehistorical events described above, which involved mixing between populations that had previously been separated by tens of thousands of years and thus developed substantial genomic differentiation. Therefore, more sophisticated analyses would be required to make inferences for more recent periods in European history using modern genetic data.

Some scholars believe that such analyses are possible, and a number of intriguing studies using modern genetic data attempt to clarify the impact of these historically attested population movements. The most intensively studied events have focused on the Anglo Saxon migrations and later Danish invasions and migrations into the British Isles at the end of Antiquity and in the early Middle Ages. Only recently have geneticists begun to investigate continental migration within the last 2,000 years.

The pioneering studies of this type concentrated on the non-recombinant portion of the human genome, that is, mitochondrial DNA inherited intact from mother to daughter, and that portion of the Y-chromosome passed without recombination from father to son. Today the results of these studies, relying as they did on single loci, are seen as too limited to be more than suggestive hypotheses. Nevertheless they raised issues that more advanced genomic studies are still addressing. A study by Michael Weale *et al.* investigating the likelihood of mass migration from the Continent to Britain at the end of Antiquity examined microsatellites in Y-chromosomes from 313 males in central England and Wales and 94 from Norway and Friesland.⁴ The results showed little difference in haplotype frequencies within Central England and no significant differences between Friesland and Central England while finding highly significant differences between the Welsh and English sites. What models of population migration might explain these findings? Assuming complete genetic identity at the time of the Neolithic and no background migration, the results can be explained by a mass migration from the continent that replaced between 65% to 100% of the Y-chromosomes in the Central English gene pool but none in Wales. If one assumes a background migration of 0.1% (still a very high estimate) plus a one-time mass migration, the mass migration contribution widens from 50% to 100%. In a follow-up study, some of the same scientists, joined by the archaeologist Heinrich Härke, estimated that if a mass migration ca. 1,500 YBP alone was invoked to explain the modern English gene pool, this would have had to be on the order of around 500,000 men. This number is entirely unrealistic given archaeological evidence as well as what we know of early medieval demographics.⁵ As an alternative explanation, they ran computer simulations postulating different original sizes of migrant and indigenous populations, but assigning a reproductive advantage to the migrants as the new conquerors of Eastern and Central Britain during 15 generations, roughly the period during which Anglo-Saxon laws gave a higher value to Saxons than to indigenous Britons. Their conclusions were that with an initial migrant population of only 10% and a selective reproductive advantage of 1.5, the socially and economically advantaged Saxons could have reached a level of 50% of the Y-chromosome gene pool within 15 generations.

4 Weale *et al.*, Y Chromosome Evidence for Anglo-Saxon Mass Migration.

5 Thomas *et al.*, Evidence of an Apartheid-like Social Structure.

A somewhat contradictory conclusion was reached by Cristian Capelli *et al.*, who compared 1,722 Y-chromosomes from 25 small British urban areas with Danish, Norwegian, German, and Irish data.⁶ With this different sampling approach, the team found that Southern England, the region presumably most heavily occupied by Anglo Saxon migrants, showed relatively little non-indigenous y-chromosomal influence. The most significant continental contribution to the Y-chromosomal profile of Great Britain in their study seems to have been that of the Danes in the north.

The models selected in the above-discussed studies derived from modern demographic studies and to some extent from estimations of numbers of migrants based on archaeology. Geneticists in Ireland took a quite different approach when attempting to estimate the impact of Scandinavian Y-chromosome DNA in the contemporary Irish population. McEvoy *et al.* investigated this question by adopting another model: surnames.⁷ The research team examined Y-chromosome diversity within a cohort of 47 Irish men bearing 26 surnames of putative Norse origin selected from geographic areas in which the Norse were known to have settled in the ninth and tenth centuries. The results were striking. On the one hand, while individuals bearing surnames such as Doyle had Y-chromosome types so different from each other that one must postulate multiple founders; others such as Arthur, Hanrik, and Gohery each bore types that were identical, suggesting a single origin for the individuals who possessed these surnames. On the other hand, no correlation was found between the Irish Y-chromosomes and the theoretical Scandinavian paternal population. Tests indicated a roughly 90 % plus Irish contribution.

In Great Britain, surnames do not begin until several centuries after their appearance in Ireland and well after the end of the Viking presence in England. Nevertheless a similar study was undertaken for Wirral and West Lancashire, regions in Northwest England that, according to written evidence, were heavily occupied by Scandinavian settlers.⁸ The study used two samples: a »modern« sample based simply on two generations of residence in the area and a »medieval« sample of individuals who not only had male ancestors who had resided in the regions for two generations but carried surnames present in the region prior to 1572. Interestingly the medieval sample was much more similar to modern Scandinavians, and consistent with the written evidence.

The differing results of these two studies raise questions about the nature of Viking conquest and settlement in the British Isles, but also about the approaches to elucidating the genetic evidence of these populations. Did Norse settlement in Ireland follow a different pattern from that in Great Britain, or were the Norse expelled from Ireland, as written sources suggest, in 902? Or could it be that the samples, analyses, and models used in one or another of these studies inadvertently provided data inadequate to judge the impact of Norse settlements in the two regions? The latter possibility makes one want to find a more direct way of approaching and analyzing the genetic impact of early medieval migrations.

The tentative conclusions of all of these pioneering studies are certainly plausible, but one can see how much depends on the appropriate selection of samples, the reliance on necessarily simplified if not simplistic models, assumed rates of background migration, and even

6 Capelli *et al.*, Y Chromosome Census of the British Isles.

7 McEvoy *et al.*, Scale and Nature of Viking Settlement.

8 Bowden *et al.*, Excavating Past Population Structures.

assumptions from archaeology and textual research that themselves are extraneous sources of model-building. Adjustments in any of these can result in quite different results. A more fundamental problem lies in the focus on a single locus, either mtDNA or the Y-chromosome, to establish population history. Unfortunately, a single locus provides only a minuscule portion of an individual's ancestry: every individual has two parents, four grandparents, eight great-grandparents, sixteen great-great grandparents, etc. Tracing one single line of descent across fifteen hundred years actually provides very little information about the genetic diversity of ancestral populations and unintentionally reinforces a tendency to essentialize complex hybrid populations into simple categories. In recent years, technical advances in SNP microarrays and whole genome sequencing has made it possible to move beyond single-locus studies and to look across the entire genome.

Building on some of this early single-locus research a recent study examined genome-wide SNP data from ca. 2,000 individuals from rural areas across the British Isles.⁹ Much like the results of Novembre *et al.*, geographic location dominates how genetic variation is apportioned, consistent with isolation-by-distance. However, incidence of above-average levels of differentiation via genetic clusters of individuals are observed, for example between Orkney, Wales and everywhere else. Even finer delineation of geographical regions is observed as one looks at increasing hierarchical levels of clustering. Mimicking the early single-locus studies by comparing modern European individuals, they associated these clusters with certain historical migrations, asserting »clear signals of some of the known historical migrations and settlements, including the Saxons and Norse Vikings«¹⁰ (via northern German/Danish and Norwegian populations respectively). They also estimated that »Saxon ancestry in C/S [Central/Southern] England as very likely to be under 50%, and most likely in the range 10%-40%.« However, they also acknowledged that »we must use modern-day groupings, in Europe and the UK, as surrogates for the sources and results of major migration events,«¹¹ identifying the major weakness of their study despite the use of highly sophisticated analytical methods.

Despite certain weaknesses, islands such as the UK and Ireland, being more isolated from other populations, represent somewhat unique opportunities to identify migrational input from an outside source via genetic data. As a consequence, relatively few studies have attempted to use modern genome-wide data to assess early medieval migration within the Continent. Ralph and Coop reanalyzed the POPRES data from Novembre *et al.* to look for specific chromosomal regions shared between pairs of individuals from the same ancestor in the past (known as tracts of identity-by-descent or IBD, not to be confused with isolation-by-distance)¹². They found that while in general pairs of individuals from the same location shared larger IBD tracts (consistent with the interpretation of Novembre *et al.* of isolation-by-distance), almost all European individuals, even when separated by large geographic distances (> 2 km), shared hundreds of ancestors within the last 3,000 years.

One of the more interesting patterns was that individuals from across eastern Europe shared a significantly higher number of IBD tracts than expected, which they determined was consistent with increased shared ancestry of a population from 1,000-2,000 years ago.

9 Leslie *et al.*, Fine-scale Genetic Structure.

10 Leslie *et al.*, Fine-scale Genetic Structure, 313.

11 Leslie *et al.*, Fine-scale Genetic Structure, 313.

12 Ralph and Coop, Geography of Recent Genetic Ancestry.

The authors speculated that this may be the result of the expansion of Slavs during the migration period, and also associated the Huns in this movement because of non-Slavic modern populations in Hungary and Romania also contributing to this signal. However, they noted that »additional work and methods would be needed to verify this hypothesis.« They also observed a lower rate of such shared ancestry from this point in time in France, Italy and the Iberian peninsula, interpreting this as possible evidence that »Germanic migrations/invasions« involved smaller amounts of population replacement.

Another study on European genome-wide data by Busby *et al.* identified substantial evidence of widespread admixture in Europe dating towards the end of the first millennium involving a population that they claim acts as a Slavic source (modern Lithuanians);¹³ they linked these events with the *Völkerwanderung* (a concept, incidentally, now increasingly discarded by historians). While the robustness of this precise conclusion is questionable, it does appear to support the results of Ralph and Coop that this general period of time may be important with regard to the structuring of modern European genetic diversity.

However, while these studies offer promising directions of research, they must necessarily assume that the living subjects from whom DNA is collected are direct descendants of the populations whose movements, dispersal, or interactions they wish to study. Can we be so sure that if all four grandparents came from the same village, that their ancestors had been in that village since time immemorial, or at least since the Danes, Anglo-Saxons, Huns, or Slavs arrived? Over centuries and millennia, populations do not necessarily remain stable. Subsequent internal migrations, the introduction of new genetic material through intermarriage with other communities, the forced resettlement of slaves or dependent labor, all have the potential to change the genetic profile of a population in a very dynamic manner that cannot easily be accounted for by population genetic models.

Perhaps even more significant an obstacle to working backward from modern DNA is the problem that the modern population will represent only a portion of the historical population, that portion which for whatever reason was successful in transmitting its genetic data to the present. For presentist-minded scientists, who naturally want to understand the genetic makeup of contemporary European populations, this is unproblematic. However, it poses a serious problem for historians who want to understand not just the present but rather the alterity of the past. Thus, modern DNA is likely to represent only a portion of the genetic diversity of past populations. It is, in essence, a way to study the winners, and ignores the losers in genetic history, regardless of how important they may have been in changing history.

A few studies have highlighted how quickly genetic profiles can change because of demographic effects, underlining the lack of inferential power when relying only on modern DNA analysis for historical research. Helgason *et al.* have performed extensive research on both modern and ancient DNA from Iceland.¹⁴ Comparing Icelanders with Norwegians on the one hand, and Irish and Scots on the other, they found that roughly 75% of founding Icelandic males were of Scandinavian origin and 25% of Irish or Scots, while the majority of female lineages had Gaelic origins and only about 37% Norse. When they compared ancient DNA extracted from Viking-age burials with that of the modern population however, they found that more than 50

13 Busby *et al.*, Role of Recent Admixture.

14 Helgason *et al.*, Estimating Scandinavian and Gaelic Ancestry; Helgason *et al.*, MtDNA and the Islands of the North Atlantic; Helgason *et al.*, Sequences From First Settlers.

% of the original genetic diversity in the founding medieval population was not represented in the modern Icelandic population. Genetic drift appears to have had an enormous influence on the genetic profile of modern Iceland, and thus understanding the differential contributions of Y-chromosomal and mtDNA in the migratory population needs to take into account not only contemporary populations but, when possible, ancient DNA as well.

More recently, a preliminary study by our research team led by Stephanie Vai and Silvia Ghirotto looked at the mtDNA from sixth century cemeteries in the Piedmont and compared it with contemporary samples from the same region.¹⁵ We found strong evidence for discontinuity with regard to matrilineal genetic diversity between the early Middle Ages and these present populations in all but one case. This, along with the studies of Iceland described above, suggests that 1,500 years of history do matter with regard to genetic diversity. Thus, while modern genetic research is significant for a spectrum of issues involving health and possibly history, assumptions about the relationship between present and past populations must be tested against ancient DNA collected from the individuals we are actually attempting to study, rather than relying automatically on modern proxies.

This is now beginning to be realized not just at the mtDNA and Y-chromosome levels, but also by examining whole genome data from ancient individuals, which should provide considerably more power to make inferences. (As described above, such data has revolutionized our understanding of prehistorical Eurasia.) Schiffels *et al.* were recently able to sequence the whole genomes from 10 individuals in Cambridge dating to the late Iron Age (n=3) as well as the early (n=4) and middle (n=3) Anglo-Saxon periods.¹⁶ By developing a novel method that examines rare shared alleles between ancient and modern samples, they demonstrated that while middle Anglo-Saxons were genetically close to modern Dutch and Danish populations, the older Iron Age individuals showed a much greater diversity of ancestors from across Northern Europe. The early Anglo-Saxon samples, despite demonstrating similar burial positions and grave goods, showed intriguing evidence of heterogeneous ancestry, with one individual being similar to the Iron Age samples, one being a likely recent immigrant, and two individuals probably being of mixed ancestry. Interestingly, in general modern British individuals appear to share more ancestry with the older Iron Age samples, with the greatest Anglo-Saxon similarity occurring in modern eastern England. While certainly more work is needed, it is clear that the patterns of migration and admixture over the time span considered by these ancient genomes were very complex, with the authors stating that their data »show that early medieval migration took a variety of forms and that these migrants integrated with the incumbent population in different ways«¹⁷. Such a resolution is only possible with ancient genomic (paleogenomic) data.

While the Schiffels *et al.* study is somewhat small in scale with regards to size and breadth of sampling, clearly, there are no longer major technical hurdles that would prevent the characterization of hundreds to thousands of paleogenomes from the historical era. We are already at this point with prehistorical specimens, which are generally harder to acquire and have less endogenous DNA.¹⁸ Thus, it should be possible to amass similar data for more

15 Vai *et al.*, Genealogical Relationships.

16 Schiffels *et al.*, Iron Age and Anglo-Saxon Genomes.

17 Schiffels *et al.*, Iron Age and Anglo-Saxon Genomes, 7.

18 Allentoft *et al.*, Population Genomics of Bronze Age Eurasia; Fu *et al.*, Genetic History of Ice Age Europe; Mathieson *et al.*, Genome-wide Patterns of Selection.

recent periods. Using such data, we then could ask what a genetic map of Europe would look like if, instead of relying on twenty-first century European genomes as in Novembre *et al.*, it examined genomes from people who actually lived during the so-called migration age. Better yet, what if we could produce a series of such maps at regular intervals across the centuries such that we could see changes in how genetic diversity is distributed across the continent? Might we then see, rather than John Novembre's »isolation-by-distance«, evidence of recent migrations resulting in geographically separate populations with close genetic profiles? Thinking still further, what would an ancient genomic map of all of Eurasia look like at discrete moments in time? Would we see the effects of the great Steppe empires of the Xiongnu, Huns, and Mongols? Would we see the presence of whole populations displaced as the result of wars or political decisions? Would men and women have different migration histories? With genome-wide ancient DNA we should be able to not only identify such events and processes, but quantify them, estimating parameters such as sizes of ancestral populations and the magnitude of population movements.

These are the kinds of questions that our research team is attempting to answer on a very preliminary and modest scale by doing deep genetic analysis of skeletal remains of over 1,200 sixth and early seventh-century individuals from what are generally seen as Langobard cemeteries in the former Pannonia (Austria, Hungary, Moravia) and Italy from the sixth century.¹⁹

Our decision to concentrate on Langobards had nothing to do with an intrinsic interest in Langobards, Pannonia, or Italy as such. It was driven by our desire to find a population with abundant archaeological and historical evidence that could be used to construct models of population histories and that could then be compared with those derived from population genetics. Of all of the various peoples who were reputed to have migrated into the Roman Empire at the end of Antiquity, the Langobards are the latest and the best documented. Accounts by Marius of Avenches,²⁰ Gregory of Tours,²¹ and especially Paul the Deacon,²² describe the early history of the Langobards from their appearance in Pannonia ca. 500 until their conquest of Italy in the 560s. Whether or not these texts are accurate, they provide what might be called a model of Langobard migration that can then be compared with other types of evidence.²³

Archaeologists studying sixth-century cemeteries throughout the region classify as Langobard hundreds of sites, based on a mixture of archaeological and historical sources.²⁴ Moreover, they attribute the appearance in Northern Italy of burial forms and grave goods similar to those from the regions of Pannonia to the arrival of Langobards. Our project remains agnostic concerning such identifications, based either on textual or archaeological evidence.

19 Geary, *Rethinking Barbarian Invasions*.

20 Marius of Avenches, *Chronica*, ed. Mommsen, 238.

21 Gregory of Tours, *Historiarum Libri X*, IV, 41, ed. Krusch and Levison, 174.

22 Paul the Deacon, *Historia Langobardorum*, II, 7, ed. Waitz, 78.

23 On Langobard history in general see Ausenda *et al.* (eds.), *Langobards before the Frankish Conquest*; Pohl and Erhart (eds.), *Langobarden – Herrschaft und Identität*.

24 On Langobard archaeology: Landschaftsverband Rheinland and Rheinisches Landesmuseum Bonn, *Langobarden*; Tejral *et al.* (eds.), *Langobardische Gräberfelder in Mähren*; Bóna and Horváth, *Langobardische Gräberfelder in West-Ungarn*; Pejrani Baricco (ed.), *Presenze Langobarde*; Bemmman and Schmauder (eds.), *Kulturwandel in Mitteleuropa*.

We are not claiming that any of our samples are »Langobards.« After all this term could be cultural, political, or ethnic. Clearly people both in Pannonia and in Italy would have identified themselves as Langobards, but we cannot be certain that all of the individuals buried in this way would have done so, or that they would have identified themselves as Langobards for all purposes and on all occasions. A legal identity could be quite different from a political adhesion, a linguistic tradition, or a cultural practice. However, these cultural patterns present another model that can be compared with the historical record and the genetic record to construct a comprehensive image of the population of the region.

Again, the focus of our study is not one of Langobard identity: with apologies to the numerous, excellent scholars studying early medieval ethnic identities, our project offers no answers to their debate. It does, however, have the potential to examine whether, in the course of the sixth century, closely interrelated communities existed in modern Hungary and the surrounding region who differed in their genetic profile from their neighbors, thus suggesting recent arrival or long-established populations. It also can determine whether populations south of the Alps that followed the same cultural norms in burying their dead were more closely related to those practicing similar traditions in the North and East, or whether, despite a unique cultural identity manifested in their burial customs, they sprang from the same stock as their Italian neighbors. Our project offers, in other words, a different way of conceptualizing space, this time in terms of genetic affinities and that can be compared with other spaces such as those constructed by material culture, language, law, and politics.

This work is necessarily interdisciplinary, something notably lacking in the majority of genetic studies. The Ralph and Coop study, while highly rigorous at the level of the population genetic analysis, included no historians or archaeologists, and the only historical literature cited, presumably to »identify« the Hunnic contribution to European population, was a general history of Europe,²⁵ a survey of Slavic history,²⁶ and two articles in the *New Cambridge Medieval History*.²⁷ The Busby *et al.* study also included no historians or archaeologists on its team, and the only historical literature cited was a Penguin *History of the World*, Peter Heather's survey of the Early Middle Ages, and a survey of Muslims in Italy.²⁸ Unlike these studies, designed and executed exclusively by geneticists who then look through a few general historical handbooks to try to find stories that might explain their data, historians and archaeologists are integrated from the start in our project. Their role is both to develop the historical questions that we seek to answer and also to identify and understand the nature of the specimens that we are analyzing. However, just as geneticists cannot execute the project in isolation, historians cannot simply ask geneticists to confirm the stories they find in their texts. And certainly archaeologists must develop independent typologies and chronologies for their data and not rely on either textual sources or genetics to identify and date material culture ensembles. We believe then that such research must be from its inception an intimate collaboration among these disciplines; together, our team has developed a series of historical questions that we hope genetic research might answer.

25 Davies, *Europe*.

26 Barford, *Early Slavs*.

27 Halsall, *Barbarian Invasions*; Kobyliński, *Slavs*.

28 Heather, *Empires and Barbarians*; Metcalfe, *Muslims of Medieval Italy*; Roberts, *New Penguin History of the World*.

Essentially, we want to understand the social structure of the militarized communities within and without the Empire in the sixth century. This means determining the genetic relationships that existed among individuals buried in what have been termed Langobard and non-Langobard cemeteries. It also requires investigating the biological relationships between individuals buried in neighboring »Langobard« and non-»Langobard« cemeteries. Do these communities show any significant genetic structure or are they simply part of the same biological community? If there is some differentiation and we find evidence of gene-flow between groups, is there evidence that this differentiation is sex-biased? Do all of these characteristics differ between presumed Langobard communities in Pannonia and those in Italy? Are the populations that are buried in so-called Langobard cemeteries primarily a portion of the indigenous population that took on the cultural, social, and behavioral models of the new powers in Italy? And finally, is there evidence of genetic continuity between pre-(Pannonia) and post-(Italy) migration »Langobard« cemeteries?

These are large questions, and it will take many years and millions of euros to properly sequence skeletal remains from the over 1,200 graves in our sample. We must then analyze our data using statistical methodologies developed by population geneticists, and then confront the results with those developed from the analysis of stable isotopes, historical evidence, and cultural archaeology. Our project, although under way for four years, is still at the beginning. However we hope, through close collaboration between disciplines and mutual respect for the contributions of historians, geneticists, and archaeologists, to begin to uncover the demographic history of the migration period and in so doing contribute to a map similar to that produced by Novembre *et al.*, but of Europe's population a millennium and a half ago.

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Geneticizing Bantu: Historical Insight or Historical Trilemma?

Manfred K. H. Eggert*

This paper is devoted to the much debated problem of the expansion of Bantu languages over most of the southern half of Africa. Apart from being a major linguistic phenomenon it is a culture-historical and, more specifically, an archaeological topic as well. The reasoning focuses on three aspects: (1) Bantu languages; (2) rainforest archaeology; and (3) Bantu genetics. While the Bantu language dispersal and sub-Saharan archaeology are in some sense historically linked, Bantu genetics is a kind of ›newcomer‹ to the field. As the title indicates, the impact of molecular anthropology on finding an answer to the Bantu expansion – here epitomized by the term ›geneticizing Bantu‹ – claims some importance in this presentation. It has to be stressed, however, that human genetics is by no means the principal topic here. Rather, the emphasis lies on the interplay between Bantu linguistics, archaeology and Bantu genetics. Consequently, it is the combination of all three which is at stake. As the subtitle puts it: we may well ask whether this trinity leads jointly to historical insight or hides a historical trilemma. The paper tries to enumerate some basic points of each field. Likewise, it aims to assess each field's strengths and weaknesses in order to arrive at an answer to the subtitle's question.

Keywords: historical linguistics; prehistoric archaeology; molecular genetics; sub-Saharan Africa; Central African rainforest; Bantu languages; rainforest archaeology; Bantu genetics; Münchhausen trilemma.

Introduction

The problem at the heart of this contribution involves three disciplines, that is: Bantu linguistics as a field of historical linguistics, sub-Saharan archaeology as a field of prehistoric archaeology, and Bantu genetics as a specialty of molecular genetics. Each of these subfields is highly complex and consequently the domain of rather specialized cultural and molecular anthropologists. Generally, as, for instance, Peter Robertshaw has stressed,¹ the mutual understanding of each other's units of analysis, methodologies and theoretical underpinnings is rare. Hence, regarding the Bantu languages, one wonders about the potential for solving their dispersal from some homeland in northwestern Central Africa to over most of the southern half of Africa. For almost six decades, linguists and archaeologists have been

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1 Robertshaw, *African Archaeology*, 100-101.

engaged in resolving this enigma.² In recent years, it has especially been linguists in cooperation with geneticists and other scholars such as archaeobotanists, geographers and (although rarely so) archaeologists who have been active in bridging the interpretative gap created by different data and different procedures.³ Unfortunately, however, such cooperations should not, *a priori*, be considered well-integrated interdisciplinary endeavors.⁴

This paper aims at a relatively high level of abstraction. Rather than becoming immersed here in summarizing and analyzing ongoing work in detail – which would not be possible considering the complexity of the arguments and the space allotted – only a very brief general summary of each field is intended.⁵ The main focus of the following concerns the innate potential of each field to generate a solution to the so-called »Bantu Expansion« as a major historical phenomenon in the southern half of Africa. Thus, the question is whether or not the current state of the art gives reason to be optimistic in this regard. The contribution is organized along three lines of reasoning: (1) Bantu languages, (2) rainforest archaeology and (3) Bantu genetics. For a start, some rather general aspects of the historical reconstruction of Bantu languages and related problems will be discussed. Then the argument will switch to the second line, namely, equatorial rainforest archaeology. The archaeology of this habitat is of some importance in the context of the expansion of Bantu languages. This is followed by the third line of reasoning, the relevance of molecular genetics in the context of linguistics and archaeology.⁶ In conclusion, an attempt will be made to bind together the different strands of the argument and relate them to the heading of this paper.

However, to allow for an understanding of the perhaps somewhat enigmatic title of this paper, the historic personality of the Baron von Münchhausen⁷ needs to be introduced here. Later, von Münchhausen, or rather one of his tall tales, will help to integrate the reasoning of this paper.

Hieronymus Carl Friedrich Freiherr von Münchhausen

Hieronymus Carl Friedrich Freiherr von Münchhausen was born in 1720 at his father's estate in Bodenwerder in the Duchy of Brunswick-Lüneburg (now within the state of Lower Saxony in Germany). He served as an officer in the Russian cavalry and participated in the Russian-Turkish war. After having retired to his estate in Bodenwerder he died there in 1797. In his later years, he became a legendary figure in aristocratic circles of the region, since he used to entertain his guests with extraordinary tall tales of his travels and adventures during and

2 See Eggert, Bantu Problem and African Archaeology.

3 See, *e.g.*, Bostoen *et al.*, Middle to Late Holocene Paleoclimatic Change; de Filippo *et al.*, Bringing Together Linguistic and Genetic Evidence; Grollemund *et al.*, Bantu Expansion; Kahlheber *et al.*, Early Plant Cultivation; Li *et al.*, Genetic Variation; Pakendorf *et al.*, Molecular Perspectives on the Bantu Expansion.

4 As an example might serve Bostoen *et al.*, Middle to Late Holocene Paleoclimatic Change; see Eggert, Comment on Bostoen *et al.*

5 For an in-depth consideration of the underlying difficulties the reader is referred to Eggert, Bantu und Indogermanen.

6 The verb »to geneticize« which I use in this context and, more specifically, in the main title of this paper, is certainly uncommon; it was invented here for the sake of my reasoning.

7 In the English-speaking world he is known as »Baron Munchausen«; however, I am using the original German version of von Münchhausen's patronym.

after his military service. Münchhausen never wrote down any of these stories, but some of them were anonymously put into literary form in a series of newspaper articles in German. Later published in English, they were soon translated into other languages and became a great success. From the very beginning, the various editions and re-editions transformed Münchhausen into a fabulous fictional character whose glamor and bravado made him much more interesting than the real-life baron had ever been. However, in Germany the two barons remained and remain largely intertwined as attested by the nickname *Lügenbaron* (literally ›Baron of Lies‹) given to the Bodenwerder Münchhausen. Here is one of the baron's tall tales:

»At another time I wanted to jump with my horse over a morass which did not appear as wide to me as it actually was when I was in the middle of the jump. Hovering in the air I thus turned back to from where I started so as to take a longer run-up. Nonetheless, I again jumped too short and found myself up to my neck in the morass near its other edge. Here I surely would have perished were it not for the strength of my own arm such that I pulled myself out on my own pigtail, together with my horse, which I took firmly between my knees.«⁸

This is what one might call a three-dimensional tale in that there are three clearly identifiable, though improbable, contentions: first, Münchhausen turns his horse in the middle of the jump, second, he pulls himself out of the morass on his own pigtail, and third, in taking the horse firmly between his knees he rescues it as well.⁹ In fact, the whole setting implies what the German sociologist and philosopher Hans Albert has called this the *Münchhausen-Trilemma*.¹⁰ As said, I will come back to that later.

Bantu Languages

Since the Bantu languages are the focus of this paper, some basic points need to be enumerated. The study of the ancestry of languages and thus their internal and spatial change over time falls within the field of historical linguistics. Its foundation goes back to the nineteenth century, when in Germany, the Indo-European languages were studied by what came to be known as the »comparative method«. In the 1850s, the German linguist Wilhelm Heinrich Immanuel Bleek (1827–1875), who resided in the Cape Colony, discovered the genetic relationships of a number of languages spoken in the southern half of Africa. He termed them »Bantu«, after the Zulu word *aba-ntu* which means »men«. Today, the number of Bantu languages is estimated to be between about 300 and 680,¹¹ with a tendency to settle for about 500.¹² Bantuists agree that the *Ursprache* of Bantu, that is proto-Bantu, originated somewhere in the borderland of what is now Nigeria and Cameroon (*Fig. 1*).¹³

8 Translated by the author from Anonymous, *Wunderbare Reisen*, 54-55.

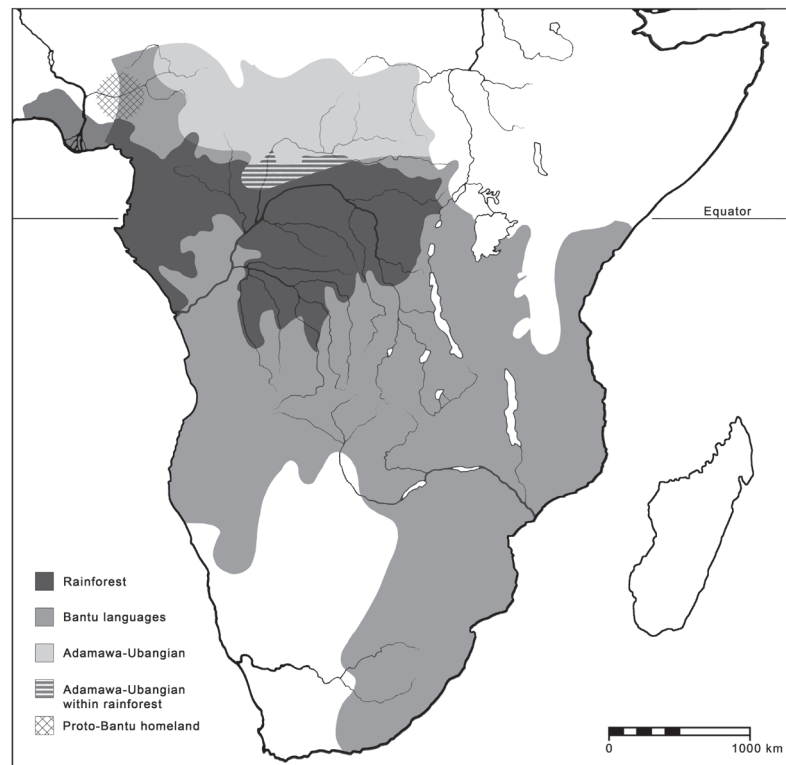
9 In both the English and the German *Wikipedia* there are several informative entries on von Münchhausen.

10 Albert, *Traktat über kritische Vernunft*, esp. 13-15.

11 See, e.g. Nurse, *Contributions of Linguistics*, 367; Nurse, *Survey Report for the Bantu Languages*. Nurse (*Contributions of Linguistics*, 367) himself estimates the number of Bantu languages »slightly more than 300«.

12 See, e.g., Bostoen *et al.*, *Middle to Late Holocene Paleoclimatic Change*, 354.

13 For the major lines of the development of Bantu linguistics and its relationship to archaeology see Eggert, *Bantu Problem and African Archaeology*.



*Fig.1: Distribution of Bantu and Adamawa-Ubangian languages in relation to the rainforest (after Eggert et al., *Pits, Graves and Grains*, 275, fig. 1)*

The most hotly debated question regarding Bantu concerns the mechanisms and routes of its dispersal over most of sub-Saharan Africa. This question represents one of the continent's greatest linguistic and cultural-historical problems. Unfortunately, from the very beginning, the debate was marred by intermingling linguistic and archaeological arguments, in a word, by circular reasoning.¹⁴ The whole problem of Bantu language origins and dispersal bears a striking resemblance to that of the Indo-European languages. In a recent paper, both were analyzed together with archaeo- or historical genetics, in considerable detail.¹⁵ Principally, language change and language dispersal have been generalized in a number of models. The main models discussed today include the so-called »migration model«, the »wave-of-advance model«, the »discontinuous spread model«, the »wave model« and the »language shift« or »dominance model«. Except for the wave model, all others opt for concrete migrations of people, although on different scales. The wave model assumes language dispersal via contact between speech communities, that is, by means of diffusion rather than migration.¹⁶ With respect to Bantu, most if not all bantuists figure its dispersal in terms of migratory movements of some kind. In recent years, Koen Bostoen in particular has been intensely working on this.¹⁷

14 See, e.g., Eggert, *Bantu Problem and African Archaeology*, 307-312.

15 Eggert, *Bantu und Indogermanen*.

16 On the modeling of language spread see Eggert, *Bantu und Indogermanen*, 14-17, and Eggert, *Bantu Problem and African Archaeology*, 317. Both are referring back to Nurse, *Contributions of Linguistics*.

17 See, e.g., Bostoen *et al.*, *Middle to Late Holocene Paleoclimatic Change*, 358-362, with figs. 2 and 3; Pakendorf *et al.*, *Molecular Perspectives on the Bantu Expansion*, 54-57, with figs. 1 and 2.

In the following, I will focus on the Central African rainforest for two reasons: (1) because of my extensive first-hand experience as an archaeologist with this ecosystem, and (2) because the rainforest represents an almost homogeneous linguistic territory. Except for some languages of the Adamawa-Ubangian language family spoken in its northern part, the forest is peopled by Bantu-speaking populations (*see Fig. 1*). From a linguistic point of view there are a number of more or less divergent hypotheses of how Bantu came to be spread throughout the forest. Since this immense biome is counted among the first territories to have been settled by Bantu speakers, it is closely linked with the initial dispersal of Bantu from its proto-Bantu homeland in northwestern Central Africa. In assessing the various hypotheses of the penetration of Bantu speakers into the tropical forest, as well as their subsequent splittings, one has to be aware of the temporal dimension of Bantu. Since Bantu languages only came to be written down in dictionaries, grammars, texts and so forth in the nineteenth century, there are no genuine linguistic sources in the narrow historical sense of the term prior to that time. That is to say, Bantu languages are not attested by authentic evidence before the nineteenth century. That is to say, that even the earliest written Bantu material is all but contemporaneous with the temporal context historical Bantu linguists tried to reconstruct. Thus, all Bantu reconstruction is based on the comparative method of historical linguistics (or some derivatives of it) developed in the nineteenth century. By contrast, a number of Indo-European languages are attested to by original texts, some of which go back to the first half of the second millennium BC.¹⁸ Also, while we are dealing with about 300 to 500 Bantu languages, Indo-European is restricted to about 140 languages, which have been intensely studied since the beginning of the nineteenth century. Today, Indo-European is considered the most exhaustively analyzed language family on a global scale.¹⁹ The important point to remember here concerns the fact that with regard to Bantu, the comparative method is not capable of furnishing any information on the absolute time depth of the reconstructions achieved by it. As just indicated, these are exclusively based on what one might call a kind of linguistic »presence«. Consequently, this is also true for all speculative efforts of linking all language detachments or splits in the rainforest and elsewhere to an absolute temporal framework.²⁰

All attempts of breathing time into Bantu linguistic data – in terms of both relative as well as absolute time – proceeds by means of what linguists call »lexicostatistics« and »glottochronology«. While the first aims at relative time, the second maintains to produce more or less precise time spans in relation to fixed points, that is, absolute time. As has been detailed elsewhere, both procedures have been intensely discussed for decades. While lexicostatistics appears more or less accepted as a means of generating rough relative datings, rare today are those who consider glottochronology a suitable technique for establishing absolute age.²¹ P. Sims-Williams, for example, speaks in this context of »the ›glottochronological‹ fallacy«. ²² As

18 Meier-Brügger, *Indogermanische Sprachwissenschaft*, 142-143, 148-149.

19 Bußmann, *Historisch-vergleichende Sprachwissenschaft*, 285-288; Meier-Brügger, *Indogermanische Sprachwissenschaft*, 133-141.

20 Eggert, *Bantu und Indogermanen*, 34, with note 116.

21 Thus, the Bantuist Schadeberg, *Historical Linguistics*, 160, states: »Historical linguistics is strong in relative chronology but has no credible means to provide absolute datings.«

22 Sims-Williams, *Genetics, Linguistics, and Prehistory*, 509.

of late, however, it is Bayesian statistics in which linguistic reconstructions of phylogenetic language trees are clad as, for instance, in the papers of both Bostoen *et al.* and Grollemund *et al.*²³ These impressive looking statistics seem to add considerable weight to the argument, but, as Roger Blench claims, behind the »glamorous graphics« lurks »just the discredited old lexicostatistics.«²⁴ The answer of Bostoen and coauthors, against whom Blench's remark was directed, shows to which degree complex statistical procedures might obscure underlying empirical data. In consequence, the question of what temporal distance might separate us from the reconstructed proto-Bantu is not solvable within historical linguistics. We therefore have to think about other means of getting at the time dimension in regard to the influx of Bantu speakers in the Central African forest and beyond. Quite naturally, as in the case of the Indo-European languages, attention focuses on archaeology. Blench remarked that it is the interplay between linguistics and archaeology that is crucial here. To him, this interplay depends on reconstructible lexical items that bear potential associations with the archaeological record.²⁵ Unfortunately, however, associations of this kind are relatively rare and usually do not have much explanatory power. Shared words – as Blench himself is fully aware of²⁶ – might as well indicate technical or social change as not have an impact on the archaeological record at all. In this contribution then, archaeology is considered as the second line of reasoning. Since its history of research has been spelled out elsewhere,²⁷ there is no point in discussing it here again. Rather, I will briefly comment on the current state of rainforest archaeology, and then move on to archaeo-genetics.

Rainforest Archaeology

Since 1977 I have been engaged in archaeological fieldwork in the Central African rainforest, which covers parts of the modern states of the Democratic Republic of the Congo (Congo-Kinshasa for short), the Republic of the Congo (Congo-Brazzaville) and Cameroon. According to current knowledge, pottery-producing groups began to penetrate into the forest at about 800 BC. Between 400 and 300 BC, early ceramics are present over a large area stretching from central Cameroon into the Inner Congo Basin.²⁸ However, although widely distributed, this ceramic evidence does not constitute a geographically interrelated net of archaeological sites which one might consider sufficiently dense. Rather, the evidence is spotty, with large gaps of archaeological *terra incognita* in between. As for shape and decoration, the pottery in question is complex and certainly not homogeneous. Nevertheless, there are some formal and decorative elements that the different ceramic groups have in common. This has led several authors to contemplate a possible relationship on the level of pottery. Others, however, use these similarities to postulate an outright historical connection between the populations which made this pottery.²⁹

23 Bostoen *et al.*, Middle to Late Holocene Paleoclimatic Change; Grollemund *et al.*, Bantu Expansion.

24 Blench, Comment, 367, an argument which the authors disapproved of: Bostoen *et al.*, Middle to Late Holocene Paleoclimatic Change, 376; see also Dimmendaal, Comment on Bostoen *et al.*, 369.

25 Blench, Language, Linguistics, and Archaeology, 53-54.

26 Blench, Language, Linguistics, and Archaeology, 54, 60.

27 Eggert, Archaeology of the Central African Rainforest, 185-186, 189-190; Eggert, Bantu und Indogermanen, 25-26.

28 Eggert, Bantu und Indogermanen, 27-28, with fig. 9; Wotzka, Records of Activity, 279-281.

29 Eggert, Bantu und Indogermanen, 25-28.

Since about the mid-1960s archaeological evidence has been used in many efforts to trace the dispersal of Bantu languages over the southern half of the African continent. As mentioned above, this led to circular reasoning within historical Bantuistics as well as African archaeology. Regarding the Central African forest it was and is tempting to link the influx of farmers and potters with the arrival of Bantu speakers. Unfortunately however, there is no genuine association between languages on the one hand and farming and making pottery on the other. As we all know, this is true for the whole realm of material culture in general. In other words, non-written languages do not leave material traces. In contrast, migrations in the sense of any larger movement of populations – regardless of which language or languages are being spoken by the migrants – can be expected to leave at least some sort of material imprint.

Thus, our argument has gone full circle: in order to lend some plausibility at all to the linkage between the migratory movement of speakers of whatever languages and the material traces of times past, we need to have a well-dated and sufficiently interconnected archaeological record at our disposal. Even then, however, the possibility that these migrants spoke a specific language remains just that: a possibility which might or might not be plausible. At any rate, the current archaeological record in the Central African rainforest is extremely spotty and consequently far from convincing so as to be taken as a reflection of a steady influx of Bantu speakers into the forest, let alone movement on a larger scale. In general, archaeology, with its material record of bygone times, is uniquely suited to provide a rather fine absolute time-scale for phenomena of the past. While, as Scott MacEachern has stressed, historical linguists and geneticists routinely make use of archaeological data and its associated radiocarbon datings,³⁰ this does not resolve the inherent difficulty in linking these fields in the first place. But he is certainly right that radiocarbon dating is based upon a fairly well-known physical process, whereas chronological estimates in both historical linguistics and archaeogenetics are dependent on linguistic and biological processes that are »not well-constrained physically«. And, he continues, since archaeological data are so often adopted beyond archaeology, it is all the more important that archaeologists understand the basis and limitations of chronologies proper to these other fields.³¹ Having thus dealt briefly with rainforest archaeology, I will now switch to the third line of my argument. It is constituted by molecular genetics or, rather, to its possible impact on the decipherment of the dispersal of Bantu.

Bantu Genetics

As archaeo-genetics in general, molecular studies of Bantu-speaking populations are increasing at a rapid pace. The latter are proceeding with a clear historical aim: they want to contribute to, if not to solve, the riddle of the dispersal of Bantu languages. Nevertheless, what Lara B. Scheinfeldt, Sameer Soi and Sarah A. Tishkoff stated in 2010 is still true: the results of studies on genetic variation in Africa and their correlation with cultural and linguistic diversity have not been sufficiently studied yet.³² Sometimes, however, geneticists seem to overestimate the historical potential of their field in their common endeavor.³³

30 MacEachern, *Holocene History*, 265.

31 MacEachern, *Holocene History*, 266.

32 Scheinfeldt *et al.*, *Working toward a Synthesis*, 8931.

33 The Scheinfeldt *et al.* paper with its pretentious title is a good example. In it, roughly three-quarters of a page are devoted to the »Bantu Expansion« (Scheinfeldt *et al.*, *Working toward a Synthesis*,) and there the authors inadvertently demonstrate their lack of knowledge of the linguistic and archaeological problems involved.

Being trained in linguistics as well as in molecular anthropology, Brigitte Pakendorf has recently discussed some important issues involved in linking up historical linguistics and molecular anthropology. She posits a coevolution of genes and languages in that both are passed on by socially interacting males and females. On the other hand, as she stresses, languages are also submitted to contact-induced change. Thus, while genes are passed on only vertically from parents to offspring, culture contact between speech communities enables languages to be influenced on a horizontal level as well.³⁴ Since it is not possible to discuss the relationship of historical Bantu linguistics to Bantu genetics here in any detail, the following will concentrate on a few aspects only.³⁵ First, there is the problem of the origin of the genetic data analyzed. Phrased differently, it is important to know according to which ethnolinguistic criteria the donor groups of the samples were defined.³⁶ From general experience it seems fair to say that these definitions, considered from a cultural anthropological and linguistic perspective, are more often than not rather vague. Even more questionable appears the genetic makeup, and thus the genetic variability, within however-defined ethnolinguistic groups, let alone the correspondence between ethnolinguistic boundaries and changes within intragroup genetic variability.³⁷ Second, we are faced with the problem of how genetic patterning is to be correlated with linguistic patterning and language change. For although genes and languages are passed on through sexual and cultural interaction, there are no genes for language. The capacity of man to principally master any language, however imperfectly, is more than sufficient proof of this point. Third, the current state of the art of molecular genetics in Bantu Africa is all but satisfying. In fact, and especially in central, southwestern and southern Africa, only a fairly restricted number of genetically studied farming groups has been examined yet.³⁸ The same applies to Bantu speakers in eastern Africa.³⁹ While being generally true for the tropical rainforest as well, this applies most notably to the Congo Basin.⁴⁰ Thus, the scarcity of genetic data is directly related to the potential for comparison with the quantity and quality of other datasets, be they linguistic or archaeological. But even if such comparisons were to be established, we would still be left with the question as to whether »patterning in one dataset has anything to do with patterning in the other,« as Scott MacEachern put it.⁴¹ Fourth and last, since the expansion of the Bantu languages over the southern half of Africa is a historical phenomenon, the historical impact of genetic data seems important. While it is one thing to agree on the immense temporal dimension inherent in genes, it is quite another to come up with genuine ancient DNA from Bantu Africa. Needless to say that due to the acidity of tropical soils, human skeletal material is, if at all, almost nonexistent beyond a very narrow temporal limit of two or three centuries at most. In contrast, despite the inbuilt time factor in genes, modern DNA is contemporary and thus the outcome of an inextricably complicated mixture of genetic and social factors. Although there

34 Pakendorf, *Historical Linguistics and Molecular Anthropology*, 627-628.

35 For a more detailed discussion see Eggert, *Bantu und Indogermanen*, 34-38.

36 Pakendorf, *Historical Linguistics and Molecular Anthropology*, 630.

37 MacEachern, *Genetics and Archaeology*, 68.

38 MacEachern, *Genetics and Archaeology*, 67-68.

39 See, e.g., Pakendorf *et al.*, *Molecular Perspectives on the Bantu Expansion*, 58, 59, 61.

40 DeFilippo *et al.*, *Bringing Together Linguistic and Genetic Evidence*, 3258, fig. 2b.

41 MacEachern, *Genetics and Archaeology*, 67.

are a number of techniques of estimating genetic distance,⁴² one wonders how far the quality and quantity of the data at hand from Bantu Africa will lead to convincing results. It may be noted in passing, that when it comes to measuring linguistic distance, Pakendorf is rather skeptical. However, her proposition of the coevolution of genes and languages is dependent on correlations between genetic and linguistic distances.⁴³ This last point is worth keeping in mind, since it implies that the coevolution of genes and languages is all but a foregone conclusion. That is to say, while coevolution is possible, its actual presence in each particular case has to be demonstrated rather than assumed. Consequently, a mismatch between genetic and linguistic data does not appear as telling as it is represented in the literature. It would be misleading to look for an explanation only in terms of language shift or intermarriage in which the married-in maintain their language.⁴⁴ Rather, it seems to be the coevolution model which is at stake here.

Finally, MacEachern in his paper on genetics and archaeology has directed attention – as has Robertshaw before him⁴⁵ as well as Pakendorf in her paper on historical linguistics and molecular anthropology – to the necessity of interdisciplinary work.⁴⁶ One could only agree, since otherwise we would be constantly faced with a situation strongly reminiscent of the intermingling of linguistic and archaeological reasoning of times past. In fact, circular reasoning seems forever looming nearby were it not for the special attention given to that danger.⁴⁷ There is a certain tendency to refer oneself to the conclusions of a paper of another discipline in the search for supporting arguments of one's own case. With regard to molecular genetics, MacEachern has termed this the »Last Paragraphs Problem«, since it is often in the concluding section of molecular papers where genetic patterns are linked to historical processes.⁴⁸ Needless to say, the same is true for historical linguistics and archaeology as well. Also, Robertshaw does not quite see how molecular genetics fits into his proposed new, potentially interdisciplinary, approaches.⁴⁹ According to him, genetic data tell us something about the biotic outcomes of past events but much less about African history as such.⁵⁰ It has to be stressed, however, that his concept of »history« is a rather rigid one, revolving, as it were, around the notions of »how« and »why«. In this, neither archaeology nor historical linguistics are any better off than molecular genetics. As far as the current situation is concerned, it is quite obvious that with regard to the Bantu problem, molecular genetics and historical linguistics have been cooperating rather intensely in recent years in publishing research papers. Under these circumstances it is all the more surprising that archaeology, as the only discipline capable of generating authentic historical evidence – that is, evidence which is part and parcel of the time it is supposed to elucidate – is not or is only rarely being cited in this context.⁵¹

42 Pakendorf, *Historical Linguistics and Molecular Anthropology*, 628.

43 Pakendorf, *Historical Linguistics and Molecular Anthropology*, 628-629.

44 But see Pakendorf, *Historical Linguistics and Molecular Anthropology*, 630.

45 Robertshaw, *African Archaeology*, 100-102.

46 MacEachern, *Genetics and Archaeology*, 69, 74; Pakendorf, *Historical Linguistics and Molecular Anthropology*, 630, 631.

47 See also Eggert, Comment on Bostoen *et al.*, 370 on this.

48 MacEachern, *Genetics and Archaeology*, 69.

49 Robertshaw, *African Archaeology*, 101.

50 Robertshaw, *African Archaeology*, 100, 102.

51 See, *e.g.*, Pakendorf, *Historical Linguistics and Molecular Anthropology*, 631, where in a number of fields mentioned archaeology is missing.

Insight or trilemma?

It has been argued here that historical Bantu linguists agree on an origin of the Bantu languages in northwestern Central Africa. If so, the speakers must have penetrated from this *Urheimat* into the equatorial rainforest on their way south. However, although there are almost no non-Bantu languages spoken in the forest, we do not possess any material evidence – which, under the given circumstances, could only be ceramics – to infer any kind of population movement. Likewise, the link between Bantu languages and molecular genetics appears as tenuous as that between languages and material culture. In any case, for want of ancient DNA, genetics is being barred from basing its arguments on authentic evidence in the sense explicated above. As mentioned, this is true for historical linguistics as well.

To sum up, it is indeed far from being established that the molecular, linguistic and archaeological data used in the Bantu expansion endeavor can rightly be considered a reflection of a common historical process.⁵² As Blench observed, wide-ranging correlations of archaeo-genetics, archaeology and historical linguistics seem still to be far in the future.⁵³ In other words: (1) we are a far cry from linking what might be called the inherent »presence« of Bantu linguistics to the authentic material evidence of archaeology; (2) there appears to be about an equal distance between the extraordinarily spotty molecular dataset and the much more solidly constituted set of Bantu languages; and (3) there is as yet not even a hint of any linking of contemporary molecular data to the archaeologically documented human past.

At this juncture it is time to come back to the Baron von Münchhausen who was briefly characterized earlier. Hans Albert has demonstrated that the aim of any process of epistemological justification resides in establishing the truth of the respective propositions and, consequently, their formulation. Truth has to be based on proof. However, as soon as a justification, in other words proof, is demanded for each proposition, this implies first, either an infinite regress; or, second, a logical circle in the deduction; or, third, an arbitrary suspension of the principle of sufficient reason.⁵⁴ As mentioned, this is what Albert, with direct reference to the Münchhausen tale quoted above, has called the »Münchhausen-Trilemma«. Considering the state of the elucidation of the Bantu problem, one is very much reminded of the Münchhausen trilemma. Or, to put it differently, the joint efforts of historical Bantu linguistics and archaeology have not come up with convincing solutions yet. Unfortunately, the impact of molecular genetics in recent years has not significantly changed the overall picture. Although »issues of scale« and, by implication, »Big Science directed toward Big Questions,« as MacEachern observes,⁵⁵ play a role here, they are certainly not the key to the problem. Rather, as I have attempted to show here, molecular genetics have added another »procedural« puzzle,⁵⁶ so that instead of a dilemma, we may now confidently speak of a trilemma.

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52 See also MacEachern, *Genetics and Archaeology*, 68.

53 Blench, *Language, Linguistics, and Archaeology*, 55.

54 Albert, *Traktat über kritische Vernunft*, 11-15.

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With *víkingr* into the Identity Trap: When Historiographical Actors get a Life of their Own

Kerstin P. Hofmann*

As the field of genetic history has grown, academic interest in migration, peoples and ethnic identities has also grown apace. The people of the British Isles have been a focus of research in this area. Specifically, researchers have been fishing for Vikings in the gene pool. My paper begins, therefore, with some brief remarks on the etymology of the term »Viking«, its historical usage and the reception of Vikings in modern times. I address practices of naming as well as the role of romanticization and mythologization as constituents of the popular image of »the Vikings«. The discussion makes it apparent that the term »Viking« has a wide variety of associations and that behind the shared designation, which functions as a kind of semantic shorthand, lie many relationships that have yet to be studied. For that reason, in a second step, this paper outlines what are, in some cases, the greatly diverging conceptualizations of time, space, mobility and identity on which archaeological and genetic interpretations are based. I discuss in particular the problem posed by the essentialization of archaeological subjects as well as the »naturalization« of protagonists of historiographical narratives and their equation with historical actors. Finally, I address the dangers associated with identity politics, which go on both outside the academic discourse and within academia itself. Our duty now is to steer clear of mere battles over the prerogatives of interpretation. Instead, we must cultivate academic and political reflexivity, as well as mutual acceptance. Only by doing so will we be able to explore questions – and they are important questions – concerning the constitution and historicization of identities, interactions among migrations, mobility and identity, and about the relationships between biological and social reproduction.

Keywords: Vikings; historiography; Britain; genetic history; archaeology.

Is it possible to »fish for Vikings¹ in the gene pool«? Is there such a thing as »Viking DNA«? We often see phrases like these, not framed as questions as they are here, but as headings in the context of projects and publications investigating human genetic diversity, and the

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1 In some historical studies, putting the word »Viking« in upper case gives it in English the status of a nationality. More and more scholars are now abandoning that practice and leaving it in lower case. This might signal a deliberate distancing from the loaded usage of the past, but there is also an argument that it gives the word a clearer frame of reference as a descriptor based on something to do with activity. In the archaeological and genetic studies quoted here this distinction is not made. Furthermore, in my mother tongue, German, this differentiation cannot be made. For these reasons, I have decided not to distinguish between upper and lower case Vikings in this paper.

history of the population of the British Isles in particular.² My answer to all such questions is no, but not out of any wish on my part to reject the results of genetic analysis or because I do not find the relevant studies extremely interesting and fruitful. Rather, we need to ask different questions if we are to have a constructive collaboration between archaeology, history and genetics. And besides, it is not terminology alone which is at issue.³ To avoid raising false expectations or even fears, it is essential to communicate clearly that DNA, though it can be an identity resource for contemporary people, was irrelevant for the constitution of identities in the past. Nonetheless, the emerging discipline of genetic history does pose an important challenge both for our current Western academic conceptions of identities, human communities and persons, and for our historiographical narratives. Moreover, genes do constitute an important historical source, one whose value we are only now, slowly, learning to assess correctly.

When grappling with issues of identity, a subject that always seems fraught with danger these days, more and more people are turning to geneticists for an answer to the question of who they are. This is not surprising: genetics is seen as an exact natural science, and one of its applications is the identification of individuals in law enforcement contexts. Outside of the academic sphere, this situation has resulted in the establishment of genetic ancestry testing companies that serve private individuals, and the publication of a steadily growing number of popular science books and newspaper articles on questions of who is descended from which peoples/cultures. The thought processes reflected in the answers these publications provide tend to be outdated, and though occasionally one does see evidence of new thought processes, even these are relatively simplistic.⁴ The situation has had an impact within the academic sphere as well: many researchers today either try to avoid the racially and *völkisch* charged tendencies and interpretations that often quickly infuse discussions of these topics these days, or they deliberately attempt to combat them. Some do so while continuing to use genetics, while in the humanities some scholars completely reject the use of those particular methods to answer questions of identity.⁵ Just what is it though that lies behind the – at times extremely controversial – field of genetic history? In the following, I will attempt to shed light on certain aspects and basic premises of research in genetic history, and point up future challenges for the field and its integration into society, taking as my example the current focus on »Vikings«, and the genetic survey of Wirral and West Lancashire in particular.⁶

2 Phrases borrowed from the title of a lecture by Mark A. Jobling, »Fishing in the Gene Pool for Vikings«, unpublished lecture given at the conference »Genetic History: A Challenge to Historical and Archaeological Studies«, Humboldt-Universität zu Berlin, 2 October 2015; www.genetic-history.com/wissenschaft/programm.htm (retrieved on 21 April 2016) and Harding *et al.*, *Viking DNA*.

3 This paper is written from the point of view of a German archaeologist. The remarks are addressed mainly to archaeologists, but much of the discussion applies to all students of the Viking age, including historians, literary scholars and linguists, as well as scientists such as physical anthropologists and geneticists. Furthermore, I hope that some of the general points might also be of interest for all kinds of scholars to become involved with genetic history.

4 Sykes, *Blood of the Isles*; Oppenheimer, *Origins of the British*; cf. Wiwajorra, *Ethnische Anthropologie*.

5 E.g., Bamshad *et al.*, *Deconstructing the Relationship between Genetics and Race*; Pluciennik, *Genetics, Archaeology and the Wider World*, 14.

6 Bowden *et al.*, *Excavating Past Population Structures*; Harding *et al.*, *Viking DNA*; Harding *et al.*, *In Search of the Vikings*; Griffiths *et al.*, *Looking for Vikings in North-West England*; see also Goodacre *et al.*, *Genetic Evidence for a Family-based Scandinavian Settlement*; McEvoy *et al.*, *Scale and Nature of Viking Settlement*.

My paper starts with the question of what lies behind the word »Viking«. In my analysis, I look at practices of naming as well as semantic simplifications, and at romanticization and mythologization as constituents of the popular image of »the Vikings«. I also examine the divergent concepts of time, space, mobility and identity on which archaeological and genetic interpretations are based. I then turn to the dangers of identity politics, which occur both outside of the academic discourse and within academia itself. In my conclusion, I argue that both more reflexivity and mutual acceptance are needed if we are to establish good ways of collaborating with each other.

Vikings: what's in the name?

»Names go with identities and identities go with names.«⁷

Recently, Turi King and Mark Jobling posed the elegant and succinct question, »What's in a name?« for the field of genetics.⁸ Admittedly, their focus at the time was on heritable surnames, not on the meaning of the term »Vikings«.⁹ King and Jobling wanted to increase the probability of acquiring new information about past population movements from modern DNA samples through the selection of sample subjects whose surnames have long been present in the region under study. In general, however, publications relating to genetic ancestry usually fail to provide in-depth treatment of the potential ancestral peoples involved. It is also rare to find researchers systematically tackling questions of eponymy.¹⁰ Far more common is the preference to rely on »proper names already filled«,¹¹ i.e., to use proper nouns about which readers have pre-existing knowledge because the terms are already familiar from other contexts.¹² This was long the standard practice in the fields of prehistoric and early historic archeology – and one to some extent still standard today – when referring to the *ethne* mentioned in written sources, for instance.¹³ Thus, scholars intentionally use the »significance of names«¹⁴ as a way of integrating their findings within familiar narratives.

7 Brendler, *Identity of Name(s)*, 29.

8 King and Jobling, *What's in a Name?* This is the rhetorical question about the meaning of proper names, frequently quoted in studies on names, that Shakespeare has Juliet ask as she laments the fact that her beloved Romeo bears the hated name of Montague; see, for example, Zabeeh, *What is in a Name?*; Carroll, *What's in a Name?*; Haubrichs, *Einleitung*.

9 For further literature on the relation of surnames and genes see Jobling, *In the Name of the Father*; King and Jobling, *Founders, Drift, and Infidelity*; Redmonds *et al.*, *Surnames, DNA, and Family History*; Sykes and Irven, *Surnames and the Y Chromosome*; Winney *et al.*, *People of the British Isles*.

10 Though this has not been not unheard of recently, from the history of science and classical studies perspectives: Cancik-Kirschbaum and Wiedemann, *Historische Variablen und narrative Identität*.

11 De Certeau, *Writing of History*, 95.

12 One exception here is Bryan Sykes, Professor of Human Genetics (now emeritus) at the University of Oxford; however Sykes has also since come under criticism among geneticists for other premature, since disproven assertions. Sykes published a book presenting research on human mitochondrial haplogroups for a general audience in which he wrote the stories of hypothetical prehistoric »clan mothers«, not only assigning them specific women's names, but also including a brief description of their lives and environments (Sykes, *Seven Daughters of Eve*).

13 Cf. Brather, *Ethnische Interpretationen*; Fehr, *Germanen und Romanen im Merowingerreich*.

14 According to the Swiss philologist Stefan Sonderegger, the term »significance of a name« (*Namensbedeutsamkeit*) should be understood as the sum of all of the associations, ideas and emotions associated with that name. The significance of a name at any given time, Sonderegger says, arises through the interplay among (i) the name itself in the expressivity of its sound-gestalt and written form; (ii) the category of people who bear the name, as a reference subject/object and (iii) the use of the name by speakers or the speech community (Sonderegger, *Bedeutsamkeit der Namen*).

In the face of criticism, however, those same scholars often take up a nominalistic position vis-à-vis these names: i.e., the designation is presented as a *terminus technicus*. The names of persons or groups serve purposes of identification and individuation. Through names, we can identify that which is meant at a single stroke, as it were,¹⁵ because the moment we give someone or something a proper name, we have also – usually implicitly – defined a rule for its usage. By doing so we have also established an identity criterion for the person or thing named, one that is intended to make it possible to individuate it according to its type.¹⁶ In addition, the names of groups are intended to denote, as far as possible, persons or things that are the same, or similar; however, this also amounts to a delimitation excluding other persons or things. In addition, group names are also used to establish affiliations. They can be used to express positions and relationships within a single matrix of meaning, albeit one in constant flux.¹⁷ It is essential to bear in mind in this regard, however, that names also serve as containers for meaning, containers to which characteristics and actions are assigned, though such assignments can also be revoked at times.

How do and did people understand the word »Viking«? In the effort to find out, it is helpful to differentiate among the analyses of its etymology, historical usage and current usage.¹⁸ Two Old West Norse words, *vikingr* and *viking*, commonly serve as references for our contemporary term »Viking«. Despite a century of intensive study, though, no consensus about the origin of those words has emerged.¹⁹ Only on the following points is there broad agreement: The two words probably both came from the North-West Germanic dialect, and both appear to have been very closely linked with ships and seafaring. While there is no surviving evidence in Scandinavia of either the masculine noun *vikingr* (for a person) or of the feminine noun *viking* (for an activity) in Old West Norse that dates from before the second half of the tenth century, counterparts for both words in Old English are found in glossaries dating as far back as the seventh/eighth century. There is also evidence of the words in poems written in Old English, though their chronological positioning is the subject of dispute. The general meaning of the words as common nouns denoting pirates and piracy appears to pre-date the geographical restriction to the Scandinavian region and the use of the word as part of a personal name. The earliest evidence of the above-mentioned two specifications *vikingr* and *viking* is found in Ælfric's *Grammar* and on rune stones from the tenth and eleventh centuries.²⁰

This brings us to the historical usage of the words, since the Viking period is normally dated as lasting from the late eight until the mid-eleventh century on the basis of events recorded in writing. The only clue in the continental European sources, is found in the writings of the Adam of Bremen, who mentions that northern pirates were called *wichingos* by others.²¹ Otherwise, the Frankish chronicles always speak in terms of *normanni* or *nort-*

15 »Durch sie identifizieren wir gleichsam mit einem Schlage das Gemeinte« (Debus, *Namen in literarischen Werken*, 19).

16 Descombes, *Rätsel der Identität*, 68-69.

17 Gruner, *Gestatten mein Name ist Hase*.

18 Jesch, *Viking Diaspora*, 4-8.

19 Andersson, *Wikinger*.

20 Krüger, »*Wikinger*« im Mittelalter, 2-3, 42-47.

21 *Ipsi vero pyratae, quos illi Wichingos alleanni, nostri Ascomannos* (Adam of Bremen, *Gesta Hamburgensis ecclesiae pontificum IV*, 6, ed. Trillmich and Buchner 440, 23-26).

manni.²² By contrast, the Old English sources refer to *wicinge*, *hæðen*, *Dene* and *Norðmenn*.²³ On the whole, the non-Norse sources present a quite stereotypical picture of the Vikings, one that adheres largely to the barbarian cliché of the Ancient World. The Vikings are firmly established in the role of the heathen pirate, their raids seen as a punishment for past sins; hence they function as a representation of »the Other« for Christian civilization.²⁴ One finds only scattered mention of Viking voyages/voyagers in the contemporary runic writings from Denmark, Sweden and Gotland.²⁵ In those contexts, these ventures are described as bringing glory, as they are later, in the early phase of the sagas.²⁶ It is important to note, then, that the temporary activity of piracy and the category of origin (though the latter to only a limited degree) – and not the category of ethnicity as a self-defined collective identity – applied as the defining criteria for the contemporary term denoting Viking. However it must be said that this reconstruction of the concept »Vikings« is based on only a small number of biased sources, which include terminological conventions more than anything else.

Not until the narrative vernacular sources of the High Middle Ages do we find a more comprehensive, but also highly mythologized, picture of the Viking voyages.²⁷ These texts, along with the works of sixteenth century Gothicism, constitute the reference sources for the »Vikings«, which figure prominently in public discourse and historiography in the eighteenth and nineteenth centuries. Here the »Vikings« function as an antithesis to the Occidental tradition, one that is assessed positively in multiple respects and is linked with a topos of freedom. Only Franco-centric historiography takes a considerably more negative attitude vis-à-vis the »Vikings«. Thus »Viking«, once a narrow term, had long since become a broader, *völkisch* term. In this newer meaning it even served as source material for fascist models of society.²⁸

References to the grievously misused Vikings become more rare in the aftermath of World War II. In Germany, in particular, they did not return to prominence again until the 1960s/70s, when they begin to figure as the antiheroes of children's books, animated films and comic books.²⁹ Today we encounter them both as highly versatile advertising characters and as reference figures for religious and political groupings.³⁰ The word »Viking« also serves

22 Cf. Hellberg, *Vikingatidens vikingar*; Zettel, *Bild der Normannen*.

23 It was long assumed that *Dene* and *Norðmenn* were used to distinguish separate ethnic groups – in fact, they were often equated with the national labels »Dane« and »Norwegian«, but today scholars are relatively certain that *Dene* and *Norðmenn* were more or less interchangeable in English sources from the Viking Age (Downham, »Hiberno-Norwegians« and »Anglo-Danes«).

24 Bödl, *Wikinger*, 698-700.

25 Krüger, »*Wikinger*« im Mittelalter, 42-47.

26 Cf. Jesch, *Ships and Men in the Late Viking Age*.

27 In addition to the skaldic poetry – here it is argued that much of the surviving verses, although preserved in later narratives, is early, perhaps even contemporary – it is particular true for the sagas and the *Gesta Danorum of Saxo Grammaticus*.

28 Bödl, *Wikinger*, 705-707; cf. Müller-Wille, *Political Misuse of Skandinavian History*; Wawn, *Vikings and the Victorians*.

29 Particularly popular, aside from »Vicke Viking«, a series of children's books by Swedish author Runer Jonsson, which served as the inspiration for several other works including two animated television series and two films, was »Hågar the Horrible«, an American comic strip created by Dik Browne, and which first appeared in 1973. The caricatures were widely disseminated, primarily through syndication in numerous newspapers.

30 Hein, *Mythos und Legende*.

as a possible designation of origin, and, lately, Vikings have begun to appear in the role of heroic protagonists again, e.g., in the much-watched Irish-Canadian historical drama television series *Vikings*.³¹

Meanwhile, another concept of Viking has been evolving in the field of archaeology. This concept has contributed to the production and reception of the many images of Vikings, but done so very unevenly.³² Archaeologists associate what they view as a characteristic material culture – which includes certain fibula and sword types, steatite, ship and building forms, stone monuments, but also a series of art styles and burial forms – with Scandinavia or the presence of Scandinavians.³³ This bundle of characteristics is supplemented, primarily by historians, with data and descriptions relating to historical events,³⁴ as well as with the names of persons and places supplied by historical linguists,³⁵ and, lately, with haplotypes from geneticists.³⁶ Despite criticism of the ethnic interpretation and the overly close association of things or actions with the bearers of a geographically referenced culture, the classification remains in use to a great extent, though increasingly with the qualification that it constitutes an analytical category, ideal type or narrative figure. And although some researchers deliberately focus on aspects of diversity in small-scale investigations, rarely is the superordinate entities – »the Vikings« in our example – challenged at a fundamental level.

Yet archaeologists are co-producers³⁷ of the images of Vikings and as such they cannot be careful enough.³⁸ One need only look at the cover of the album »This Time the World« (which was placed on Germany's official list of media harmful to young persons) by British skinhead band No Remorse to see why: it depicts what for neo-Nazis is the perfect ancestral line-up, a skinhead, a Nazi-soldier and a Viking warrior.³⁹

31 www.history.com/shows/vikings; retrieved on 7 June 2016.

32 The horned helmets so frequently associated with Vikings reveal just how immune the popular image of Vikings can be to the influence of archaeological knowledge. This invention of Romanticism goes back to artists such as Gustav Malmström, who illustrated an edition of Frithiof's Saga, and Carl Emil Doepler, who created horned helmets for the first Bayreuth Festival production of Wagner's opera »Der Ring des Nibelungen« in 1876. However, there is no archaeological evidence that Scandinavians in the Viking Age wore them (Richard, *Vikings*, 120; cf. Frank, Invention of Viking Horned Helmet).

33 See e.g., Brather, Lindisfarne; Brink and Price, *Viking World*.

34 E.g., Sawyer, *Kings and Vikings*; Smyth, *Scandinavian York and Dublin*.

35 E.g., Fellows-Jensen, *Scandinavian Personal Names*; Fellows-Jensen, *Vikings in the British Isles*.

36 Bowden *et al.*, *Excavating Past Population Structures*; Harding *et al.*, *Viking DNA*, 62-68, 102-109.

37 Jasanoff, *Idiom of Co-Production*; Cf. M'charek *et al.*, *Topologies of Race*; Schramm, *Neue Technologien*; Schreiber, *Vergangenheit als personaler Wissensraum*.

38 This applies in particular to major exhibitions such as the 22nd Council of Europe exhibition »From Viking to Crusader – Scandinavia and Europe 800–1200« in Paris, Berlin and Copenhagen, 1992–1993, and the international exhibition »Vikings: Life and Legend« in Copenhagen, London and Berlin, 2013–2014 (Roesdahl and Wilson, *From Viking to Crusader*; Williams *et al.*, *Vikings*). Particularly vigilant regarding the various political entanglements is the current exhibition in Rosenheim »Wikinger!« (Helmbrecht, *Wikinger!*). A systematic comparative study of archaeological Viking exhibitions and their reception is still to be made.

39 The album was released in 1988 by the French white power rock record label *Rebelles Européens*. No Remorse was one of the most influential and radical right-wing rock bands. The band was part of the Blood & Honour network (Helmbrecht, *Wikinger und die politisch Rechte*, 267; Raabe and Schlegelmilch, *Rezente extreme Rechte*, 174-175; cf. Menhorn, *Skinheads*, 115-116).

Applied to »Vikings«, the question »What's in a name?« can ultimately only be studied contextually, e.g., through what are known as topological analyses.⁴⁰ Nonetheless, my survey points up concepts that have repeatedly been of relevance for the definition of the term »Vikings«: time, space, mobility and identity. In the following, I provide a brief outline describing how each of these four concepts is used in the context of the analysis of Vikings in archaeology and population genetics. It should also have become clear from my survey that while the shared name increases the potential for tie-ins, it also works as a smokescreen, obscuring the interconnections that may have existed in some form among individual characteristics/features, persons and ways of living, and thus preventing their examination or scrutiny. What is actually needed is systematic differentiation.

Central Concepts

Time

In archaeology, past and present are seen as two separate, but relationally conceived worlds. Their relationship to one another is defined through continuity and discontinuity and through distance and proximity, and is renegotiated over and over again through othering, historical traditions and nostrification⁴¹ (Fig. 1).

The notion of an irretrievable past results in the creation of insurmountable distance, and thus, discontinuity. There is a reason that archaeologists and historians researching far-off periods say that they study dead cultures.⁴² On the other hand, though, they assume that

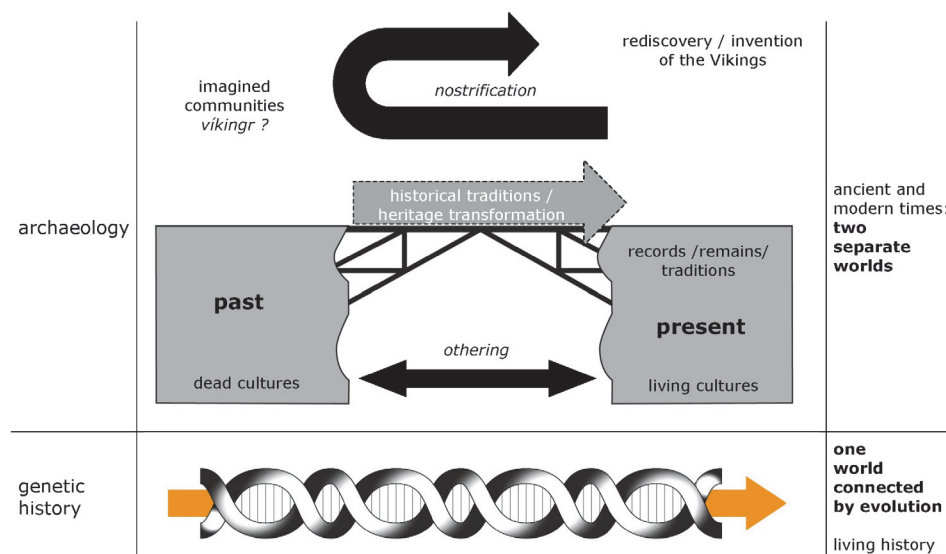


Fig. 1.: Time concepts in archaeology and genetic history: a comparison (Layout: Kerstin P. Hofmann and Blandina C. Stöhr)

40 M'charek et al., *Topologies of Race*; Serres, *Aufklärungen*; Schramm, *Neue Technologien – alte Kategorien*.

41 Cultural appropriation of the other, sometimes even accompanied by claims that the formerly other has always been part of one own's culture.

42 Eggert, *Prähistorische Archäologie*, 112; Eggers, *Einführung in die Vorgeschichte*, 258-262; cf. Lucas, *Understanding the Archaeological Record*, 54-55, 59, 100.

remnants or traces left behind in their transformed residuality project out of the past and into the present, and they usually even grant our historical sources a power of veto on false or unreliable representation of the past.⁴³ They further assume that past actions and structures have effects, some of which carry over into the present. The historical potency/efficacy and degree of path dependence⁴⁴ varies considerably, however. In many cases these are gauged as being fairly minor, particularly for cultures and periods that do not stand in direct relation to one another. Moreover they can be influenced by the actors of the respective present(s). For instance, it is possible to surmount the divide between ancient and modern times with the help of constructions of meaning, e.g., genealogies⁴⁵ or invented traditions,⁴⁶ but also through development thinking.⁴⁷ Continuities and coherences postulated in this manner re-link the past and the present, lending archaeology a particular appeal, even in the eyes of the public, and particularly at times of social upheaval. In the end, this is the only way to explain the significant role that archaeology has played for the construction of identities and in the current history and heritage boom.⁴⁸ Identity narratives established in this way, however, are predominantly part of *intentional history*⁴⁹ or also applied history.⁵⁰ Archaeological analysis, though, requires us to consider archaeological cultures as alien.⁵¹ We use distancing as a means to try to prevent the unthinking transfer of unexamined premises of the present day onto prehistory and early history. This issue also came up above, in my consideration of the term Viking.

In the field of genetics, and also that of genetic history, scholars assume the existence of a world that links past and present through evolution. In this context the meaning of DNA appears to be self-referential: there is a trajectory that leads directly from the past to the present (*Fig. 1*). In his 2006 bestseller *Blood of the Isles*, Bryan Sykes, Professor of Human Genetics (now emeritus) at the University of Oxford and founder of the genealogical DNA testing firm *Oxford Ancestors* expressed this as follows: »It is a living history, told by the real

43 Hofmann, *Dinge als historische Quelle in Revision*, 286; cf. Koselleck, *Standortgebundenheit und Zeitlichkeit*; Jordan, *Vetorecht der Quelle*.

44 Concept developed by economic historian Paul A. David and the economist and mathematician W. Brian Arthur, that is now used in a less deterministic sense in other fields, such as the social sciences and history of science, though not without extensive criticism. Path dependencies refer to critical junctures of the past, which substantially define or at least restrict the trajectory of future development, because once paths have been taken it becomes easier to continue along them due to the regular antecedent conditions associated with them, such as institutional settings, high fixed costs, feedback processes, reduced coordination costs, etc.; see Beyer, *Pfadabhängigkeit*; Werle, *Pfadabhängigkeit*.

45 Renger and Toral-Niehoff, *Genealogie und Migrationsmythen*.

46 Hobsbawm, Introduction; cf. Boschung *et al.*, *Reinventing »The Invention of Tradition«?*

47 For a critical view: Cesana, *Geschichte als Entwicklung*.

48 Cf. Lowenthal, *Heritage Crusade*; Tschofen, *Antreten, ablehnen, verwalten?*

49 Term coined by the historian of antiquity Hans-Joachim Gehrke in 1994. »Intentional history [...] is the projection in time of the elements of subjective, self-conscious self categorization which construct the identity of a group as group«; Foxhall and Luraghi, Introduction, 9; cf. Gehrke, *Mythos, Geschichte, Politik*, 247; Foxhall *et al.*, *Intentional History*; Gehrke, Hans-Joachim, *Geschichte als Element antiker Kultur*.

50 Applied history is history that is applied to real-world issues. Sometimes the term was used synonymously and interchangeably with public history, but applied history better highlights that this kind of historiography especially takes account of the intellectual and practical needs of society and often goes hand in hand with commercialization; cf. Hardtwig and Schug, *History Sells*; Nießer and Tomann, *Angewandte Geschichte*; Sommer, *Angewandte Geschichte auf genetischer Grundlage*; Tomann *et al.*, *Diskussion Angewandte Geschichte*.

51 Röder, *Jäger sind anders*; Veit, *Archäologie und das Fremde*.

survivors of the times: the DNA that still lives within our bodies. This really is the history of the people, by the people.«⁵² Certainly, this assertion has also served the marketing of Sykes' business. (Concerns about situations like this, incidentally, were one of the motivations behind the development of honour codes in the field of archaeology – regrettably only very late in the day – which include a provision barring archaeologists from simultaneously being collectors and/or antique dealers).⁵³ Nonetheless, more recent studies on Viking DNA have also emphasized the direct link to history, and also their ideologically less-problematic approach to history.⁵⁴ Despite the advances in aDNA analysis, these studies usually start from modern populations whose data are also better suited for other forms of use, such as in medical or forensic investigations. Human biologists' interest in studying the genetic legacy of the Vikings on the British Isles can also be traced to the desire to understand what it means to be British.⁵⁵ And the new »Impact of Diasporas...« research project is interested above all in diasporas' impact »...on the Making of Britain.«⁵⁶ These issues are embedded in a larger research environment that, since early in this millennium, has increasingly been shifting away from earlier tendencies to emphasize biological equality and towards the study and mapping of the 0.1 percent difference among people.⁵⁷ In this context, the intent is not to learn through the past or history through contrasted otherness and diversity – an approach increasingly prevalent in historiography and archaeology – but instead to do so through the understanding of origin, descent and difference, and recently, to a greater extent also, through an understanding of the admixtures of populations.

Other differences in the treatment of time can also be identified, however. For instance, the »molecular clock«⁵⁸ still ticks considerably more slowly than its archaeological counterpart. Nonetheless, long-term developments are linked with data and persons associated with historic events mentioned in written sources – as was the standard practice in archaeology for a long time, and, despite criticism,⁵⁹ is still, in some respects, standard. The *histoire de longue durée* or *histoire conjoncture*, which the underlying data actually should be used to write, is usually linked, without any more thorough analysis of the nature of that link, to an

52 Sykes, *Blood of the Isles*, 288; cf. Sommer, *It's a Living History*.

53 See, e.g., *Ehrenkodex »Ethische Grundsätze für archäologische Fächer«* www.wsva.net/fileadmin/wsva/dokumente/ehrenkodex_659_1.pdf (retrieved on 15 June 2016); cf. Beaudry, *Ethical Issues in Historical Archaeology*; Scarre and Scarre, *Ethics of Archaeology*.

54 It is claimed to be less problematic, because phenotype irrelevant, so-called junk DNA was investigated; e.g., Griffith and Harding, *Interdisciplinary Approaches*, 22; cf.; Harding *et al.*, *Viking DNA*; Sommer, »Wer sind Sie wirklich?«, 56; cf. Dietrich, *Origins of the Neutral Theory*. Nadia Abu El-Haj expresses a very critical view of the neutrality of even so-called junk DNA (Abu El-Haj, *Genetic Reinscription of Race*; Abu El-Haj, *Genealogical Science*).

55 The opening statement in the text accompanying a short video that appeared on 26 November 2010 featuring the work of a project entitled »People of the British Isles«, funded by the *Wellcome Trust*, is worded as follows: »What does being British mean to a scientist?« (Nash, *Genome Geographies*, 193; see also www.youtube.com/watch?v=PCwHCMfyW88 (retrieved on 15 June 2016)).

56 For the project website see www2.le.ac.uk/projects/impact-of-diasporas/ (retrieved on 15 June 2016).

57 Schramm, *Neue Technologien*, 234.

58 Metaphorical term introduced in 1962 by Emile Zuckerkandl and Linus Pauling denoting a method in genetics which uses the mutation rates of biomolecules to deduce when two or more life forms diverged in prehistory. Unfortunately, mutation rates are non-constant. In addition, in order to provide specific dates, the molecular clock has to be calibrated with fossil or archaeological records (Zuckerkandl and Pauling, *Molecular Disease*); Ayala, *Molecular Clock Mirages*; cf. Sommer, *History in the Gene*.

59 E.g., Brather, *Ethnische Interpretation*, 344-354; Brather, *Lindesfarne*.

histoire événementielle, whose characters and events then dominate the migration narratives.⁶⁰ To give one example: the high proportion of the »genetic legacy of Vikings« found in the population of Wirral and West Lancashire has been linked to the expulsion of Norwegian Vikings from Dublin and their settlement in Wirral in 902 under the leader Ingimund.⁶¹

Space

Concepts of space underlying archaeological and genetic analyses are considerably more similar, however. A »methodological territorialism«⁶² is often inherent in studies of both types, though it is easier to avoid in genetic history.

In archaeology, the findings related to a group of people with its lived social space are usually associated with a more-or-less clearly delimited territory. Designations of administrative and natural-geographical units often serve to localize these geographically. This is frequently associated with an amalgamation of the different kinds of spaces, which can be better separated analytically: social spaces, natural spaces and modern administrative spaces. Moreover, in many cases archaeologists address only the structural spaces, which are so nicely (re)producibile in maps, while failing to address the spaces for movement hidden behind them. Furthermore, the use of information acquired from the location of finds is also indispensable for the field of archaeology. Localization will therefore always play an important role. In my view, however, rather than locations inside »container spaces«, one should start from interrelated networks of locations, and if one does posit the existence of correlations between enclosed cultural spaces and features or boundaries of the natural landscape, one should always specify one's rationale for doing so.⁶³ However, there is still a dearth of constructive approaches for conceptualizing and researching dynamic, overlapping scapes rather than static territories. Still, researchers studying the Viking period in particular have tended in recent years to focus more on analyses relating to individual archaeological sites or small geographical regions because these permit them to produce »denser« descriptions.

Geneticists also argue with territorial areas of distribution. These used to be defined mainly on a global or continental scale,⁶⁴ but smaller scales are being used now as well, as the Wirral and West Lancashire project demonstrates. The term »genome geography« is understood as: »how, through the tools and practices of human genetics, bits of genomic sequence become associated with specific geographic locations, posited as the place of origin of people who possess these bits.«⁶⁵ Another argument put forth by population geneticists is that gradients of human genetic variation are geographically structured.⁶⁶ People living closer together who, or rather, whose ancestors, did not migrate over long distances during the last centuries, or who were separated from other populations by topographical barriers,

60 Cf. Braudel, *Geschichte und Sozialwissenschaften*.

61 Though this event-oriented historical [ereignisgeschichtliche] interpretation is reported as merely »one version of events« in the paper aimed at the scientific community, it is discussed in considerably more detail than any other »version« in the popular science book *Viking DNA*, and is reinforced by the book's cover; Bowden et al., *Excavating Past Population Structures*, 302; Harding et al., *Viking DNA*, front cover illustration, 11, 16-18, 121. Cf. Harding, *Ingimund's Saga*.

62 Brenner, *Beyond State-Centrism*, 46; Langthaler, *Orte in Beziehung*.

63 Hofmann, *Fundverbreitungen*; cf. Krämer, *Was eigentlich ist eine Karte?*

64 Thomas, *Gene-Flows and Social Processes*, 51.

65 Fujimura and Rajagopalan, *Different Differences*, 7; cf. Nash, *Genome Geographies*.

66 Novembre et al., *Genes Mirror Geography*.

are likely to bear greater similarity to one another than they do to people who live farther away. This results in the creation not only of genome geographies – usually mapped with reference to nation states – of present-day populations, but also of imagined geographies of ancient populations and their homelands.⁶⁷ In connection with data collection, therefore, there is a preference for drawing on »indigenous populations«:⁶⁸ researchers seek proof of residence or, lately, stock their sample populations with people whose surnames are old and relatively rare, which increases the statistical probability of their local specificity.⁶⁹ However, these days, scholars studying the British Isles during the Viking period assume that a variety of colonization strategies were pursued, and that responses to them were subject to regional and chronological variation.⁷⁰ Along with toponyms, various settlement and building forms in particular have been interpreted as indications of the composition of populations specific to each. Thus settlements have been termed Viking or Scandinavian, Hiberno-Norse, Anglo-Scandinavian and Anglo-Saxon.⁷¹ Despite these questions, which are clearly worthy of research, so far only genetic studies based on entire regions instead of single settlements have been carried out.

In the context of the genetic analysis conducted for North-west England, researchers were able to work on a regionally differentiated basis and to some extent with »reconstructed« random samples from the Middle Ages, but for the necessary comparison with Scandinavia they drew only on data for the present-day population of Norway.⁷² The broad term »Viking« is thus geographically restricted in this study – although with reference back to the written sources.

Mobility

The object geographies of archaeologists and the genome geographies of geneticists are all based on specific notions of mobility. Though the early equation »pots equal people« has come under fire on multiple occasions,⁷³ it is still common to find specific names and cultures associated with specific artifacts. For instance, archaeologists often continue to interpret finds of oval brooches as an indicator of the presence of Scandinavian women in England, although the fibulae could have also been traded, given as gifts etc.⁷⁴ The growing numbers of object biographies being published have made it increasingly clear that objects are not necessarily accompanied by their manufacturers or even by their former users when they travel.⁷⁵ Selected material culture can serve as a marker of identities in certain situations, but

67 Nash, *Irish DNA*, 196.

68 Schramm, *Neue Technologien – alte Kategorien*, 244; Sommer, »Wer sind Sie wirklich?«, 66.

69 Bowden *et al.*, *Excavating Past Population Structures*; King and Jobling, *What's in a Name*.

70 Richards, *Viking Settlement in England*, 372.

71 E.g., Fellows-Jensen, *Scandinavian Settlement in England*; Hall, *Scandinavian Settlement in England*; Richards, *Identifying Anglo-Scandinavian Settlements*; Wallace, *Archaeological Identity*.

72 Nash, *Genome Geographies*, 199-200.

73 Carol Kramer was already arguing against the equating of pots with people back in 1977 (Kramer, *Pots and People*); cf. Ucko, *Introduction*, 12.

74 E.g., Kershaw, *Viking Identities*, 216; cf. Lee, *Viking Age Women*.

75 E.g., Boschung *et al.*, *Biography of Objects*; Gosden and Marshall, *Cultural Biography of Objects*; Hahn and Weiss, *Mobility, Meaning and Transformation of Things*; Kopytoff, *Cultural Biography of Things*.

its interpretation must always be context-specific. Where once researchers thought in terms of human migration or the diffusion of ideas, today more and more researchers want to study the entire spectrum of mobility, though the interactions and effects of different kinds of mobility have not yet been adequately researched.⁷⁶

Geneticists probably have it easier in this respect, since genes do indeed travel within the bodies of potentially mobile persons. However during the Viking period, the term Viking, while it did denote an activity, was not associated with a line of descent that can be localized territorially within present-day Scandinavia. These days, geneticists' interest is largely confined to spatial mobility and in our context to migration – also called demic diffusion, i.e., permanent changes of place of residence resulting in a population of descendants in a region far removed from the place of origin. Three basic premises underlie their work: (i) that migrations have more effects than other forms of mobility; (ii) that, in percentage terms, more people migrate in the modern age and in urban areas than did/do in earlier periods or in rural areas; and (iii) that the most significant population movements are known to us through archaeological and/or historical sources. However, since the so-called Anglo-Saxons invaded Britain before the Vikings, and differentiating between these two »migration movements« has proven difficult, the isolation desired can only be achieved by concentrating on »the« Norwegians for the time being.⁷⁷ This flaw is very important to keep in mind, because written and material evidence alike make it clear that England and Denmark were closely linked by many different networks – a fact that this Norwegian focus necessarily ignores.

In the context of debates about transnationality and globality, diasporas, as one possible consequence of migrations, have attracted the interest of archaeologists, historians and literary scholars as well as geneticists.⁷⁸ However, researchers interested in diasporas seldom consequentially examine their influence on the land of origin; doing so would require them to thoroughly reexamine the questions about provenience of material culture that keep cropping up. In that case, for instance, the decision to use modern-day Norwegians for genetic constructions of a Viking period diaspora in England would no longer appear so straightforward. Questions about male and female mobility have also arisen in connection with the differences in the results obtained in analyses of mtDNA and Y-DNA.⁷⁹ Traditionally, both population geneticists and archaeologists have tended to consider men as more likely to be interested in migration than women;⁸⁰ very rarely has research looked at what such assumptions imply for the populations in question. Moreover, new results coming in from isotope analyses have called into question the degree of validity of generalized statements about the relationship between gender and mobility/migration.⁸¹

76 Gramsch, *Culture, Change, Identity*; Kaiser and Schier, *Mobilität und Wissenstransfer*.

77 Bowden *et al.*, *Excavating Past Population Structures*; Leslie *et al.*, *Fine-Scale Genetic Structure*; Winney *et al.*, *People of the British Isles*.

78 Cf. Abrams, *Diaspora and Identity*; Jesch, *Viking Diaspora*; Sommer, *Population-Genetic Trees, Maps, and Narratives*; Sørensen, *Gender, Material Culture, and Identity*; see also the website of the project »The Impact of Diasporas«: www2.le.ac.uk/projects/impact-of-diasporas (retrieved on 26 April 2016).

79 Helgason *et al.*, *Estimating Scandinavian and Gaelic Ancestry*; Helgason *et al.*, *MtDNA and the Islands*; Wilson *et al.*, *Genetic Evidence*.

80 Koch, *Geschlechterrollen zwischen den Zeilen*; Sommer, »Wer sind Sie wirklich?«, 64.

81 Johannes Krause, *Die genetische Herkunft der Europäer: Migration in der Vorgeschichte*, lecture given on 1 June 2016, as part of the lecture series *Migration. Wanderungsbewegungen vom Altertum bis in die Gegenwart*; Kerstin Hofmann, *Identität durch Mobilität? Wikinger in Großbritannien*, lecture given on 6 July 2016: migration.hypotheses.org (retrieved on 30 October 2016). E.g., Sjögren *et al.*, *Diet and Mobility*.

Identity

Diverging approaches to time, space and mobility have repercussions for the conception of identity associated with them. Following the philosopher Vincent Descombes, one can distinguish at a fundamental level among three different questions associated with the riddle of identity: (i) who/what is this; (ii) who am I; and (iii) who are we.⁸² While the first question permits a pure identification from a bird's eye view, the other two cannot be answered without examining why someone identifies with something. Yet answering even the first question requires clarification of what is called the ›sortal dependency of individuation‹,⁸³ i.e., the question »what does it mean for an x of the sort/type/category y to continue to exist?«, or in our case here, »what does it mean for (ancient and/or modern) Vikings to exist?«, and to which kind of category do they belong? What is needed, therefore, is not only a synchronic but also a diachronic principle of individuation. I would like to clarify this briefly in the following.

History is one of several fields that have taken up narratological theories and concepts in recent years.⁸⁴ In this context, historian Felix Wiedemann, whose fields are modern history and the history of science and scholarship, has proposed that we differentiate between historical actors and historiographical protagonists.⁸⁵ Applying this suggestion to our example, both modern Vikings and ancient Vikings would, in the first instance, be nothing other than the protagonists of historiographical narratives.⁸⁶ Pirates as well as explorers, traders and settlers of the eighth to eleventh centuries, who came from the area now known as Northern Europe, on the other hand, would be historical actors, just as other persons who lived in the period would be. The hunt for, and above all, the definition of Viking DNA, however, results in the »naturalization« of protagonists of historiographical narratives and their equation with historical actors. This is because ultimately researchers need stories – whether they be factual narratives provided by historians or even myths – if they are to produce an extensive interpretation of the nucleotide sequences that they treat as objective or neutral.⁸⁷ Similar considerations apply, of course, for the interpretation of material cultures and historical texts. So this practice of essentializing identities was not and is not now unusual, even in the work of a purely archeological or historical character.

In connection with the ethnological critique of so-called primordialist approaches (*Fig. 2*), archaeologist Lynn Meskell, for one, has specifically criticized the recourse to supposed biological facts as a way of »naturalizing power«.⁸⁸ Meskell also defined the systematic deconstruction of these supposed facts as one of the key tasks of an archaeology of identity.⁸⁹

82 Descombes, *Rätsel der Identität*.

83 Wiggins, *Sameness and Substance Renewed*, 22.

84 E.g., Saupe and Wiedemann, *Narration und Narratologie*; Spinozzi and Hurwitz, *Discourses and Narrations in Biosciences*; Strohmaier, *Kultur – Wissen – Narration*; White, *Auch Klio dichtet*.

85 Wiedemann, *Völkerwellen und Kulturbringer*; cf. Wiedemann, *Stones and Stories*; Wiedemann *et al.*, *Wanderungsnarrative*.

86 Cf. Nelson, *England and the Continent*.

87 Sommer, *Angewandte Geschichte auf genetischer Grundlage*, 140-142; Sommer, *History in the Gene*; cf. Morning, *And You Thought We Moved beyond all That?*

88 Yanagisako and Delaney, *Naturalizing Power*.

89 Meskell, *Archaeologies of Identity*.

primordialist definition of identity	(de)constructivist definition of identity
immediate and primary, acquired by birth	discursive practice, generated by demarcation
belonging	strategy, legitimation, power
change only slowly	easy to change, flexible
essence, substance	code, social artifact

Fig 2. Primordialist versus (de)constructivist definition of identity

In addition, some years ago, Adam T. Smith issued an impressive call for the »end of the essential archaeological subject« and warned of the dangers of transferring present-day categories of identity onto the past.⁹⁰ In archaeology today, the usual answer to the question of what characterizes a collective identity is situation- and context-specific self-identification.⁹¹ In this understanding of collective identity, one person can put on, but also cast off again, multiple identities. Thus, the historical identity of Vikings, if there ever was such a thing, would not have been tied to a biological organism or the rules of inheritance associated with it. Establishing a link between genes and identity using archaeology's wider concept of Viking identity as a specific set of material culture would not be so simple either: one would first have to show a causal relation between the use of specific material culture and biological descent, since the latter is the sortal determination of identity in genetics.⁹²

There are a great many different definitions of sortal dependencies in the worlds we inhabit, and there were a great many of them in the worlds that existed in the past. Until we are familiar with them and their interdependencies, shared names only conceal what we seek to illuminate. Semantic shorthands may be helpful in »the universally pre-logical logic of practice«,⁹³ but for academic research they are usually more of a hindrance.

90 Smith, *End of the Essential Archaeological Subject*.

91 E.g., Brather, *Ethnische Interpretation*, 97; Díaz-Andreu and Lucy, Introduction, 1; Jones, *Archaeology of Ethnicity*, 13.

92 The fact, that one of the few things that we know about some of these people's sense of themselves is that they thought they spoke the same language – the so-called »dønsk tunga«, »Danish tongue« – could be an indication of self-identification (cf. Jesch, *Viking Diaspora*), but is not a sufficient due cause for an existing supra-regional identity of inhabitants of Scandinavia and their overseas settlements. Language is certainly an important communication medium, but again it is necessary to analyze the concrete relations between language, geography and descent.

93 Bourdieu, *Logic of Practice*, 12.

Identity politics

After this rather cursory and greatly simplified discussion of different conceptions of time, space and mobility and their repercussions for the concept of identity one uses, I would now like to turn to identity politics.

Gene and identity narrative in the public sphere

Genetic anthropology has become tangled up in the identity discourse to an even greater degree than that discussed with respect to archaeology and archaeological research,⁹⁴ according to Marianne Sommer, a scholar who studies the history of science and scholarship.⁹⁵ While there has been a great deal of theoretical discussion and speculation about the potential impacts of the science of genetics – ranging from the production of *biosociality*,⁹⁶ to a restoration and remediation of the identity discourse⁹⁷ on to the danger of a new eugenics and the racialization and essentialization of ethnicity⁹⁸ – thus far actual case studies have been few and far between.⁹⁹ This makes it all the more gratifying that the new interdisciplinary project »The Impact of Diasporas on the Making of Britain« envisions a systematic analysis of the impacts of genetic research on the general public.¹⁰⁰ I will therefore only mention two of the discussions conducted in the media in which the linkages between personal and collective identities on the one side, and genes, ethnic groups and nations and the assessment thereof on the other have emerged with particular clarity.

In Scotland, as in many other regions of the world, the supply of sperm donated for the purpose of artificial insemination failed to keep up with demand in the late 1990s.¹⁰¹ As a result, physicians came up with a plan to import sperm from a Danish sperm bank. The media picked up the story under headlines like »The Viking Baby Invasion«. ¹⁰² They also evoked images of earlier contributions by Northern Europeans to the British gene pool, one of which was put on paper by David Austin in a cartoon printed in the *Guardian*, showing a Viking, who has just come ashore from his dragon ship, telling a woman: »We are here to burn pillage and donate.«¹⁰³ The media hype also led to a temporary boom in sperm donation by Scottish

94 Cf. Brather, *Ethnische Interpretationen*; Gardner, Paradox and Praxis.

95 Sommer, »Wer sind Sie wirklich?«, 53; she believes that genetic anthropology is bound up in identity politics, from A as in »Antragstellung« (applying [for a grant]) to Z as in »Zusammenfassung der Forschungsergebnisse« (summarizing the research results).

96 Rabinow, *Artificiality and Enlightenment*.

97 Bolter and Grusin, *Remediation*; Scully *et al.*, *Remediating Viking Origins*.

98 Bradby, *Genetics and Racism*; Morning, *And You Thought We Had Moved beyond All That*; Simpson, *Imagined Genetic Communities*.

99 Positive exceptions are Scully *et al.*, *Remediating Viking Origins*; Sommer, »Wer sind Sie wirklich?«.

100 For further details see: www2.le.ac.uk/projects/impact-of-diasporas (retrieved on 26 April 2016). For an example of what kind of reactions the work of Richard Jones provoked in France see www.theguardian.com/world/2015/jun/16/hunt-for-viking-dna-among-normandy-residents-rites-anti-racism-activists; <http://www.anthrogenerica.com/showthread.php?6993-Normandy-Most-convincing-viking-markers-present-in-59-of-the-samples> (retrieved on 30 October 2016). (Jones was part of the Leicester Impact of Diaspora project.)

101 Cf. Simpson, *Imagined Genetic Communities*, 4-5; Sommer, *Angewandte Geschichte*, 143.

102 Hillmore, *Viking Baby Invasion*.

103 Simpson, *Imagined Genetic Communities*, 4.

men. It is difficult to tell just what motivated these donors. Apparently, though, some of them felt that it was important for the genes being passed on to be Scottish. For instance, one Scot who lived in London offered to travel to Glasgow regularly in order to donate. On the other hand, one *Glasgow Herald* reader wrote in to say that it did not matter where the sperm came from, as long as it came from a nation that could play soccer. Just an anecdote from the last millennium, one might think, if it were not for the fact that the discussion broke out again only recently, triggered by the BBC broadcast »Modern Times: The Vikings are Coming«. ¹⁰⁴

As a second example I would like to point to the international project on surnames and Y-DNA initiated by hobby genealogists and carried out by *FamilyTreeDNA*, a private sector business. ¹⁰⁵ Contrary to expectations, the project's certainly questionable finding was that the Barra-based McNeil clan is descended not from Niall of the Nine Hostages, the legendary Irish king, but from Vikings. This news triggered newspaper articles and discussions all over the world early this year. ¹⁰⁶ Reactions of the sampled individuals and other members of the McNeil family varied greatly, running the gamut from rejection to references to the Irish maternal line, and from playful approaches to the presumed new line of descent all the way through to acceptance and even a willingness to rewrite the family's history. ¹⁰⁷

Many people, then, are able to wear, shed or recombine different identities like garments, without placing any great importance on it. ¹⁰⁸ As individuals, we appear to be so well practiced as wanderers among major collective memories ¹⁰⁹ in the free market of collective identities on offer, that we often have no trouble embedding a new genetic identity into our multiple I-narratives. However, when central concepts relating to the identity of individuals or groups that struggle for recognition are involved, the results can lead to profound transformations of the I-consciousness and we-consciousness. The Vikings would not appear to present a very apt example for this: they may have had a bad reputation in the contemporary sources written by their victims, but they enjoy an astounding degree of popularity today (one responsible for the predominantly lighthearted tone in which the danger of the invasion of Viking babies was discussed).

Academic tribes and territories

Identity politics is not confined to the public sphere, however: it also plays out in the hallowed halls of alma mater. Immanuel Kant was already reflecting on the »conflict of the faculties« back in 1798. ¹¹⁰ Later, Norbert Elias noticed that academic departments are similar in some respects to sovereign states, ¹¹¹ and then in 1989 Tony Becher published a study on

104 Brian, *Invasion of the Viking Babies*; Johnston, *Rise of the Baby Vikings*.

105 For further information see: www.familytreedna.com/public/MacNeil?iframe=ysnp (retrieved on 28 April 2016).

106 E.g., Ayers, *Scandinavian MacNeils*; Kane, *DNA Tests Prove*.

107 By way of illustration, here are some of the reactions cited in some of the newspaper articles: »I nervously awaited the results, and was emotionally devastated when we received them. [...] I found solace in the fact that, if not a Celt, I am nevertheless a Gael« (Paul McNeil); »... my two Irish grandmothers will ensure the Irish« (Stephen McNeil); »I will be adding a new horned helmet to my kilt ensemble« (Ian MacNeil); »I'm pretty good with being of Viking descent. ... You are what you are« (Michael MacNeil); »But mother nature knows who we are. Oral history is wonderful and often there is truth in it. But everybody's family history is in their DNA« (Vincent MacNeil).

108 Sommer, »Wer sind Sie wirklich?«, 54-62; cf. Scully *et al.*, *Remediating Viking Origins*.

109 »Wanderer zwischen Großgedächtnissen« (Patzel, »Alle Erinnerung ist Gegenwart«, 192).

110 Kant, *Streit der Fakultäten*.

111 Burke, Norbert Elias. I would like to take this opportunity to thank Hans-Peter Hahn for the inspiring discussions upon interdisciplinarity and the bibliographical reference.

several different disciplines in Britain and the USA under the title »Academic Tribes and Territories«.¹¹² In 1950, Charles Percy Snow diagnosed the emergence of two cultures at odds with each other, the sciences and the humanities.¹¹³ Snow's thesis in particular has been labeled unproductive on several occasions and is considered outdated,¹¹⁴ and rightly so in my view given the present-day plurality in cultures of knowledge. Yet it is a notion referred to again and again by scholars defining the cognitive identity of archeology or discussing the possibilities of collaboration between archaeologists and geneticists.¹¹⁵ It may be that part of the explanation lies within archaeology itself, that is, in a divergence – within a discipline that supposedly bridges the sciences and the humanities – between one branch tending to rely more on natural-science methods, and another branch leaning more towards the humanities/literary studies.¹¹⁶ It is important to be aware in this respect that the research on identity, diasporas and cultural contacts at issue here is currently closely linked to the humanities and cultural studies, which means that the extensive criticism of genetic anthropology is also an expression of internal conflicts within archaeology.

However, academic primacy, and with it the prerogative of interpretation, are also at stake. Over the last few decades archaeology has held clear title to these for the period of what is called pre- and proto-history. A new and very ambitious player has entered the arena recently though, one that has reaped a great deal of premature praise and garnered stupendous amounts of research funding. Struggles for recognition and in defense of status, i.e., statements within the scope of identity politics, are to be expected here, but they should not be permitted to distract scholars from their proper work for long. A historical comparison with the situation associated with the introduction of radiocarbon analysis,¹¹⁷ and also with that during the establishment of medieval archaeology as distinct from or as part of the field of history,¹¹⁸ would certainly bring to light many interesting parallels and identify certain pitfalls we should watch out for.

In my view, however, if the desired genuine collaboration between archaeology and genetic anthropology is to take place, it is important that scholars on both sides become familiar with the epistemological, methodological, conceptual and terminological¹¹⁹ differences

112 Becher, *Academic Tribes and Territories*; resp. Becher and Trowler, *Academic Tribes and Territories*.

113 Snow, *Two Cultures*; cf. Kreuzer, *Literarische und naturwissenschaftliche Intelligenz*; Reinalter, *Natur- und Geisteswissenschaften*.

114 Meier and Tillessen, *Von Schlachten, Hoffnungen und Ängsten*, 26-27; cf. Bachmaier and Fischer, *Glanz und Elend der zwei Kulturen*; Mittelstraß, *Häuser des Wissens*.

115 Pluciennik, *Clash of Cultures?*; Samida in: Eggert and Samida, *Zum historischen Potential des Materiellen*, 199-200; cf. but without mentioning Snow: Samida and Eggert, *Über Interdisziplinarität*; Samida and Eggert, *Archäologie als Naturwissenschaft?*.

116 Succinctly characterized by Ulrich Veit as *archaeologist-as-scientist* and *archaeologist-as-author* (Veit, »Mission Impossible!«, 100); cf. Gramsch, *Jenseits der »Zwei Kulturen«*. There is a certain trend towards new holistic approaches though, e. g. Hofmann, *Anthropologie als umfassende Humanwissenschaft*; Hodder, *Entangled*; Kristiansen, *Genes versus Agents*.

117 Cf. Delley, *Au-delà des chronologies*; Delley, *Long Revolution of Radiocarbon*; Renfrew, *Before Civilization*.

118 Cf. Dymond, *Archaeology and History*; Jankuhn and Wenskus, *Geschichtswissenschaft und Archäologie*; esp. Wenskus, *Randbemerkungen*; Burmeister and Müller-Scheeßel, *Fluchtpunkt Geschichte*.

119 Just by way of example, let me refer here to the different meanings of the words *colonization* and *origins*, which frequently result in misunderstandings; see also Gautier, *Du danger des mots transparents*; Hofmann, *What Have Genetics Ever Done for Us?*, 460.

between the two academic subjects, as well as with the differences associated with pragmatic concerns that arise from the differing research traditions. With this knowledge, we will hopefully be able to work together to overcome those differences in practice and to use them constructively.¹²⁰ The scope of this paper allows no more than a brief list of a few points of divergence in simple terms:¹²¹ there are differing epistemological positions (constructivism vs. realism); different sources and their ties to individuals and groups; differences in research strategies when dealing with complexity (starting with initially simple/testable vs. already complex hypotheses); different focuses on geographical and chronological units; and, last but not least, differing traditions with respect to publications and lecture styles (*Fig. 3*). Together, these hold out more than enough potential to result in a failure to understand or misunderstand, but also for polemics, such as those launched from both sides in recent years in the battle over attention, funding or simply the »right« way to conduct research.¹²²

	archaeology - humanistic branch	genetic anthropology
epistemology	constructivism	realism
research strategy	like to deal with the already complex	from simple hypotheses and dichotomizing question to complexity; major focus on testability
data	material culture (produced and used by various persons and communities)	genes (within individual bodies, passed from generation to generation)
scales (geographical, chronological)	focus on the local, regional decades/centuries	focus on the global/continental/national milleniums
publishing traditions	slow; long papers or books, single authors; regional journals; multilingual; main results normally at the end of the paper (conclusion)	quick; preliminary results, short papers, many contributors; international journals; English; main results normally at the beginning of the paper
lecture style	reading out fully formulated texts, text-heavy presentations	free speech, structured, many statistics

Fig. 3: Differences in the research between the humanistic branch of archaeology and that of genetic anthropology

120 A similar call was issued by de Chadarevian, *Genetic Evidence and Interpretation*, 302; Cf. Fuest, *Ethnologie in der Arena*; Schmidt, *Towards a Philosophy of Interdisciplinary*.

121 Cf. Brown and Pluciennik, *Archaeology and Human Genetics*, 103-104.

122 E.g., Evison, *Genetics, Ethics and Archaeology*; Hedges, *Comment*; Mirza and Dungworth, *Potential Misuse of Genetic Analyses*; Pluciennik, *Genetics, Archaeology and the Wider World*. Cf. de Chadarevian, *Genetic Evidence and Interpretation*. Unfortunately, in my opinion, these also include a statement made in the announcement of a joint workshop for geneticists, historians and archaeologists: »These geneticists promise answers: using analysis of DNA to discover what »really« happened during the Bronze Age and the Viking sagas and replace »biased« histories with cold, hard data« (Nature Publishing Group, Source Material).

Conclusion: Should we stay with or leave the troubled helix?

Yet is it sensible for us, as archaeologists, to continue to actively engage with the »troubled helix«¹²³ and its study at all? Might it be better for us to simply ignore it – due, e.g., to time considerations or the complexity involved? Let me refer to an expression from Donna Haraway that the cultural anthropologist Katharina Schramm recently introduced to the discussion about new technologies and old categories: »staying with the trouble«.¹²⁴ In the past, scholars, particularly German-speaking archaeologists, spent far too much time refining problem-avoidance strategies and, as a result, failed to adequately fulfill their actual social task. Although much has been done in recent years – as many new projects demonstrate, including those studying the Vikings in Great Britain – the situation remains complicated. This should certainly have become apparent through my comments about the widely diverging practices associated with the constitution and assertion of identities. Like Donna Haraway, though, I see it as our common task and challenge to develop methods and theories that are both testable and capable of analytically capturing the complexity of life,¹²⁵ and to find descriptions that are not reductionist or redundant, or both.¹²⁶ Many geneticists take up master narratives and categories that were formulated and shaped in the past by historians and archaeologists. In this respect, we historians and archaeologists must demonstrate the same sense of responsibility that we are now demanding from geneticists. We must do so not only in our academic publications on our research findings, but also in the popular works we write on those topics.¹²⁷ In other words, we have to make our research more easily accessible to and more easily comprehensible by both the scientific community and the general public in a way that limits the potentials for distortion and political instrumentalization.

The constructivist concept of identity often preferred by scholars of humanities and the social sciences these days is weighted with discourse and voluntarism. To avoid earlier biologisms, and due to our current sociopolitical situation, we have tended to ignore our bodies as well as other so-called biological factors. This is not without its dangers over the long term however. On the contrary, it has become imperative that we join together to subject certain questions to rigorous scrutiny, such as how the body and identity or sexual and social reproduction interact with and shape one another.¹²⁸ This task requires us to go beyond modernity's binary distinction between the biological and the social.

Through my discussion of the case of Vikings and the research on them, I have also shown how we have, by using semantic shorthand and applying one shared name, facilely equated – and without considering the interactions among them – historical, linguistic, narratological and socio-cultural and biological entities whose natures are defined quite differently. This error has often been coupled with a naturalization and essentialization of identities. Yet what is interesting, in my opinion, is not the existence of identities, but their *historicization*, the highly complex interplay among the widest variety of actors and elements and the doing und undoing of differences.¹²⁹

123 Marteau and Richards, *Troubled Helix*.

124 Haraway, *When Species Meet*; Haraway, *When Species Meet*; Schramm, *Neue Technologien*, 235.

125 See also Grupe and Harbeck, *Isotopen- und DNA-Analysen*, 22.

126 Haraway, *When Species Meet*; cf. Lidén and Eriksson, *Archaeology vs. Archaeological Science*.

127 Wiwjorra, *Ethnische Anthropologie*, 140.

128 Voss, *What's New?*, 663-664.

129 Cf. Hirschauer, *Un/doing Differences*; Pohl, *Comparing Communities*.

We are still all too often falling victim to numerous identity traps (most of which we ourselves constructed), whether they take the form of such historical designations as *vikingr*, which we use for multiple referents and interpret in ethnic terms, ignoring other aspects; or the forms of old myths, categories, concepts or axioms; or even the pitfalls that result from the boundaries established between academic fields. The systematic exposure of these traps would take us an important step in the right direction. Studies in the sociology of knowledge and the history of science and scholarship, as well as ideology-critical questioning, can surely contribute here. But the examination of whether a cultural marker in a specific region, such as an inherited name, is also associated with shared gene patterns, can also further this project. Moreover, a combination of different bio-archaeological investigations, such as analyses of modern and ancient DNA, as well as stable isotope analyses, would certainly also be helpful for the study of protohistory.¹³⁰ It would allow researchers to grapple with the question, still too rarely asked, of how large-scale population movements interact with the spatial and social mobility of individuals.¹³¹ Another promising approach, in my view, would be to attempt to tell not one sweeping meta-narrative of the kind so often dominated by the history of events, but a multitude of different stories that would more accurately reflect differing approaches and varying quality of our sources. The plausibility of these stories could then be assessed case by case, rather than universally. Hence, we have a great deal of work to do: conferences like »Genetic History: A Challenge to Historical and Archaeological Studies« can shed light on the various pitfalls and, hopefully, contribute to more intense and productive dialog.

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130 Hofmann, *What Have Genetics ever Done for Us?*, 464.

131 Müller puts this in similar terms (Müller, Kossinna, Childe and aDNA, 36).

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Genetic History and Identity: The Case of Turkey

Celine Wawruschka*

With the rise of genetic studies of human history over the last two decades, criticism has arisen among the disciplines traditionally concerned with this subject, i.e. anthropology, archaeology and history. This criticism is concerned with the biological construct of historical communities – whether they be called tribes, (ethnic) groups, migrants or populations – that neglects decades of scholarly discourse on these matters by transferring these entities into primarily biological spheres. This essay is based on a systematic analysis of scientific articles reporting genetic research in the context of the history of what is now Turkey. Analysing the structure, methods and contents of this genetic research from the perspective of an archaeologist and historian, I discuss the issue of past and present identity according to both sampling criteria and the major research question, i.e. the Central Asian origin of the Turks.

Keywords: genetics; history; identity; sampling; Anatolia; Central Asian origin.

Introduction

Genetic history, the topic of this thematic volume and the preceding conference in Berlin in October 2015, is but one of several terms – such as Anthropological Genetics¹, Archaeogenetics², Historical Genetics³, Molecular Anthropology⁴ or Population Genetics – that attempt to reconstruct not only human evolution but also the history of human populations and peopling processes through genetic information.⁵

Encountering genetic history for the first time several years ago, I did so in an exclusively non-European context. What intrigued me most – to give but one example – was the socio-political dimension of projects that attempted to correlate geographical, linguistic and genetic borders in troubled regions such as the Caucasus,⁶ and the societal and political consequences the results might bear. This led me to consider the origin of such research questions, the composition of research teams that pursued them, the institutions that funded them, and the dissemination and use of their results. Additionally, genetics, as part of biotechnologies, plays a slightly different role in advanced developing countries, as Yulia

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1 See e.g. Sommer, *DNA and Cultures of Remembrance*.

2 Renfrew and Boyle, *Archaeogenetics*.

3 Renfrew, *Archaeology, Genetics and Linguistic Diversity*, 446.

4 See e.g. Destro-Bisol *et al.*, *Molecular Anthropology in the Genomic Era*.

5 The coinage of ›genetic history‹ may be ascribed to a division of the relevant disciplines in German-speaking countries, whereas in English-speaking countries anthropology essentially comprises all the disciplines that are involved in human history, physically, socially and culturally.

6 Nasidze and Stoneking, *Mitochondrial DNA Variation*.

Egorova shows with the example of India.⁷ The development of science and technology serves not only to become a power to reckon with in the international arena, it is also often allied to nationalist efforts to overcome past humiliations and install a national identity and political ambition.⁸ I would like to add here that not only the state but also the general public in advanced developing countries shows a greater openness to new technologies and their applications as a whole as they are regarded part of the modernisation process. It seemed reasonable then to address these questions in relation to the framework of a current nation state and advanced developing country – Turkey.⁹

Genetic studies in Turkey

For the study at hand, I analysed 24 genetic research articles from high impact journals, published from 1996 to 2016 (*Fig. 1*), according to two selection criteria: the studies should have (1) exhibited a historical research question, and (2) involved genetic data from Turkey,¹⁰ including studies that relied on genetic data collected by earlier studies or databases of any kind whatsoever.¹¹ The studies were analysed according to their structure (composition of research teams, funding, place of publication), their methods (sampling, analysis methods, references to historical literature) and their content (research questions, results/interpretations).

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- 7 Egorova, *The Substance that Empowers*. For the analysis of genetic studies on other non-European countries and regions see, for example, MacEachern, *Genes, Tribes and African History*; Sanchez-Mazas *et al.*, *Genetic Focus on the Peopling History of East Asia*.
- 8 Ong, *Introduction*.
- 9 Additionally, in Africa and the Middle East, Turkey has the biggest market for gene expression services that is continually increasing (Parker, 2009-2014 *World Outlook*, 11, 61. See also TÜBITAK, *Special Focus*).
- 10 Alkan *et al.*, *Whole Genome Sequencing of Turkish Genomes*; Arnaiz-Villena *et al.*, *HLA Alleles and Haplotypes in the Turkish Population*; Berkman *et al.*, *Alu Insertion Polymorphisms*; Berkman *et al.*, *Asian Contribution to the Turkish Population*; Calafell *et al.*, *From Asia to Europe*; Cinnioğlu *et al.*, *Excavating Y-Chromosome Haplotype Strata in Anatolia*; Comas *et al.*, *Geographic Variation in Human Mitochondrial DNA*; Di Benedetto *et al.*, *DNA Diversity and Population Admixture*; Gokcumen *et al.*, *Biological Ancestries, Kinship Connections, and Projected Identities*; Hodoğlugil and Mahley, *Turkish Population Structure and Genetic Ancestry*; Machulla *et al.*, *Genetic Affinities among Mongol Ethnic Groups*; Mergen *et al.*, *Mitochondrial DNA Sequence Variation*; Omrak *et al.*, *Genomic Evidence*; Ottoni *et al.*, *Mitochondrial Analysis of a Byzantine Population*; Ottoni *et al.*, *Comparing Maternal Genetic Variation*; Quintana-Murci *et al.*, *Where West Meets East*; Rasterio and Chikhi, *Female and Male Perspectives*; Richards *et al.*, *Tracing European Founder Lineages*; Rosser *et al.*, *Y-Chromosomal Diversity*; Schönberg *et al.*, *High-Throughput Sequencing*; Torroni *et al.*, *A Signal from Human mtDNA*; Underhill *et al.*, *Phylogenetic and Geographic Structure*; Wells *et al.*, *Eurasian Heartland*; Yunusbayev *et al.*, *Genetic Legacy*.
- 11 Four studies were not included to this analysis: In one study, aDNA was extracted from 100 bones from a site in Borkuçu, Muğla, dating to various periods of Classical Antiquity; however, the study addressed only technological aspects of the extraction procedure (Vural and Tirpan, *Comparison and Development*). Similarly, Arslan *et al.* focused on texting sex determination with morphological and genetic methods, extracting sDNA of Bronze Age individuals from Oylum Höyük (Arslan *et al.*, *Optimization of aDNA Extraction Protocol*). Furthermore, I did not consider another study that lacked a historical research question (Çakır *et al.*, *Y-STR Haplotypes in Central Anatolia*). This study was only concerned with the method of aDNA extraction. Another study was improved and reprinted in 2009 (Berkman and Togan, *Asian Contribution to the Turkish Population*), therefore I considered only the latter.

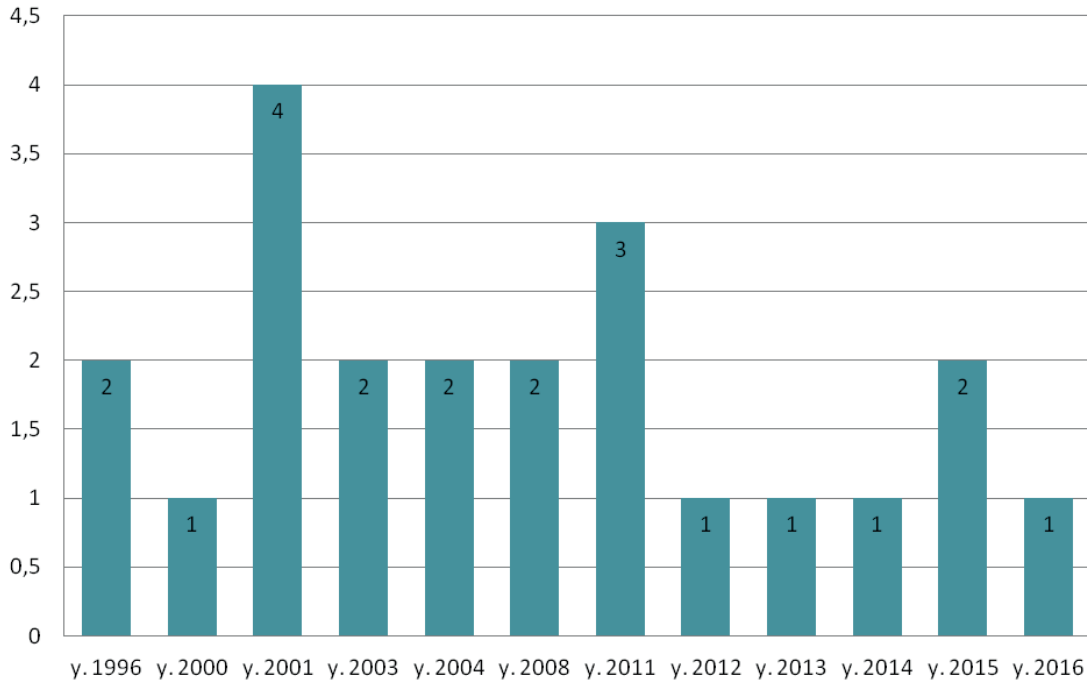


Fig. 1: Dates of publication

Structure: composition of research teams, funding, place of publication

The composition of research teams was determined according to the authors' institutional affiliation at the time of the study. Eleven studies (46%) had no Turkish participation;¹² nine studies (37%) were conducted by an international project with Turkish participation;¹³ and four studies (17%) were solely Turkish projects (Fig. 2).¹⁴ Interestingly, no international study has been conducted under Turkish project leadership. This composition of research teams did not change throughout the period investigated.

12 Ottoni *et al.*, Mitochondrial Analysis of a Byzantine Population; Ottoni *et al.*, Comparing Maternal Genetic Variation; Quintana-Murci *et al.*, Where West Meets East; Rasterio and Chikhi, Female and Male Perspectives; Richards *et al.*, Tracing European Founder Lineages; Schönberg *et al.*, High-Throughput Sequencing; Torroni *et al.*, A Signal from Human mtDNA; Underhill *et al.*, Phylogenetic and Geographic Structure; Wells *et al.*, Eurasian Heartland; Yunusbayev *et al.*, Genetic Legacy.

13 Calafell *et al.*, From Asia to Europe; Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia; Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities; Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry; Machulla *et al.*, Genetic Affinities among Mongol Ethnic Groups.

14 Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes; Berkman *et al.*, Alu Insertion Polymorphisms; Berkman *et al.*, Asian Contribution to the Turkish Population; Mergen *et al.*, Mitochondrial DNA Sequence Variation.

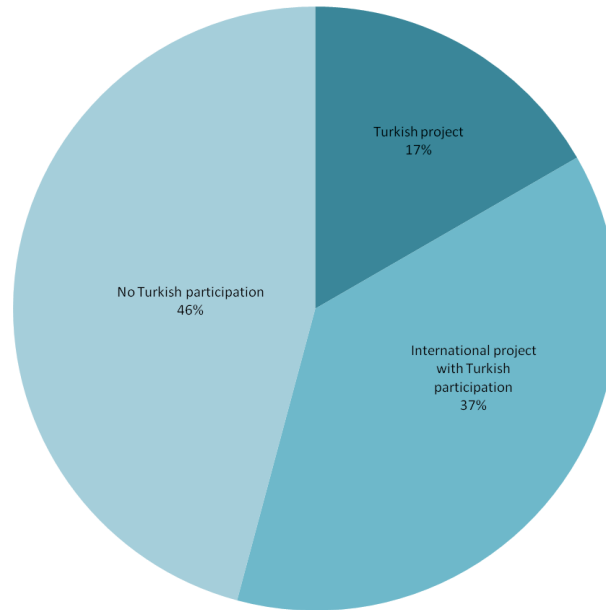


Fig. 2: Composition of research teams

Gathering the data on funding, it became evident that the result appears to be considerably different when including large international projects with many different (and mostly single) national collaborators. Such research projects exhibit research questions that cover at least a continent. As soon as these studies are added to the analysis, a good amount of smaller national or university funding comes in, that supported in nearly all the cases only one of the co-authors and only once. Therefore, I excluded the three studies of this kind from the analysis on funding.¹⁵

The remaining 21 genetic studies on Turkey were funded by 49 research institutions from thirteen different countries and the European Union (Table 1, Fig. 3). Most of the genetic research on Turkey has been funded by Italian institutions: ten funding institutions sponsored five studies.¹⁶ Four of these funding institutions were state-owned (Beni Culturali, Fondo per gli Investimenti della Ricerca di Base, Italian Ministry of Universities, National Research Council of Italy), five were university funds (universities of Ferrara, Pavia, Rome, Urbino and the Italian Consortium of Universities, all of which are public universities) and one was private (*Fondazione Telethon*). Whereas the private institution and the university funds all sponsored only one research project each, the state-owned institution (National Research Council of Italy, *Progetti Ricerca Interesse Nazionale*) funded three or four projects (*Beni Culturali*, Italian Ministry of Universities) respectively.

15 Rosser *et al.*, Y-Chromosomal Diversity; Underhill *et al.*, Phylogenetic and Geographic Structure; Yunusbayev *et al.*, Genetic Legacy.

16 Quintana-Murci *et al.*, Where West Meets East; Rasterio and Chikhi, Female and Male Perspectives.

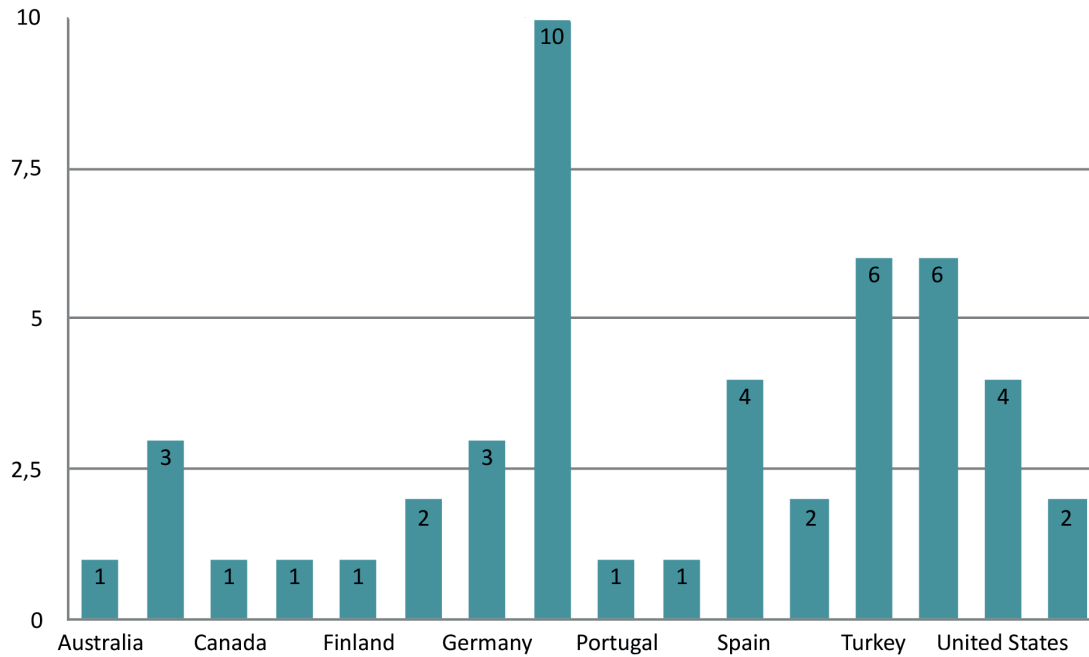


Fig. 3: Funding according to countries (including the European Union)

Six different institutions from Turkey have funded seven different genetic studies of which four were solely Turkish projects¹⁷ and three were international projects with Turkish participation¹⁸. Four of the Turkish funding institutions were university funds (Ankara University, Boğaziçi University, Hacettepe University and Middle Eastern Technical University), three projects were funded by the national research agency, The Scientific and Technological Research Council of Turkey (*Türkiye Bilimsel ve Teknolojik Araştırma Kurumu, TÜBİTAK*) and one by the Turkish State Planning Administration (*Devlet Planlama Teşkilatı, DPT*), one of the most important governmental organizations in Turkey that provides advice to the government on economic, social and cultural state goals. Thus, funding from Turkey derived entirely from state resources.

Six different genetic studies received funding from four different institutions in the United Kingdom,¹⁹ of which the Wellcome Trust sponsored three studies, the Royal Society and the Leverhume Trust two apiece, and the Imperial Cancer Research Fund and the Medical Research Council one each. With the exception of the *Royal Society*, the funding institutions from the United Kingdom are private.

17 Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes; Berkman *et al.*, Alu Insertion Polymorphisms; Berkman *et al.*, Asian Contribution to the Turkish Population; Mergen *et al.*, Mitochondrial DNA Sequence Variation.

18 Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities.

19 Ottoni *et al.*, Comparing Maternal Genetic Variation; Quintana-Murci *et al.*, Where West Meets East; Richards *et al.*, Tracing European Founder Lineages; Torroni *et al.*, A Signal from Human mtDNA; Wells *et al.*, Eurasian Heartland.

Funding institution	Projects
Academy of Finland (FI)	1
Alfred P. Sloan Foundation (US)	1
Belgian Programme on Interuniversity Poles of Attractions (BE)	2
Beni Culturali (IT)	4
Boğaziçi University Research Funds (TR)	1
CNRS (FR)	1
CNRS/NATO Cooperation (FR)	1
Complutense University (ES)	1
Comunidad de Madrid (ES)	1
Department of Forensic Sciences at Ankara University Medical School (TR)	1
Deutsche Forschungsgesellschaft (DE)	1
Deutscher Akademischer Austauschdienst (DE)	1
Dirección General de Investigación Científica y Técnica (ES)	2
ERC Advances Grant (EU)	1
EU Science and Technology Cooperation (EU)	1
Fondo d'Ateneo, University of Pavia (IT)	2
Fondo per gli Investimenti della Ricerca di Base (IT)	1
Fundação para a Ciência e Tecnologia (PT)	2
Grandi Progetti Ateneo Università di Roma "La Sapienza (IT)"	1
Hacettepe University, Department of Physical Anthropology (TR)	1
Imperial Cancer Research Fund (UK)	1
Italian Ministry of Universities (IT)	4
La Trobe University (AU)	1
Leverhulme Trust (UK)	2
Max Planck Society (DE)	1
Medical Research Council (UK)	1
Middle Eastern Technical University Research Fund (TR)	2
Ministerio de Educación y Ciencia (ES)	1
Ministry of Science and Technology of the Republic of Croatia (HR)	1
National Institutes of Health (US)	6
National Research Council of Italy (IT)	3
Progetti Ricerca Interesse Nazionale (IT)	3
Research Foundation Flanders (BE)	2
Research Fund of the K.U. Leuven (BE)	2
Romanian Ministry of Research and Technology (RO)	1
Royal Society Visiting Fellowship (UK)	1
Royal Society/NATO Postdoctoral Fellowship (UK)	1
Social Sciences and Humanities Research Council (CA)	1
Spanish Ministry of Education (ES)	1
Swedish Foundation for Humanities and Social Sciences (SE)	1
Swedish Research Council (SE)	1
Telethon-Italy (IT)	1
TÜBİTAK (TR)	3
Turkish State Planning Administration (TR)	1
University of Ferrara (IT)	1
University of Pennsylvania (US)	2
University of Urbino (IT)	1
Wellcome Trust (UK)	4
Wenner Gren Foundation (US)	1

Table 1: Number of projects according to funding institutions

Three Belgian institutions funded two genetic studies²⁰, three German institutions sponsored three projects²¹, two French institutions funded two projects²², four Spanish institutions supported five studies²³, two Swedish institutions sponsored one project²⁴ and four US institutions funded four projects²⁵. Funding from Australia, Canada, Croatia, Finland, Portugal and Romania supported in each case only one single project each. Besides solely Turkish projects that were supported only by Turkish institutions, as described above, three more projects received such a ›national‹ funding, each from a German²⁶, a Spanish²⁷ and a US institution²⁸.

All of the 24 studies were published in high impact journals (*Table 2*)²⁹. Only one of these journals covers arts and humanities and social sciences (*American Anthropologist*), one journal addresses sciences and social sciences (*American Journal of Physical Anthropology*), while all of the other journals are dedicated solely to the sciences.

Journal	no. of studies
American Anthropologist	1
American Journal of Human Genetics	4
American Journal of Physical Anthropology	2
Annals of Human Genetics	2
BMC Genomics	1
Current Biology	1
Discrete Applied Mathematics	1
European Journal of Human Genetics	3
Human Genetics	1
Journal of Genetics (Indian Academy of Sciences)	1
Molecular Biology and Evolution	1
PLOS Genetics	1
PLOS ONE	1
PNAS (Proceedings of the National Academy of Sciences)	1
Royal Society Open Access	1
Tissue Antigens	2

Table 2: Places of publications and numbers of studies

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- 20 Ottoni *et al.*, Mitochondrial Analysis of a Byzantine Population; Ottoni *et al.*, Comparing Maternal Genetic Variation.
- 21 Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Schönberg *et al.*, High-Throughput Sequencing; Richards *et al.*, Tracing European Founder Lineages.
- 22 Quintana-Murci *et al.*, Where West Meets East; Rasterio and Chikhi, Female and Male Perspectives.
- 23 Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population; Calafell *et al.*, From Asia to Europe; Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Rosser *et al.*, Y-Chromosomal Diversity; Torroni *et al.*, A Signal from Human mtDNA.
- 24 Omrak *et al.*, Genomic Evidence.
- 25 Calafell *et al.*, From Asia to Europe; Cinnioglu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia; Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities; Omrak *et al.*, Genomic Evidence.
- 26 Schönberg *et al.*, High-Throughput Sequencing, from the Max Planck Society.
- 27 Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population, from the Spanish Ministry of Education and the Comunidad de Madrid.
- 28 Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry, from the National Health Institute.
- 29 In accordance with the San Francisco Declaration on Research Assessment (see www.ascb.org/dora/; retrieved 27 August 2016), I refrained from listing the journals' impact factor.

Methods: sampling, analysis methods, references to historical literature

Sampling was defined not only as the geographical region from which the samples were obtained, but also where and how the researchers acquired the tissue samples or genetic data – whether they were obtained from a tissue or databank, collected at a hospital or were already in the researcher’s possession.

Three studies analysed ancient DNA (aDNA),³⁰ one study combined modern and aDNA by using one of the largest aDNA datasets available.³¹ The remaining 20 studies drew their conclusions from modern DNA (*Fig. 4*). Eight of the studies that analysed modern DNA generated it from blood samples only (33%),³² one study amplified DNA from hair roots (4%),³³ one from a combination of blood and buccal samples (4%)³⁴ and another one from a combination of blood samples, saliva samples and buccal swab (4%)³⁵. Of these 20 studies, one obtained DNA from the Turkish Heart Study,³⁶ one from the International Society of Genealogy database³⁷ and another one from two laboratories in Istanbul where the samples were already typed.³⁸ Five studies did not specify the nature of their samples³⁹, three studies did not specify the nature of their samples and combined their data with data from literature,⁴⁰ and two studies relied entirely on samples from literature⁴¹; these nine studies were summarised in one category (42 %).⁴² The three studies that analysed aDNA extracted it from excavated bones or bones and teeth respectively (9 %)⁴³ (*Fig. 5*).

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- 30 Omrak *et al.*, Genomic Evidence; Ottoni *et al.*, Mitochondrial Analysis of a Byzantine Population; Ottoni *et al.*, Comparing Maternal Genetic Variation.
- 31 Rasterio and Chikhi, Female and Male Perspectives.
- 32 Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes; Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population; Calafell *et al.*, From Asia to Europe; Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry; Machulla *et al.*, Genetic Affinities among Mongol Ethnic Groups; Mergen *et al.*, Mitochondrial DNA Sequence Variation.
- 33 Comas *et al.*, Geographic Variation in Human Mitochondrial DNA.
- 34 Berkman *et al.*, Alu Insertion Polymorphisms.
- 35 Schönberg *et al.*, High-Throughput Sequencing.
- 36 Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry, 129.
- 37 Underhill *et al.*, Phylogenetic and Geographic Structure, 126.
- 38 Machulla *et al.*, Genetic Affinities among Mongol Ethnic Groups, 293.
- 39 Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities; Quintana-Murci *et al.*, Where West Meets East; Rosser *et al.*, Y-Chromosomal Diversity («collections from the authors»); Torroni *et al.*, A Signal from Human mtDNA; Wells *et al.*, Eurasian Heartland.
- 40 Richards *et al.*, Tracing European Founder Lineages; Underhill *et al.*, Phylogenetic and Geographic Structure; Yunusbayev *et al.*, Genetic Legacy.
- 41 Berkman and Togan, Asian Contribution to the Turkish Population; Rasterio and Chikhi, Female and Male Perspective.
- 42 Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities; Wells *et al.*, Eurasian Heartland.
- 43 Omrak *et al.*, Genomic Evidence; Ottoni *et al.*, Mitochondrial Analysis of a Byzantine Population. Ottoni *et al.*, Comparing Maternal Genetic Variation.

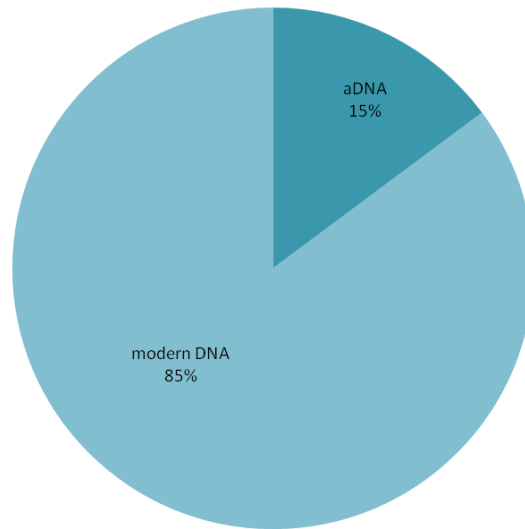


Fig. 4: Percentage of studies with aDNA and modern DNA

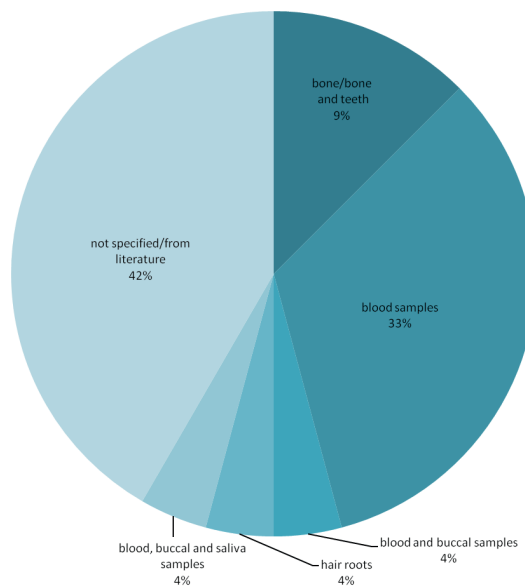


Fig. 5: Provenance of samples

The ›Turkish‹ feature of DNA samples is generally inferred from the geographic origin of the samples.⁴⁴ Information on the geographic origin of samples varies from simply ›Turkey‹⁴⁵ or ›a large territory of Turkey excluding main cities and coastal areas‹⁴⁶ or ›Anatolia‹⁴⁷, to regions in Anatolia⁴⁸, unspecified villages in Anatolia⁴⁹ or specified cities⁵⁰ or unspecified cities in Turkey⁵¹. In several studies, regional aspects formed an additional criterion in the sampling. Three research teams tried to avoid urban areas due to ›a higher probability to be recent (im)migration‹⁵² or to ›ensure the autochthony of the sample‹⁵³ when sampling in villages and rural areas. Four studies, on the other hand, collected their samples in urban areas.⁵⁴ Two studies added language to geographical features as an expression of Turkishness.⁵⁵ Three studies affiliated the Turkishness of their samples primarily or entirely with language, either by excluding non-Turkish speakers⁵⁶ or by establishing sampling criteria according to language families and languages.⁵⁷ One study assessed the Turkish feature in sampling via self-assessed ancestry of the donors.⁵⁸

Among the 15 studies in which the origin and nature of samples were given seven emphasised the fact that the donors were ›not related individuals‹⁵⁹ or ›not related and healthy‹⁶⁰ respectively. Two studies were careful to generate DNA from healthy individuals.⁶¹ In one

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- 44 Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes; Berkman *et al.*, Alu Insertion Polymorphisms; Calafell *et al.*, From Asia to Europe; Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia; Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry; Machulla *et al.*, Genetic Affinities among Mongol Ethnic Groups; Mergen *et al.*, Mitochondrial DNA Sequence Variation; Richards *et al.*, Tracing European Founder Lineages; Schönberg *et al.*, High-Throughput Sequencing; Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities; Torroni *et al.*, A Signal from Human mtDNA.
- 45 Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes; Richards *et al.*, Tracing European Founder Lineages; Torroni *et al.*, A Signal from Human mtDNA.
- 46 Calafell *et al.*, From Asia to Europe.
- 47 Machulla *et al.*, Genetic Affinities among Mongol Ethnic Groups.
- 48 Berkman *et al.*, Alu Insertion Polymorphisms; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Mergen *et al.*, Mitochondrial DNA Sequence Variation.
- 49 Comas *et al.*, Geographic Variation in Human Mitochondrial DNA.
- 50 Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry; Schönberg *et al.*, High-Throughput Sequencing.
- 51 Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia.
- 52 Calafell *et al.*, From Asia to Europe, 37; Di Benedetto *et al.*, DNA Diversity and Population Admixture, 145.
- 53 Comas *et al.*, Geographic Variation in Human Mitochondrial DNA, 1068.
- 54 Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia, 128; Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry, 129; Schönberg *et al.*, High-Throughput Sequencing, 989; Quintana-Murci *et al.*, Where West Meets East, 828.
- 55 Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Di Benedetto *et al.*, DNA Diversity and Population Admixture.
- 56 Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population, 309.
- 57 Wells *et al.*, Eurasian Heartland, 10244; Yunusbayev *et al.*, Genetic Legacy, 5.
- 58 Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities.
- 59 Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population, 309; Di Benedetto *et al.*, DNA Diversity and Population Admixture, 145; Comas *et al.*, Geographic Variation in Human Mitochondrial DNA, 1068; Berkman *et al.*, Alu Insertion Polymorphisms, 12.
- 60 Mergen *et al.*, Mitochondrial DNA Sequence Variation, 40; Quintana-Murci *et al.*, Where West Meets East, 828.
- 61 Calafell *et al.*, From Asia to Europe, 36 (›unaffected families with common Mendelian disorders‹); Wells *et al.*, Eurasian Heartland, 10244.

study, the mother's birthplace was additionally recorded,⁶² one study documented the birth place of the paternal grandfather,⁶³ one study the donor's birthplace,⁶⁴ one the paternal residency⁶⁵ and one study the birthplace of the donors, their parents and their grandparents.⁶⁶ Finally, one study tried to avoid donors from ethnic minorities.⁶⁷

In only 15 of 24 studies (68%) were the absolute numbers of samples given.⁶⁸ The ratio of Turkish samples to the total samples of these 15 studies is shown in Figure 6, with the exception of Torroni *et al.*'s study, as its total sample number is so large that it would have undermined all the other studies on this illustration.⁶⁹

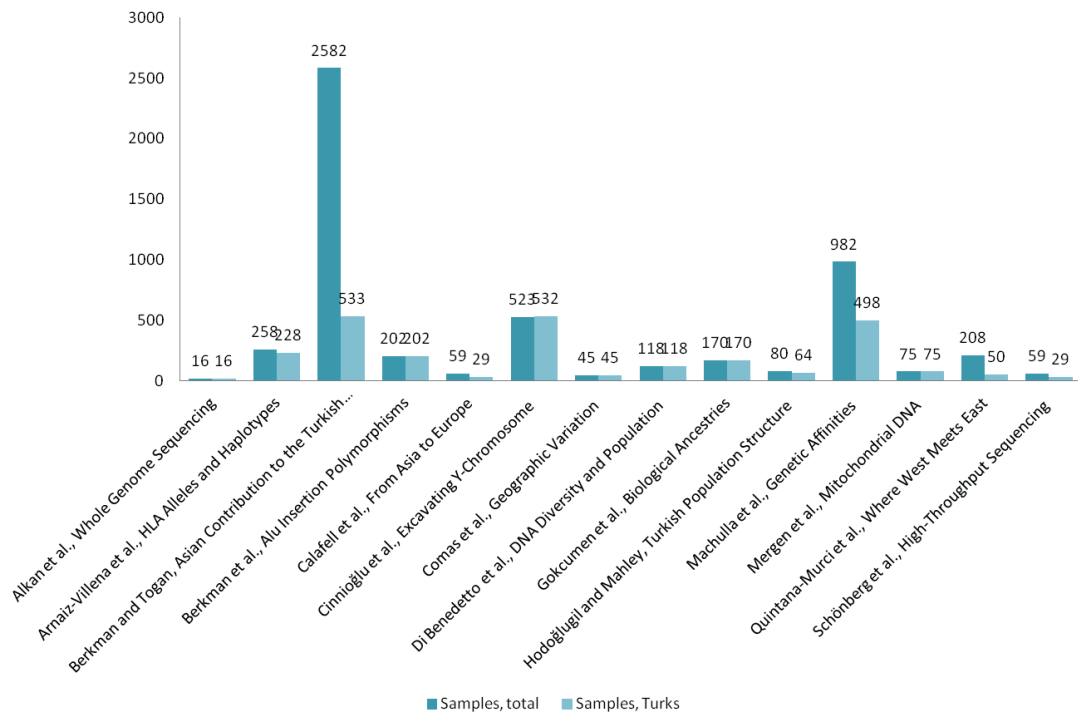


Fig. 6: Ratio of Turkish samples to the total amount of samples

62 Comas *et al.*, Geographic Variation in Human Mitochondrial DNA, 1068.

63 Rosser *et al.*, Y-Chromosomal Diversity, 1528.

64 Calafell *et al.*, From Asia to Europe, 37.

65 Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia, 128.

66 Schönberg *et al.*, High-Throughput Sequencing.

67 Calafell *et al.*, From Asia to Europe, 36.

68 Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes; Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population; Berkman and Togan, Asian Contribution to the Turkish Population; Berkman *et al.*, *Alu* Insertion Polymorphisms; Calafell *et al.*, From Asia to Europe; Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia; Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities; Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry; Machulla *et al.*, Genetic Affinities among Mongol Ethnic Groups; Quintana-Murci *et al.*, Where West Meets East; Schönberg *et al.*, High-Throughput Sequencing; Torroni *et al.*, A Signal from Human mtDNA.

69 Torroni *et al.*, A Signal from Human mtDNA, had a panel of 10,365 individuals from 56 populations of western Eurasia and northern Africa of which 606 were Turkish samples; this is about four times more total samples than the 2583 samples of Berkman and Togan, Asian Contribution to the Turkish Population, and about 647 times more samples than the study of Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes (see Fig. 6).

Studies of genetic variation in the Turkish population examined mtDNA sequence variation, polymorphic markers on the Y-chromosome, polymorphic loci on autosomal chromosomes, *Alu* insertions (YAP), HLA (Human leukocyte antigen) allele frequencies and whole genome sequences (Fig. 7).

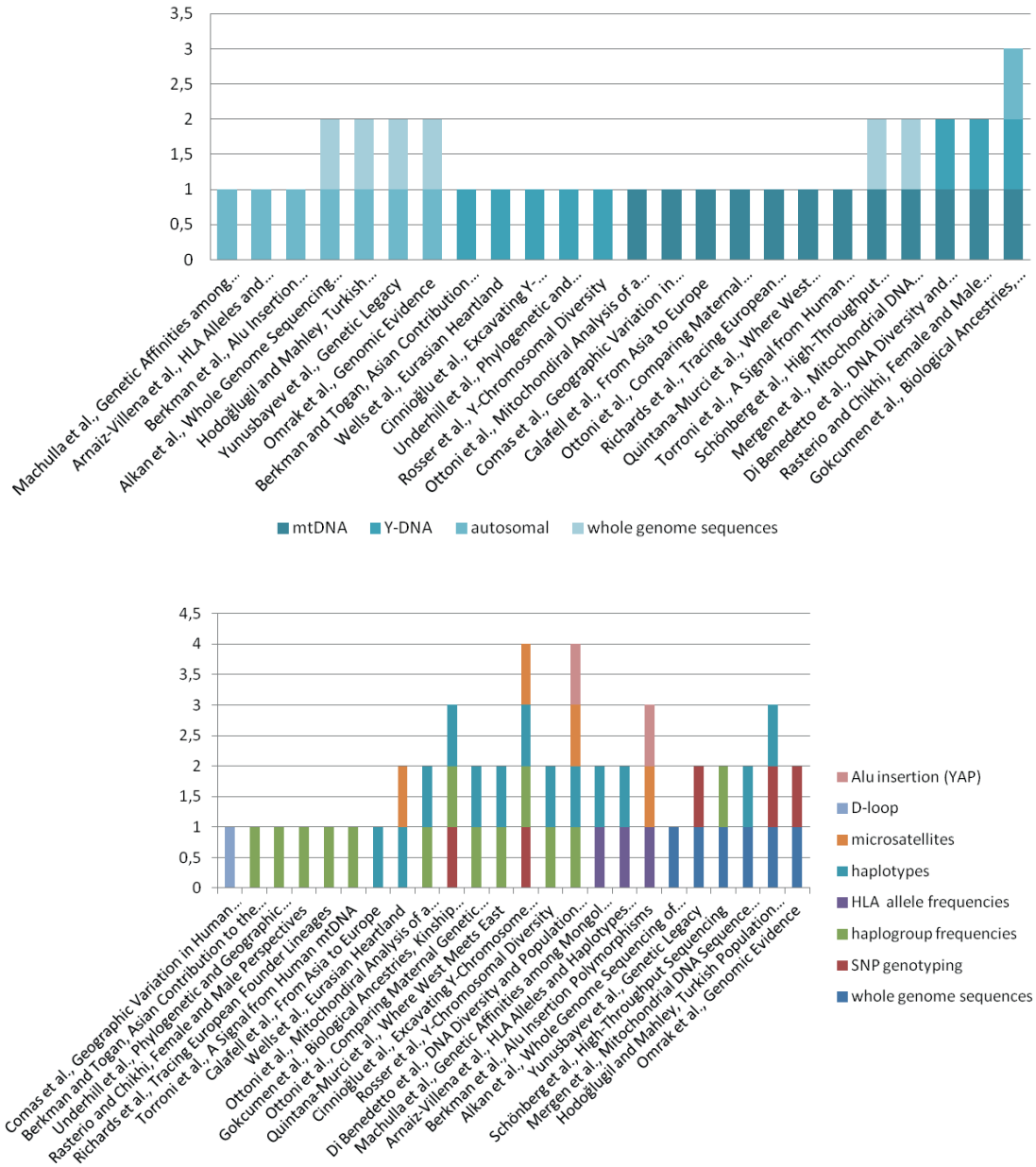


Fig. 7: Elements of DNA analysed

70 Admixture analysis: 2000-2016; phylogenetic trees: 1996-2014; principal component analysis: 2000-2014.

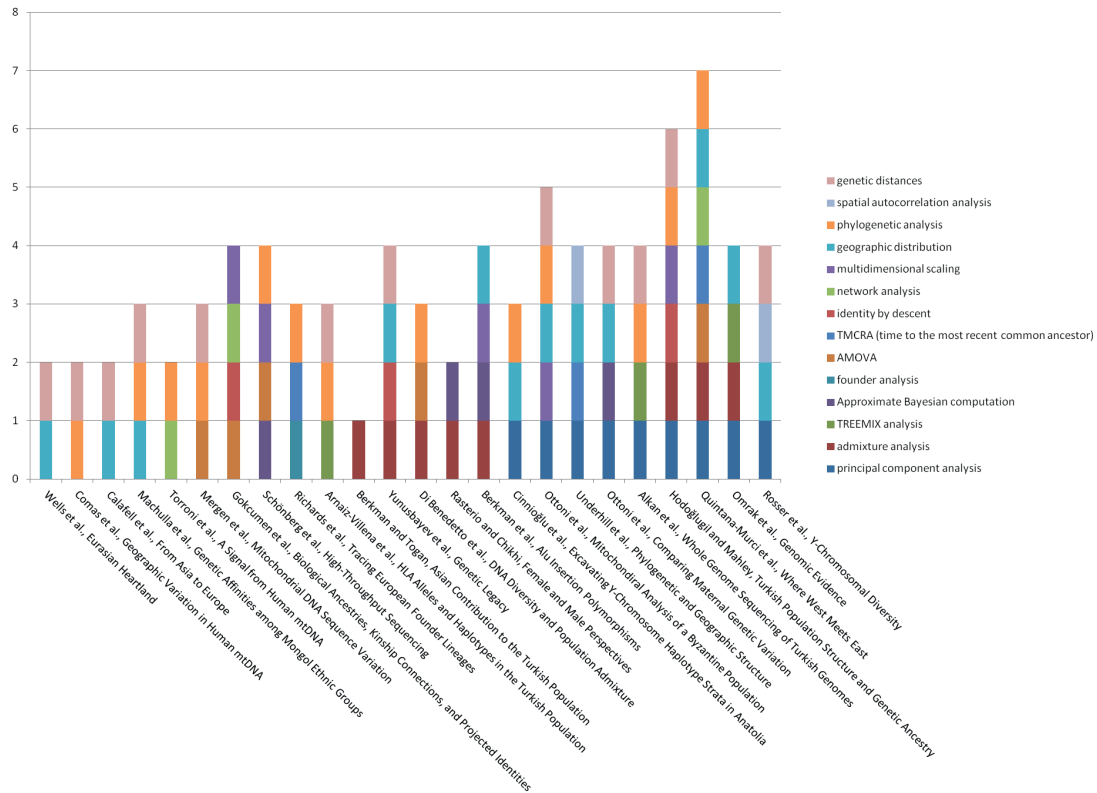


Fig. 8: Biostatistical methods applied

Among biostatistical methods for interpreting the data, three methods were favoured: phylogenetic trees (13 studies), principal component analysis (9 studies) and admixture analysis (8 studies); all of these methods were used throughout the 20 year period investigated (Fig. 8).⁷⁰

All of the genetic studies included in this analysis had an underlying historical research question, and accordingly all of them used historical literature, including archaeological and anthropological scholarship. However, there were differences in the quantity and quality of the historical literature. Compared to all of the references in the bibliographies of each study, the percentage of historical references amounts to between 3% and 59%, with an average of 16% (Fig. 9). The largest share of historical literature was used in the genetic studies that featured an interdisciplinary research setting; one of them displayed a social-anthropological context,⁷¹ two were embedded in an interdisciplinary project in the context of archaeological excavations and additionally analysed aDNA.⁷² One study, which referred to a comparatively great amount of historical literature (27%), consulted somewhat outdated literature as well

71 Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities: 50% of all references.

72 Ottoni *et al.*, Comparing Maternal Genetic Variation: 42%; Ottoni *et al.*, Mitochondrial Analysis of a Byzantine Population: 26 %.

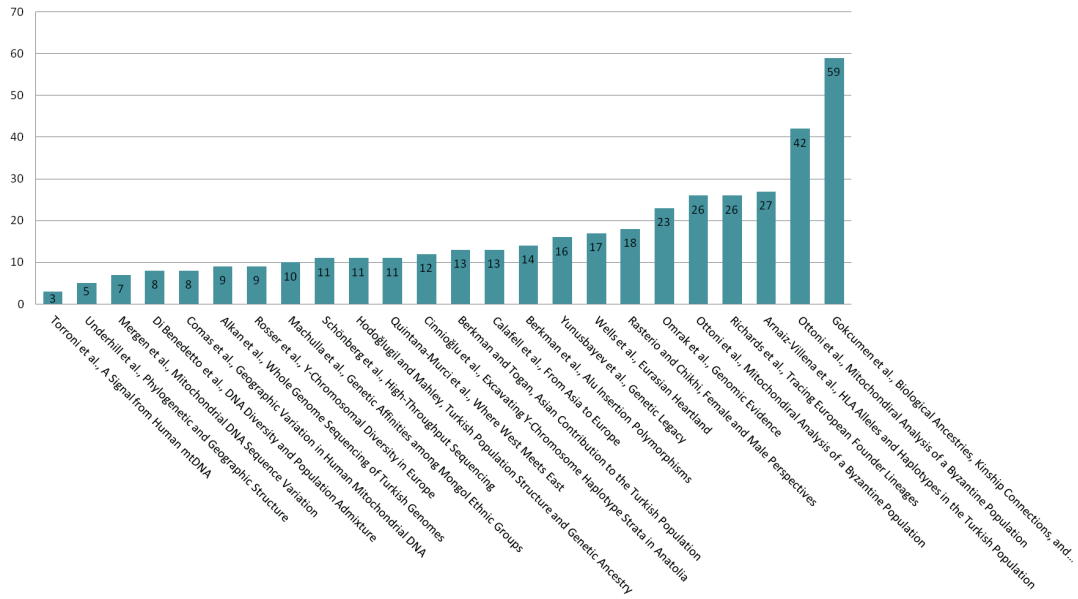


Fig. 9: Quantity of historical references in the studies analysed

as popular scientific literature and exhibited a focus on linguistics.⁷³ Four of the five studies that used the least amount of historical literature favoured historical-linguistic literature as well.⁷⁴ A lower quantity of historical literature, though, does not imply lesser quality: Schönberg *et al.* quoted few references that were all up to date;⁷⁵ Alkan *et al.*, made their point using a lot of literature on population exchanges;⁷⁶ the Rasterio and Chikhi and Richards *et al.* studies were in the mid-range in regards the total amount of referred literature, but also exhibited an excellent choice of historical references in terms of up-to-dateness and diversity.⁷⁷ However, the way the authors made use of historical references in their interpretation of the genetic data differed considerably. Whereas Rasterio and Chikhi used genetic data to shed new light on to two traditional historical models of the Neolithic transition, i.e. the demic and the cultural model, Richards *et al.* referred to historical literature mainly in their introduction but hardly included it in their discussion. The same holds true for Hodoğlugil

73 Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population, 316-317.

74 Torroni *et al.*, A Signal from Human mtDNA; Underhill *et al.*, Phylogenetic and Geographic Structure; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Comas *et al.*, Geographic Variation in Human Mitochondrial DNA – in this order according to the amount of historical literature they used.

75 Schönberg *et al.*, High-Throughput Sequencing.

76 Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes.

77 Rasterio and Chikhi, Female and Male Perspectives; Richards *et al.*, Tracing European Founder Lineages.

and Mahley who made only marginal use of their well-chosen literature on the early Middle Ages.⁷⁸ Mergen *et al.* seems even more intriguing as the selected historical literature focuses on Turkish identity in the past and in the present.⁷⁹ The most popular author referred to was by far Colin Renfrew, being quoted in 12 (of 24) studies with 8 different publications.⁸⁰

Content: research questions, results and interpretation

Two major research questions emerged in the analysed genetic studies: the Central Asian origin (10 studies/25%)⁸¹ and the Anatolian impact on the Neolithic transition (6 studies/41,7%)⁸² – one study aimed to analyse both topics⁸³. The remaining studies exhibited individual research questions (*Table 3*).

Results and interpretations of these two main topics, however, differ considerably, especially on the question of the Central Asian impact on the Turkish gene pool (*Table 4*).

78 Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry.

79 Mergen *et al.*, Mitochondrial DNA Sequence Variation, quoted Güvenç, *Türk Kimliği*, and Roux, *Histoire des Turcs*.

80 Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population; Berkman *et al.*, *Alu* Insertion Polymorphisms; Calafell *et al.*, From Asia to Europe; Cinniöglü *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia; Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Omrak *et al.*, Genomic Evidence; Quintana-Murci *et al.*, Where West Meets East; Richards *et al.*, Tracing European Founder Lineages; Rosser *et al.*, Y-Chromosomal Diversity, Schönberg *et al.*, High-Throughput Sequencing; Wells *et al.*, Eurasian Heartland.

81 Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes; Berkman and Togan, Asian Contribution to the Turkish Population; Berkman *et al.*, *Alu* Insertion Polymorphisms; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Machulla *et al.*, Genetic Affinities among Mongol Ethnic Groups; Cinniöglü *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia; Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Quintana-Murci *et al.*, Where West Meets East; Wells *et al.*, Eurasian Heartland; Yunusbayev *et al.*, Genetic Legacy.

82 Omrak *et al.*, Genomic Evidence; Mergen *et al.*, Mitochondrial DNA Sequence Variation; Rasterio and Chikhi, Female and Male Perspectives; Richards *et al.*, Tracing European Founder Lineages; Rosser *et al.*, Y-Chromosomal Diversity.

83 Cinniöglü *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia.

Research question	Reference
Investigate the complex population history of Turkey via clustering genetic variation with South European and ancestral East Asian populations	Alkan <i>et al.</i> , Whole Genome Sequencing of Turkish Genomes, 1.
Obtain for the first time the Turkish HLA gene profile and characteristic haplotypes, studying the relative contribution of ancient Mediterraneans to the genetic pool of present day Turkish people. A Kurd group is also analyzed and both ethnic groups will be compared with the HLA genetic structure of neighbouring Armenians and other Mediterraneans	Arnaiz-Villena <i>et al.</i> , HLA Alleles and Haplotypes in the Turkish Population, 309.
Male genetic contribution from Central Asia to the Turkish population	Berkman and Togan, Asian Contribution to the Turkish Population, 2341.
Genetic contributions of Central Asia to Anatolia with respect to the Balkans	Berkman <i>et al.</i> , <i>Alu</i> Insertion Polymorphisms, 11.
Gain insight in Turkish and Bulgarian population and knowledge of mtDNA variation in Europe and West Asia	Calafell <i>et al.</i> , From Asia to Europe, 35.
Understand how the succession of events spanning millennia have contributed to the current genetic composition of Turkey to illuminate the Holocene expansions, the contributions of agriculturalists to the European gene pool and the genetic assessment of Caucasian and Central Asian gene flows	Cinnioğlu <i>et al.</i> , Excavating Y-Chromosome Haplotype Strata in Anatolia, 128.
Understand the role of Turkey in the history and making of European populations	Comas <i>et al.</i> , Geographic Variation in Human Mitochondrial DNA, 1068.
Contribution of Central Asian genes to the current Anatolian gene pool	Di Benedetto <i>et al.</i> , DNA Diversity and Population Admixture, 145.
Investigate the influence of recent historical and social dynamics on local population structure and explore their influence on overall Anatolian genetic diversity	Gokcumen <i>et al.</i> , Biological Ancestries, Kinship Connections, and Projected Identities, 117.
Investigate Turkish population structure in relation to Central Asia and Europe	Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry, 128.
Analyse the relationship between three Mongolian populations and their relationship to Turkish and German samples	Machulla <i>et al.</i> , Genetic Affinities among Mongol Ethnic Groups, 293.
Obtain information about the distribution of the existing mitochondrial D-loop sequence variations in the Turkish population of Anatolia which is a junction connecting the Middle East, Central Asia and Europe	Mergen <i>et al.</i> , Mitochondrial DNA Sequence Variation, 39.
Anatolian contribution to the European Neolithic gene pool	Omrak <i>et al.</i> , Genomic Evidence 270.
Investigate whether the historical events of the Plague of Justinian in the 6th century CE, an earthquake in the seventh century CE and the abandonment of Sagalassos around 1200 CE resulted in demographic changes across time	Otoni <i>et al.</i> , Comparing Maternal Genetic Variation, 1.
Reconstruct the genetic signature potentially left in this region of Anatolia by the many civilizations, which succeeded one another over the centuries until the mid-Byzantine period (13th c. AD)	Otoni <i>et al.</i> , Mitochondrial Analysis of a Byzantine Population, 571-572.
Evaluate the effect of Southwest and Central Asian migrations on the current landscape of the Iranian plateau, the Indus Valley and Central Asia	Quintana-Murci <i>et al.</i> , Where West Meets East, 827.
Test the demic diffusion model and the cultural diffusion model for the Neolithic transition	Rasterio and Chikhi, Female and Male Perspectives, 1.
Investigate the colonization of Europe and estimate the proportion of modern lineages whose ancestors arrived during each major phase of settlement	Richards <i>et al.</i> , Tracing European Founder Lineages, 1232.
Investigate the demographic history of Europe, discuss demic versus cultural diffusion	Rosser <i>et al.</i> , Y-Chromosomal Diversity, 1526.
Investigate the genetic structure of three Caucasian (Armenian, Azeri and Georgian) groups and one group from Iran and Turkey each to infer their demographic history	Schönberg <i>et al.</i> , High-Throughput Sequencing, 988.
Geographic distribution of haplogroup V mtDNA to precise geographical extent and timing of the western recolonization	Torrioni <i>et al.</i> , A Signal from Human mtDNA, 835.
Phylogenetic and geographic structure of Y-chromosome haplogroup R1a across Eurasia	Underhill <i>et al.</i> , Phylogenetic and Geographic Structure, 124.
Reveal traces of historical migrations with a particular focus on Central Asia	Wells <i>et al.</i> , Eurasian Heartland, 10244.
Prehistoric origin of nomadic Turkish speakers; identify explicit genetic signals shared by all Turkish peoples that have likely descended from putative prehistoric nomadic Turks; trace back the hypothesized "Inner Asian Homeland"	Yunusbayev <i>et al.</i> , Genetic Legacy, 3.

Table 3: Research questions

Result/interpretation	Reference
Genetic variation of the contemporary Turkish population is best described within the context of the Southern European/Mediterranean gene pool, but also shows signatures of relatively recent contribution from ancestral East Asian populations.	Alkan <i>et al.</i> , Whole Genome Sequencing of Turkish Genomes, 1, 8.
The present-day Turkish HLA profiles reflect an old Mediterranean substratum, not very different from the Jewish or Lebanese. The input from the Altai mountains was relatively low. The "out of Anatolia" origin for the Hittites and related people who are considered by some on a linguistic basis as Indo-Europeans has to be doubted according to the results of the study. Turks, Kurds and Armenians are very close genetically and all of them seem to have been living in the area for many millennia, because typical Asian HLA genes are not found. Probably, small different "elite" invaders imposed different languages on these three different groups who originally spoke a similar pre-Indo-European language.	Arnaiz-Villena <i>et al.</i> , HLA Alleles and Haplotypes in the Turkish Population, 314-315.
Anatolia is genetically more closely related with the Balkan populations than to the Central Asian gene pool. Central Asian contribution is only 13%.	Berkman <i>et al.</i> , <i>Alu</i> Insertion Polymorphisms, 11.
Male contribution from Central Asia to the Turkish population with reference to the Balkans is 13%. The genetic similarity between Anatolia and the Balkans seems to be high within males. Comparison of the admixture estimate for Turkey with those of the neighbouring populations point out that the Central Asian contribution was lowest in Turkey.	Berkman <i>et al.</i> , <i>Alu</i> Insertion Polymorphisms, 2341, 2347.
The Turkish sample showed a higher and more diverse polymorphism than the Bulgarians. Bulgarians are close to Western Europeans in terms of levels of internal differentiation and genetic distances, whereas Turks present a close affinity to Middle Eastern populations in terms of higher internal differentiation and shorter genetic distances.	Calafell <i>et al.</i> , From Asia to Europe, 39, 46.
The major components (haplogroups) are shared with European and neighbouring Near Eastern populations (94%) and contrast with only a minor share of haplogroups related to Central Asian (3,4%), Indian (1,5%) and African (1%) affinity. The variety of Turkish haplotypes is witness to Turkey being both an important source and recipient of gene flow.	Cinnioglu <i>et al.</i> , Excavating Y-Chromosome Haplotype Strata in Anatolia, 127.
The Turkish population presents the shortest genetic distance with the British, but at the same time Turkey is the population with the shortest genetic distance to the Middle East. Once again, Turkey's intermediate genetic position between the Middle East and Europe is shown.	Comas <i>et al.</i> , Geographic Variation in Human Mitochondrial DNA, 1075.
With one exception, the estimated <i>m</i> values converge in suggesting a Central Asian contribution to the current Turkish gene pool of around 30%. An instantaneous input of Asian alleles, accounting for 30% of the current gene pool, means that the 11th century invasion entailed a massive movement of people, females as well as males.	Di Benedetto <i>et al.</i> , DNA Diversity and Population Admixture, 152-153.
Strong structuring of paternal lineages among villages, but not for autosomal and maternal lineages. Based on ethnographic observations, this paternal genetic structuring is delineated from the cultural isolation between the villages, which are rationalized mostly on differences in ancestry and religion.	Gokcumen <i>et al.</i> , Biological Ancestries, Kinship Connections, and Projected Identities, 116.
Turkish population has a close genetic similarity to the Middle Eastern and European populations and some degree of similarity to South Asian and Central Asian populations. Results from the samples collected in Turkey overlapped without a clear sub-population structure, suggesting a rather homogenous and distinct genetic ancestry.	Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry, 137.
Turks and Germans are equally distant to all three Mongolian populations: lack of a strong genetic relationship between Mongols and Turks despite close relationship of languages and geographic neighbourhood. Despite a shared central Asian history and common linguistic features, Turks and Mongolians are not genetically related.	Machulla <i>et al.</i> , Genetic Affinities among Mongol Ethnic Groups, 292.
Turkic Central Asian, Turkish, British and Finnish populations are placed on one side, German, French, Bulgarian and Greek on the other side of the phylogenetic tree. Turkish samples are at a lower distance from Turkic Central Asian populations and at a somewhat higher distance from European populations. The study provides further support for the intermediate location of Anatolia between Europe and Asia.	Mergen <i>et al.</i> , Mitochondrial DNA Sequence Variation, 45-46.
Genetic similarities to the early European Neolithic gene pool and modern-day Sardinians, as well as a genetic affinity to modern-day populations from the Near East and the Caucasus. Anatoli's central geographic locations appears to have served as a connecting point with other areas of the Near East and Europe, throughout and after the Neolithic.	Omrak <i>et al.</i> , Genomic Evidence 270.

Table 4: Results and interpretations

Comparing mtDNA variation in three period groups (Roman, Middle Byzantine and modern), and by simulating possible scenarios inferred by historical and archaeological evidence, the data suggests that concurrently with the abandonment of the city of Sagalassos in the early thirteenth century CE, the population of the region may have been drastically reduced by almost 90%, most likely due to migrations towards farther regions in southwest Anatolia. Furthermore, an earlier but milder contraction in population size may have taken place in the sixth-seventh centuries CE, either owing to the Plague of Justinian and/or an earthquake in the region.	Otoni <i>et al.</i> , Comparing Maternal Genetic Variation, 8.
High haplotype diversity, all characteristic of West Eurasians. No East/South Asian haplogroup M and Sub-Saharan haplogroups; significant maternal genetic signature of Balkan/Greek populations, as well as ancient Persians and populations from the Italian peninsula. Some contribution from the Levant has also been detected, whereas no contribution from Central Asian population could be ascertained.	Otoni <i>et al.</i> , Mitochondrial Analysis of a Byzantine Population, 573.
The Central Asian Uzbeks, Turkmen, and Shugnan tend to be closer to populations from the Anatolian/Caucasus/Iranian regions, rather than to Indus Valley populations. The eastern Eurasian contribution to the west is negligible.	Quintana-Murci <i>et al.</i> , Where West Meets East 835, 838.
Males and females underwent the same admixture history and both support the demic diffusion mode. The patterns of genetic diversity found in extant and ancient populations demonstrate that both modern and aDNA support the demic diffusion model. Some differences between male and female markers suggest that the effective female population size was larger than that of the males, probably due to different demographic histories that might be connected to various shifts in cultural practices and lifestyles that followed the Neolithic transition, such as sedentarism, the shift from polygyny to monogamy or the increase of patrilocality.	Rasterio and Chikhi, Female and Male Perspectives, 1.
There has been substantial back-migration into the Near East; the majority of extant mtDNA lineages entered Europe in several waves during the Upper Palaeolithic; there was a founder effect or bottleneck associated with the Last Glacial Maximum 20,000 years ago, from which derives the largest fraction of surviving lineages; the immigrant Neolithic component is likely to comprise less than one quarter of the mtDNA pool of modern Europeans.	Richards <i>et al.</i> , Tracing European Founder Lineages, 1251.
Geographic proximity may be a better predictor of Y-chromosomal genetic affinity than is language. In the range of this genetic affinity, the Turks lie between the geographically neighbouring but linguistically distant Armenians and Greeks.	Rosser <i>et al.</i> , Y-Chromosomal Diversity, 1537
The randomly sampled complete mtDNA genome sequences indicated extraordinarily high genetic diversity in the groups from the South Caucasus, Iran and Turkey. Central/East Asian groups were found only in a few individuals from the Azeri and Turkish groups, suggesting some Central Asian influence especially on these groups; the low frequency of these mtDNA lineages is in good agreement with previous estimates of low levels of gene flow from Asia into Anatolia. The complete mtDNA genome sequences do reveal some additional genetic similarity between the two Turkish-speaking groups (Azeri and Turks) that was not evident in previous studies. The BSP for the mtDNA sequences from Turkey suggests that the ancestors of the group from Turkey have a different history than the ancestors of the Caucasian and Iranian group in this study. Specifically, these results suggest that the ancestors of the group from Turkey did not expand after the LGM.	Schönberg <i>et al.</i> , High-Throughput Sequencing, 991-993
Haplogroup V is virtually absent in the southern Balkans, Turkey, the Caucasus and the Near East.	Torrioni <i>et al.</i> , A Signal from Human mtDNA, 850.
The initial episodes of haplogroup R1a diversification likely occurred in the vicinity of present-day Iran and eastern Turkey. Possibly the R1a lineages accompanied demic expansions initiated during the Copper, Bronze and Iron Ages, partially replacing previous Y-chromosome strata.	Underhill <i>et al.</i> , Phylogenetic and Geographic Structure, 130.
The Turkish and Azeri populations are atypical among Altaic speakers in having low frequencies of M130, M48, M45, and M17 haplotypes. Rather, these two Turkic-speaking groups seem to be closer to populations from the Middle East and Caucasus, characterized by high frequencies of M96- and/or M89-related haplotypes. This finding is consistent with a model in which the Turkic languages, originating in the Altai-Sayan region of Central Asia and northwestern Mongolia, were imposed on the Caucasian and Anatolian peoples with relatively little genetic admixture—another possible example of elite dominance-driven linguistic replacement.	Wells <i>et al.</i> , Eurasian Heartland, 10248.

Table 4: Results and interpretations

<p>Turkic-speaking peoples sampled across the Middle East, the Caucasus, Eastern Europe and Central Asia share varying proportions of Asian ancestry that originate in a single area, southern Siberia and Mongolia. The findings reveal genetic traces of recent large-scale nomadic migrations and map their source to a previously hypothesized area of Mongolia and southern Siberia. Although we report a single admixture date for each population, we note that it is likely that the contemporary Turkic peoples were established through several migration waves. Indeed, Turkic peoples closer to the SSM area (those from the Volga-Ural region and Central Asia) showed younger dates compared to more distant populations like Anatolian Turks, Iranian Azeris, and the North Caucasus Balkars.</p>	<p>Yunusbayev <i>et al.</i>, <i>Genetic Legacy</i>, 2, 12.</p>
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Table 4: Results and interpretations

Discussion

The majority of the studies examined based their research on recent DNA samples (85%),⁸⁴ only four studies relied on aDNA,⁸⁵ of which one compared modern DNA with aDNA.⁸⁶ Two aDNA studies, however, were conducted under the same research project,⁸⁷ the excavations of Sagalassos, which are well known for the interdisciplinary evaluation of their results.⁸⁸ The fact that most of the studies drew their conclusions about historical migrations from modern genetic data pre-eminently represents the state of technical possibilities. As these are constantly improving, many more genetic studies of aDNA, not only from present-day Turkey, are to be expected in the near future.⁸⁹

Before discussing the contents and results of the analysed genetic studies, I would like to make some methodological remarks on sampling criteria and statistical methods. As the *Race, Ethnicity, and Genetics Working Group* has stated, sampling design can have a critical influence on the result of genetic studies.⁹⁰ In many cases of plant and animal population genetics, definition of exact boundaries and particular demes⁹¹ and the assignment of individuals of the species under study to one or another deme is not crucial, and patterns of genetic variability can be detected by a fairly straightforward random sampling procedure in

84 Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes; Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population; Berkman *et al.*, *Alu* Insertion Polymorphisms; Berkman *et al.*, Asian Contribution to the Turkish Population; Calafell *et al.*, From Asia to Europe; Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia; Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities; Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry; Machulla *et al.*, Genetic Affinities among Mongol Ethnic Groups; Mergen *et al.*, Mitochondrial DNA Sequence Variation; Quintana-Murci *et al.*, Where West Meets East; Richards *et al.*, Tracing European Founder Lineages; Rosser *et al.*, Y-Chromosomal Diversity; Schönberg *et al.*, High-Throughput Sequencing; Torroni *et al.*, A Signal from Human mtDNA; Underhill *et al.*, Phylogenetic and Geographic Structure; Wells *et al.*, Eurasian Heartland; Yunusbayev *et al.*, *Genetic Legacy*.

85 Rasterio and Chikhi, Female and Male Perspectives; Omrak *et al.*, Genomic Evidence; Ottoni *et al.*, Comparing Maternal Genetic Variation; Ottoni *et al.*, Mitochondrial Analysis of a Byzantine Population.

86 Rasterio and Chikhi, Female and Male Perspectives.

87 Ottoni *et al.*, Comparing Maternal Genetic Variation; Ottoni *et al.*, Mitochondrial Analysis of a Byzantine Population

88 Cf. the website of the Sagalassos project: www.sagalassos.be (retrieved 30 October 2016).

89 Destro-Bisol *et al.*, Molecular Anthropology in the Genomic Era, 106-107; Der Sarkissian *et al.*, Ancient Genomics.

90 Race, Ethnicity, and Genetics Working Group, Use of Racial, Ethnic, and Ancestral Categories, 521.

91 Originally, a deme describes any specified assemblage of taxonomically closely related individuals. With time, however, the use of the term 'deme' by biologists took on the added implications of a local inbreeding population, a feature not essential to the original proposal of the term (Summers, Demes).

the territory under study. Population geneticists cannot apply these procedures when studying human genetic variation. Researchers interested in the historical analysis of human genetic variability are faced with the problem of associating genetic variability with identifiable modern populations in some explicit way.⁹²

Several sampling criteria have been applied in the analysed genetic studies; however, the main criterion was geographical. Some research teams were explicitly cautious to avoid urban or coastal areas for sampling in order to bypass the genetic impact of »recent migrations«. ⁹³ The timespan of »recent« has never been indicated in any of the surveyed studies – and I cannot decide what recent means from the geneticist’s perspective. Anatolia’s prehistoric demography is subject to much discussion among specialists,⁹⁴ not least due to missing data such as cemeteries in certain periods or uncertainty upon household size, often due to partial excavation of settlements.⁹⁵ Even with the availability of written sources, the evidence of population data (censuses, tax registers, land registers) is not as comprehensive and clear as might be desired by historians. Nevertheless, it is a fact that the Ottoman Empire witnessed intensive state-induced population movements in the form of internal migrations and immigration from beyond its borders, from the sixteenth century until its dissolution in 1922. During its expansion from the sixteenth to the eighteenth century, the Ottoman Empire pursued a deportation and resettlement policy based on military, administrative, economic and political considerations, i.e. to fill empty land, to facilitate the dispatching of troops and to supply provisions as well as to disperse heterodox population groups whom the state perceived as religious and political troublemakers.⁹⁶ From the second half of the nineteenth century to 1913, the Ottoman lands became a shelter for Muslim refugees coming from the Caucasus and the Balkans, i.e. the Crimean Tatars who fled the annexation of their homelands by the Russian Empire in the last quarter of the eighteenth century; the Circassians who were subjected to the Russian policy of expulsion in the 1860s or the Muslim Turks who fled the Balkans in the aftermath of the Russo-Turkish war (1877-1878).⁹⁷ A massive deportation of Greeks from Asia Minor started with the Balkan wars (1912-1913), and especially after these wars in 1914.⁹⁸ From 1906 onwards⁹⁹, the Committee of Union and Progress (*İttihat ve Terakki Cemiyeti*) directed internal migration, following a policy of ending existing demographically homogenous regions by mixing the Turkish Muslim population with the non-Turkish Muslim population. It is estimated that nearly one million Balkan refugees, approximately 2 million Kurdish and Turcoman nomads, 5,000 Arab families from

92 MacEachern, *Genes, Tribes, and African History*, 361. For a detailed discussion of sampling by reference to the Human Genome Diversity Project see Reardon, *Race to Finish*, chapter 4.

93 Calafell *et al.*, *From Asia to Europe*, 37; Comas *et al.*, *Geographic Variation in Human Mitochondrial DNA*, 1068; Di Benedetto *et al.*, *DNA Diversity and Population Admixture*, 145.

94 Düring, *Breaking the Bond*; see there also references for details. See also Cohen, *Implications for the NDT* (as well as other chapters in the same volume).

95 Düring, *Early Holocene Occupation*.

96 Şeker, *Forced Population Movements*, 3-4; for examples see *ibid.*, 4.

97 Şeker, *Forced Population Movements*, 5.

98 Dundar, *Settlement Policy*, 35.

99 The Committee of Union and Progress was already active between 1895 and 1897, being concerned with the Armenian question, see Dundar, *Settlement Policy*, 34.

Syria, nearly 1,5 million refugees from eastern Anatolia, some Arab refugees from Tripoli and Benghazi whose number is unknown, nearly 400,000 new Balkan refugees and the Circassians who escaped from Syria, were displaced. To summarise, this means that more than one third of the Muslim population of Asia Minor was transferred from their original habitat to places far away. If the massive reduction of the non-Muslim population, i.e. nearly 1,2 million Greeks and more than 1,5 million Armenians, is added to this number, it is evident that only one half of Asia Minor's population was displaced by the Committee's policy.¹⁰⁰

Additionally, individual migration in the Ottoman Empire has to be considered: peasants, for instance, migrated for survival, for under the conditions of the fifteenth- and sixteenth-centuries, mountainous regions and islands typically did not produce enough to feed their populations. Besides seasonal migrations, some migrants who had left their villages for longer, ultimately found their way back to their home villages, while others stayed away for good, transferring their families to the localities where they had found a source of livelihood. Some permanent migrants married local women and rapidly became part of the society into which they had entered.¹⁰¹ Finally, from the Neolithic period and well into the twentieth century, a good part of the population in present-day Turkey consisted of nomads, semi-nomadic pastoralists and peripatetic nomads.

Lastly, it should be mentioned here that Turkic tribes already settled throughout the thirteenth and fourteenth centuries in Byzantine lands, adopted Christianity and Greek language, married local Greeks or Slavs and thus entered Byzantine society. Rustam Shukurov describes this Turkic minority as the »Byzantine Turks«, a term that was originally coined by the Ottomans in the first half of the fifteenth century.¹⁰² We do not know the total extent of this Turkic settlement and all the regions of the Byzantine Empire it affected. However, the fact that this minority is well documented in Byzantine sources shows that ethnocultural realities were already more complex in the thirteenth and fourteenth centuries than they are presented in the binary model that many scholars use to describe relations between Greeks and Turks.¹⁰³ Thus, genetic admixture took place in a more continuous and less sudden way than the conception of medieval nomadic invasions would suggest. Taking into account only the known migrations of the last five centuries, any suggested »autochthony« of samples taken in rural areas of present-day Turkey seems illusory.

Of all the analysed genetic studies, it was only Gokcumen *et al.* who considered the more recent Turkish migration history in greater detail and contrasted it with the self-assigned identity of their donors. Thus, they could show that, at the village level, paternal genetic diversity is structured among settlements, whereas maternal genetic diversity is distributed more homogeneously, reflecting strong patrilineal cultural traditions that transcend larger ethnic and religious structures. Local ancestries and origin myths, rather than ethnic or religious affiliations, delineate the social boundaries and projected identities among the villages.¹⁰⁴

100 Dunder, *Settlement Policy*, 39. For the population exchange with Bulgaria in 1913, see also İçduygu *et al.*, *Politics of Population*, 364. For the population exchange between Greece and Turkey in 1923, see Hirschon, *Crossing the Aegean*.

101 Faroqhi, *Ottoman Population*, 394.

102 Shukurov, *Byzantine Turks*, 9.

103 Shukurov, *Byzantine Turks*, 9.

104 Gokcumen *et al.*, *Biological Ancestries, Kinship Connections, and Projected Identities*, 119-121.

Other research teams accomplished their sampling in urban areas¹⁰⁵ which have been and still are subject to massive internal and external migrations since at least the formation of the Turkish Republic.¹⁰⁶ In all cases this choice seems to have been a pragmatic one as the investigators drew on blood samples from other studies,¹⁰⁷ simply asked the staff and students of the medical department on site to donate samples,¹⁰⁸ or both.¹⁰⁹ Given the rural migration in the last centuries, the decision to collect available blood samples in urban areas amounts to the same thing.

Five studies categorised their samples as Turkish according to language.¹¹⁰ Linguistic models and archaeological models that often originated from them influenced genetic history from its very beginnings;¹¹¹ and indeed, four of the five studies date to the early period of genetic research on human history.¹¹² Already Rosser *et al.* have shown in the same early period of genetic research that geographic proximity – at least in regards to the Y-chromosome – may be a better predictor for genetic affinity.¹¹³ In the same study, Rosser *et al.* made another important point: the Altaic language of the Turks was acquired as a result of Turkic invasions from the eleventh to the fifteenth century, and if this language is believed to be acquired by elite dominance, the genes of populations like the Turks are unlikely to be separated from surrounding populations by genetic barriers.¹¹⁴

Gokcumen *et al.* have already stated that Anatolia was a multilingual region and that it is not only likely but is also historically documented that a considerable number of communities changed their language over the past centuries.¹¹⁵ Language concerns in regard to homogenisation of language and ›proper‹ Turkish started already with the *Tanzimat* period, the process of Westernisation that began in 1839. The foundation of the Republic of Turkey that necessitated the process of forming a national consciousness, and language was used as a significant instrument to create Turkishness as a collective identity.¹¹⁶ A remarkable example

105 Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia, 128; Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry, 129; Schönberg *et al.*, High-Throughput Sequencing, 989; Quintana-Murci *et al.*, Where West Meets East, 828.

106 İçduygu *et al.*, Politics of Population in a Nation-Building Process

107 Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry, 129, from the Turkish Heart Study; Machulla *et al.*, Genetic Affinities among Mongol Ethnic Groups, 293 used samples »collected by two other studies, available from two laboratories in Istanbul where the samples were already typed.«

108 Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population.

109 Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia, used 359 blood samples from blood banks, 61 from paternity clinics, 103 from staff and students enrolled at Istanbul University.

110 Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population, 309; Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Wells *et al.*, Eurasian Heartland, 10244; Yunusbayev *et al.*, Genetic Legacy, 5.

111 Cavalli-Sforza, *Genes, Peoples, and Languages*; Renfrew, *Archaeology, Genetics and Linguistic Diversity*.

112 1996: Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; 2001: Arnaiz-Villena *et al.*, HLA Alleles and Haplotypes in the Turkish Population; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Wells *et al.*, Eurasian Heartland. Yunusbayev *et al.*, Genetic Legacy, is an exception as the study was published in 2015.

113 Rosser *et al.*, Y-Chromosomal Diversity, 1537.

114 Rosser *et al.*, Y-Chromosomal Diversity, 1528.

115 Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities, 127.

116 Aydingün and Aydingün, Role of Language, 416; see there also for details on language policy before the formation of the Turkish Republic.

is the »Citizen, Speak Turkish!« (»*Vatandaş, Türkçe konuş!*«) campaign during the first two decades of the Turkish Republic that aimed at putting pressure on non-Turkish speakers to speak Turkish in public.¹¹⁷ Starting with an initiative of students of the Istanbul University to which the Ministry of Interior granted permission, the Commission for the Protection and Expansion of Turkish Language was formed. This commission arranged newspaper announcements, the instalment of posters and above all public meetings that frequently culminated in outbursts of violence. This campaign was a minor event in the history of the Turkish Republic, but the fact that it was initiated by the state and accomplished by the people it could mobilise, shows that language homogenisation was also a concern of the general public.¹¹⁸ The »Citizen, Speak Turkish!« campaign was but one of the many state-induced means to spread Turkish language throughout Anatolia (and Thrace, too, of course)¹¹⁹ in the course of the »Turkification« (*Türkleştirme*) policy. During the 1920s and especially the 1930s, many municipalities imposed fines on those who did not speak Turkish.¹²⁰ In 1926, the parliament passed a law that made use of the Turkish language compulsory in all correspondence among corporations; in 1931, the state required all Turkish children to have their primary education in Turkish; in 1934, the Law of Surnames required all citizens to take Turkish surnames; names of cities, towns and villages were subsequently changed into Turkish.¹²¹

Therefore, it might be more valuable to document the languages the grandparents and great-grandparents of the donors spoke (and not their birthplaces) when sampling current Turkish population according to the language spoken.

The criteria of geography and language may suggest that the assumption of ethnicity mattered in some of the studies. Hodoğlugil and Mahley queried their donors about their ethnicity and included only participants who indicated Turkish or Kyrgyz ethnicity in their study.¹²² Ethnic groups in Mongolia were the point of departure for Machulla *et al.*'s study;¹²³ similarly this was the case in Arnaiz-Villena *et al.*'s study that investigated the genetic relatedness of Turks, Kurds and Armenians.¹²⁴ Torroni *et al.* equated geographic and ethnic origin.¹²⁵ Calafell *et al.* applied ethnic criteria when excluding »individuals from ethnic minorities« from their study.¹²⁶ In contrast, some studies explicitly rejected any ethnic assignment of their donors. Alkan *et al.* included their donors »irrespective of their mother-tongue/ethnicity« by referring to all of their donors »collectively as Turkish«.¹²⁷ Di Benedetto *et al.* mentioned in their sampling description that they did not record any »self-assigned ethnic affiliations« of their donors.¹²⁸

117 Aslan, »Citizen, Speak Turkish!«.

118 Aydıngün and Aydıngün, *Role of Language*, 267.

119 N.N., *Les Israélites de Turquie ; Bali, 1934 Trakya Olayları*, 12-13, 170.

120 Başak, *Citizenship and Identity in Turkey*, 61.

121 Aydıngün and Aydıngün, *Role of Language*, 252, 265.

122 Hodoğlugil and Mahley, *Turkish Population Structure and Genetic Ancestry*, 129.

123 Machulla *et al.*, *Genetic Affinities among Mongol Ethnic Groups*, 292.

124 Arnaiz-Villena *et al.*, *HLA Alleles and Haplotypes in the Turkish Population*, 309.

125 Torroni *et al.*, *A Signal from Human mtDNA*, 845.

126 Calafell *et al.*, *From Asia to Europe*, 36.

127 Alkan *et al.*, *Whole Genome Sequencing of Turkish Genomes*, 3.

128 Di Benedetto *et al.*, *DNA Diversity and Population Admixture*, 146.

The bulk of the analysed genetic research was done on the genetic affiliations of modern populations with the investigation of prehistoric and historic relationships among modern human groups in mind. Genetic studies of Turkey cover a time span of nearly two decades. Methodologies have continually developed throughout this period, so that different methods were applied. As an archaeologist and historian not trained in genetics, I cannot judge to what extent the results of classical methods (from blood protein polymorphisms and gene frequencies) and molecular methods (DNA sequencing, genomics) can be compared with one another.¹²⁹

In order to interpret modern genetic data for historical and prehistoric periods, they are extrapolated with the help of statistical methods. These statistical methods have already been subject to criticism. One issue concerns the sample size and therefore the studies' relevance and significance.¹³⁰ In all of the genetic studies, the proportion of Turkish samples when compared with the Turkish population in total¹³¹ is at best a per mille value with at least two zeros after the decimal place (*Table 5*). Robert V. Krejcie and Daryle W. Morgan provided, besides the necessary formula, a table for determining sample size from a given population, according to which the sample size for a population size of 1,000,000 has to amount to 384 or more. However, they noted that as the population increases the sample size increases at a diminishing rate and remains relatively constant at slightly more than 380 cases.¹³² Based on the total population size of 74,525,696,¹³³ with a margin of error¹³⁴ of 5% and a confidence level of 95%, the recommended sample size for the current Turkish population amounts to 385.¹³⁵ In terms of percentage, 385 samples constitute 0,00052% or 0,0052‰ of the total Turkish population respectively. Of the 15 studies which stated the absolute number of their samples, four studies exhibited this recommended sample size,¹³⁶ whereas eleven studies did not.¹³⁷ In the cases with the smallest sample sizes, this led to margins of error of 24,5%¹³⁸, 18, 2%¹³⁹ and 14, 61%¹⁴⁰. This margin of error, however, refers to the current population and I frankly assume that it must increase retrospectively to time when the data is retrojected.¹⁴¹

129 For an example of the incomparability of methods that causes a problem when comparing results, see Rasterio and Chikhi, *Female and Male Perspectives*, 5-6, who explained this in detail.

130 For early remarks on this topic see Pohl, *Identität und Widerspruch*, 26.

131 Turkish Statistical Institute, *Population and Housing Census*: total 74,525,696.

132 Krejcie and Morgan, *Determining Sample size for Research Activities*, 607, table 1.

133 Turkish Statistical Institute, *Population and Housing Census*: total 74,525,696.

134 The margin of error expresses the amount of random sampling error in a survey's result.

135 Cf. The sample size calculator: www.raosoft.com/sample_size.html (retrieved on 30 October 2016).

136 Berkman and Togan, *Asian Contribution to the Turkish Population*; Cinniöglü *et al.*, *Excavating Y-Chromosome Haplotype Strata in Anatolia*; Machulla *et al.*, *Genetic Affinities among Mongol Ethnic Groups*; Torroni *et al.*, *A Signal from Human mtDNA*.

137 Alkan *et al.*, *Whole Genome Sequencing of Turkish Genomes*; Arnaiz-Villena *et al.*, *HLA Alleles and Haplotypes in the Turkish Population*; Berkman *et al.*, *Alu Insertion Polymorphisms*; Calafell *et al.*, *From Asia to Europe*; Comas *et al.*, *Geographic Variation in Human Mitochondrial DNA*; Di Benedetto *et al.*, *DNA Diversity and Population Admixture*; Gokcumen *et al.*, *Biological Ancestries, Kinship Connections, and Projected Identities*; Hodoğlugil and Mahley, *Turkish Population Structure and Genetic Ancestry*; Mergen *et al.*, *Mitochondrial DNA Sequence Variation*; Quintana-Murci *et al.*, *Where West Meets East*; Schönberg *et al.*, *High-Throughput Sequencing*.

138 Alkan *et al.*, *Whole Genome Sequencing of Turkish Genomes*.

139 Calafell *et al.*, *From Asia to Europe*.

140 Comas *et al.*, *Geographic Variation in Human Mitochondrial DNA*.

141 Pohl, *Identität und Widerspruch*, 27, made the same assumption. See also Geary and Veeramah in this volume.

Reference	Samples, total	Samples, Turks	% Turkish population
Alkan <i>et al.</i> , Whole Genome Sequencing	16	16	0,00021
Arnaiz-Villena <i>et al.</i> , HLA Alleles and Haplotypes	258	228	0,00359
Berkman and Togan, Asian Contribution to the Turkish Population	2582	533	0,00715
Berkman <i>et al.</i> , <i>Alu</i> Insertion Polymorphisms	59	29	0,00039
Calafell <i>et al.</i> , From Asia to Europe	59	29	0,00039
Cinnioğlu <i>et al.</i> , Excavating Y-Chromosome	523	532	0,00714
Comas <i>et al.</i> , Geographic Variation	45	45	0,00064
Di Benedetto <i>et al.</i> , DNA Diversity and Population	118	118	0,00158
Gokcumen <i>et al.</i> , Biological Ancestries	170	170	0,00228
Hodoğlugil and Mahley, Turkish Population Structure	80	64	0,00086
Machulla <i>et al.</i> , Genetic Affinities	982	498	0,00888
Mergen <i>et al.</i> , Mitochondrial DNA	75	75	0,00010
Quintana-Murci <i>et al.</i> , Where West Meets East	208	50	0,00067
Schönberg <i>et al.</i> , High-Throughput Sequencing	59	29	0,00039
Torroni <i>et al.</i> , A Signal from Human mtDNA	10365	606	0,00813

Table 5: Ratio of Turkish samples to the total Turkish population

This assumption raises the issue of time depth in data simulation. The timing of biological processes that brought genetic variation into being is entirely unknown¹⁴² and is instead estimated with the help of computer simulation or bioinformatics respectively. Sometimes it seems the cart is put before the horse when genetic data is used to date demographic events instead of being interrogated as to whether it can supply proof of that kind. Richards *et al.*, e.g., used the age of mtDNA mutations and haplogroups to date major demographic events.¹⁴³ This kind of approach has been criticised as it can lead to misinterpretation of the data.¹⁴⁴

In the studies analysed, three methods of data simulation were favoured: phylogenetic trees (13 studies), principal component analysis (9 studies) and admixture analysis (8 studies); each of these methods was used throughout the 20 year period investigated. Marianne Sommer has argued extensively the problematic nature of phylogenetic trees and their mappings which freeze the hierarchical kinship systems that are meant to represent a state before great historical population movements.¹⁴⁵ Previously, Colin Renfrew called attention to the problem of correlating gene frequency maps to long-term population history as it is not known how stable spatial structures in gene frequencies are through time, even when populations are relatively isolated. On the other hand, some of these genes and their phenotypes may not be adaptively neutral, so that some of the variation is to be associated with environmental variables. Furthermore, the spatial aspect of mating patterns may vary at different periods of history and thus influence the gene flow. Finally, a gene frequency map presents a contemporary map. Although it is agreed that early demographic processes may have had a determining impact on genetic distributions, it is unknown so far which gene frequencies are pertinent.¹⁴⁶

142 MacEacher, *Genes, Tribes, and African History*, 360.

143 Richards *et al.*, *Tracing European Founder Lineages*.

144 Rasterio and Chikhi, *Female and Male Perspectives*, 5-6; see there also for further references concerning critique.

145 Sommer, *Population-Genetic Trees*. See also Pohl, *Identität und Widerspruch*, 26, who critically discussed genetic mapping some 15 years earlier.

146 Renfrew, *Archaeology, Genetics and Linguistic Diversity*, 463.

Geoffery Anderson Clark has described the way in which principal components analysis is used to establish correlation coefficient matrices for patterns in genetic polymorphisms in order to isolate a number of principal components, expressed geographically, and which are interpreted as time-successive, quasi-historical migration events in the form of a »post-hoc accommodative argument« that develops explanations after an analysis is completed to account for patterns in the data.¹⁴⁷

Furthermore, differences in patterns of exogamous marriage and post-marital residence can have significant effects on genetic distributions and genetic drift.¹⁴⁸ I estimate that this should be considered in data simulation, especially when extrapolating data to past centuries or millennia. Turkey is a country with a high level of consanguinity. The rate of cousin marriage was found to be at 28,4% in 1969,¹⁴⁹ 24,53% in 1983,¹⁵⁰ 23,06% in 1987,¹⁵¹ and 22% in 2003.¹⁵² Regional differences in this rate, however, may vary considerably; the study by Akbayram *et al.* for the Lake Van region, for instance, even showed a percentage of 34,4% cousin marriages of which 75 % were first degree cousin marriages.¹⁵³ Interestingly, Hodoğlugil and Mahley considered consanguinity in the interpretation of their results when detecting an extended homozygosity in a locus with two identical alleles in Middle Eastern and South Asian populations; however, they excluded Turkey (besides Central Asia, Europe and Northeast Asia) from these considerations as these countries showed less homozygosity in terms of number and size.¹⁵⁴ Mergen *et al.* interpreted the differences they observed in the nucleotide pairwise distributions between Eastern and Western Anatolia as being due to consanguinity and migration events.¹⁵⁵

Besides consanguinity, polygyny looks back at a rich history on Anatolian grounds: Walter Scheidel described the conditions in the Greco-Roman world as prescriptively universal monogamous marriages that co-existed with (male) resource polygyny, especially for elites;¹⁵⁶ and stated the same for the pre-Islamic and Islamic Middle East.¹⁵⁷ Laura Betzig has argued a close relationship between stratification, despotism and polygyny in early agrarian societies¹⁵⁸ that are relevant for prehistoric periods in Turkey.

With the development of bioinformatics in the last decade, computer simulation programs became increasingly complex, matching modern genetic, historical and ecological data sets, modelling life cycles, mating systems and even phenotypes, even if they still have a wide array of options, capabilities, limitations, input formats and assumptions.¹⁵⁹ For

147 Clark, Comment on MacEachern, 372.

148 Renfrew, *Archaeology, Genetics and Linguistic Diversity*, 471. See, especially, the groundbreaking study of Cavalli-Sforza *et al.*, *Consanguinity, Inbreeding and Genetic Drift in Italy*.

149 Şayli, *Anadolu'nun genetik yapısı*, 1.

150 Başaran, *Anadolu'nun genetik yapısı*, 5.

151 Ulusoy and Tunçbilek, *Consanguineous marriage in Turkey*.

152 Koc, *Prevalences and Sociodemographic Correlates*; Ulusoy and Tunçbilek, *Consanguinity in Turkey in 1988*.

153 Akbayram *et al.*, *Frequency of Consanguineous Marriage*, 212.

154 Hodoğlugil and Mahley, *Turkish Population Structure and Genetic Ancestry*, 139.

155 Mergen *et al.*, *Mitochondrial DNA Sequence Variation*, 45.

156 Scheidel, *A Peculiar Institution?*

157 Scheidel, *Sex and Empire*.

158 Betzig, *Sex, Succession, and Stratification*.

159 Hoban *et al.*, *Computer Simulations*, 110-111.

historical interpretation, computer simulation programs are used for statistical inference and evaluation of statistical genetics methods, and some of these simulators consider polygamy, polyandry and other complex mating behaviours.¹⁶⁰ Of all the analysed studies, only Rita Rasteiro and Lounès Chikhi considered polygyny (and the shift to monogamy) in the interpretation of their results.¹⁶¹

Thematically, the genetic studies on populations in Turkey analysed in this study are concerned with two main topics: the Central Asian origin of the Turks (10 studies) and the migrations in the course of the Neolithic transition (6 studies). In accordance with these topics, genetic studies were conducted on two different scales, a macro scale (covering an area of several countries, one continent or more) and a micro scale (covering regions of Turkey or Turkey entirely). In macro-scale studies, Turkish DNA samples constituted only one sample category among many,¹⁶² whereas some micro-scale studies gathered DNA samples solely from Turkey and compared them to published data (see Fig. 6).¹⁶³ This observation, though, is restricted to the 15 studies that provided information about the number and origin of their samples.

I would like to discuss here the topic of the Central Asian origin of the Turks that is of greater interest for the readers of this journal. Various estimates exist on the proportion of gene flow associated with the arrival of Central Asian Turkic speaking people to Anatolia. Di Benedetto *et al.* compared mtDNA control region sequences and one binary and six STR Y-chromosome loci analyzed in 118 Anatolian samples with those found in Central Asia and suggested roughly a 30% Central Asian impact on the Anatolian gene pool. According to Di Benedetto *et al.*, these data reflect the occurrence of a single admixture event related to the flow of Central Asian mtDNA into the Anatolian gene pool.¹⁶⁴

In contrast, according to Berkman *et al.*, who investigated 10 *Alu* insertion polymorphisms, the Central Asian contribution to the Anatolian gene pool amounts only to 13%.¹⁶⁵ Cinnioğlu *et al.* detected in their study of Y-chromosome variation only a minor share of Anatolian haplogroups related to Central Asian that amounts to 3,4%.¹⁶⁶ Hodoğlugil and Mahley attested the Turkish population only had »some degree of similarity to South Asian and Central Asian populations:«¹⁶⁷ depending upon the number of chosen components of parental ancestry,

160 Hoban *et al.*, Computer Simulations, 119. See *ibid.* also for simulation programs on historical events in general, esp. 116, Fig. 3.

161 Rasterio and Chikhi, Female and Male Perspectives, 6-7.

162 Machulla *et al.*, Genetic Affinities among Mongol Ethnic Groups; Quintana-Murci *et al.*, Where West Meets East; Rasterio and Chikhi, Female and Male Perspectives; Richards *et al.*, Tracing European Founder Lineages; Rosser *et al.*, Y-Chromosomal Diversity; Schönberg *et al.*, High-Throughput Sequencing; Torroni *et al.*, A Signal from Human mtDNA; Underhill *et al.*, Phylogenetic and Geographic Structure; Wells *et al.*, Eurasian Heartland; Yunusbayev *et al.*, Genetic Legacy.

163 Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes; Berkman *et al.*, *Alu* Insertion Polymorphisms; Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia; Comas *et al.*, Geographic Variation in Human Mitochondrial DNA; Di Benedetto *et al.*, DNA Diversity and Population Admixture; Gokcumen *et al.*, Biological Ancestries, Kinship Connections, and Projected Identities; Mergen *et al.*, Mitochondrial DNA Sequence Variation.

164 Di Benedetto *et al.*, DNA Diversity and Population Admixture, 144.

165 Berkman *et al.*, *Alu* Insertion Polymorphisms, 11.

166 Cinnioğlu *et al.*, Excavating Y-Chromosome Haplotype Strata in Anatolia, 127, 136.

167 Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry, 137.

the Central Asian contribution amounted between 9% (K = 4) and 15% (K = 3).¹⁶⁸ Several other studies confirm the small Central Asian impact on the Anatolian gene pool, even if they did not express it in numbers. Quintana-Murci *et al.*, analysing mtDNA, found »the eastern Eurasian contribution to the west negligible.«¹⁶⁹ Schönberg *et al.*, who genotyped complete mtDNA sequences, found »Central/East Asian groups only in a few individuals from the Azeri and Turkish groups, suggesting some Central Asian influence especially on these groups« that, nevertheless, confirmed »previous estimates of low levels of gene flow from Asia into Anatolia.«¹⁷⁰ Machulla *et al.*, who found in their analysis of five HLA loci that »Turks and Germans are equally distant to all three Mongolian populations and stated that »despite a shared Central Asian history and common linguistic features, Turks and Mongols are not genetically related.«¹⁷¹ Mergen *et al.* who analysed mitochondrial D-loop region sequence variations abstained from a judgment of their data when ascertaining that the »Turkish samples are at a lower distance from Turkic Central Asian populations and at a somewhat higher distance from European populations.«¹⁷²

Several studies agree with traditional Turkish historiography concerning the timing of Central Asian genetic contribution. Alkan *et al.* state that the genetic variation of contemporary Turkish population is best described within the context of the Southern European/Mediterranean gene pool; however, it »also shows signatures of relatively recent contribution from ancestral East Asian populations.«¹⁷³ Wells *et al.*, who found the »Turkish and Azeri populations atypical among Altaic speakers but closer to populations from the Middle East and the Caucasus«, applied a linguistic model of the Turkic language expansion and concluded for these both groups »a possible example of elite dominance-driven linguistic replacement.«¹⁷⁴

Of great interest are the aDNA results on this matter. In their analysis on the eleventh to thirteenth century Byzantine population of Sagalassos, Ottoni *et al.* could not ascertain any genetic contribution from Central Asia.¹⁷⁵ However, the result of a single Byzantine site might not be representative for the rest of the Byzantine Empire for which a continuous Turkic immigration since the thirteenth century is attested, as mentioned above.

Aram Yardumian and Theodore G. Schurr have discussed some of the genetic studies mentioned here – as well as the genetic evidence from Central Asia – at length and contrasted it with the linguistic historical and archaeological evidence. Based on this evidence, they concluded that the genetic profile of present-day Anatolians is not the product of mass westward migrations from Central Asia and Siberia nor of small-scale migrations into an emptied sub-continent, but instead one of small-scale, irregular punctuated migrations that engendered large-scale shifts in language and culture among the diverse autochthonous inhabitants.¹⁷⁶

168 Hodoğlugil and Mahley, Turkish Population Structure and Genetic Ancestry, 128.

169 Quintana-Murci *et al.*, Where West Meets East, 838.

170 Schönberg *et al.*, High-Throughput Sequencing, 991-993.

171 Machulla *et al.*, Genetic Affinities among Mongol Ethnic Groups, 292.

172 Mergen *et al.*, Mitochondrial DNA Sequence Variation, 45-46.

173 Alkan *et al.*, Whole Genome Sequencing of Turkish Genomes, 1, 8.

174 Wells *et al.*, Eurasian Heartland, 10248.

175 Ottoni *et al.*, Mitochondrial Analysis of a Byzantine Population, 571.

176 Yardumian and Schurr, Who Are the Anatolian Turks?

The Central Asian ancestry of the Turks is anything but a new research topic in the history of the late Ottoman Empire and the Republic of Turkey. Due to the influence of European Turkologists, particularly Léon Cahun and his *Introduction to the History of Asia* in which he portrayed a just, egalitarian, well-organised society in the Turkish states of Central Asia, and to the influx of intellectuals from the Crimea, Azerbaijan and Central Asia, pre-Ottoman Turks appeared on the scene for the first time in the late nineteenth century. The revolutionary Young Turks (1908-1918) turned from Ottomanism to pan-Turkism and introduced a new period of history writing, promoting Ottoman history on a scientific basis. In the years before the First World War, interest in pre-Ottoman Turks and in early Turkish Central Asian states increased again.¹⁷⁷ Most notably, Rıza Nur emphasized the Central Asian origin of the Turks in his *Türk Tarihi (Turkish History)*.¹⁷⁸ Ever since the foundation of the Republic of Turkey by Mustafa Kemal Atatürk in 1923, history gained particular importance for the newly created nation state. In his »Great Speech« *Nutuk*, delivered by Atatürk over six consecutive days in front of the Republican Party in Ankara in October 1927, he told the nation's story. In this speech, Atatürk stretched Turkish history from the dawn of civilisation to the present, glorified the pre-Islamic ancestors in Central Asia and offered a heroic image of a new, non-Muslim ancestor. Moreover, in his narrative, Turkish history is a linear succession of various Turkish states, such as the empire of the Huns or the Seljuqs.¹⁷⁹ Accordingly, Atatürk himself promoted a research group of ministers, parliamentarians, professors and teachers to collect all possible sources on the history of the Turks. The result was the *Türk Tarihinin Ana Hatları (Main Lines of Turkish History)* that was devoted almost entirely to ancient and medieval history and gave a major role to the ancestral Turks of Central Asia.¹⁸⁰ This conception finally culminated in the »Turkish History Thesis«, according to which the Turks from Central Asia migrated in several waves and initiated the progress of civilization in the rest of the world.¹⁸¹ The citizens of the Turkish Republic were portrayed as the direct descendants of ethnic Turks from Central Asia.¹⁸² The Turkish History Thesis could be found in Turkish schoolbooks until the late 1980s;¹⁸³ accordingly, one might assume that it is still present in the minds of large parts of the Turkish population. In 1972, the Central Asian origin of the Turks was enhanced by Islam in the framework of the »Turkish-Islamic Synthesis«.¹⁸⁴ This reappraisal of Islam, embedded in a nationalism that goes hand-in-hand with the ruling political parties and various incidents over the last few decades, paved the way to Neo-Ottomanism, the current state ideology. Therefore, it seems nearly impossible not to think about Turkish politics when questioning the Central Asian origin of the Turks.

177 Foss, Kemal Atatürk, 827.

178 Nur, Türk Tarihi, 304-305. This 14 volume *History* was reprinted in the Latin alphabet but unchanged otherwise in 1978-1981.

179 Morin and Lee, *Constitutive Discourse of Turkish Nationalism*, 492, 498-500.

180 Türk Tarihi Heyeti, *Türk Tarihinin Ana Hatları*, chapter 9, 401-546.

181 Başak, *Citizenship and Identity in Turkey*, 69.

182 Morin and Lee, *Constitutive Discourse of Turkish Nationalism*, 499. For the sake of completeness, though, it has to be mentioned here that there were simultaneous attempts to construct an explicit Anatolian identity by announcing the Sumerian and the Hittites the forefathers of the Turks; see Türk Tarihi Heyeti, *Türk Tarihinin Ana Hatları*, chapter 7; see also, i.e., Erimtan, *Hittites, Ottomans and Turks*; Foss, Kemal Atatürk; Lewis, *Turkish Language Reform*.

183 Kabapınar, *Başlangıcından Günümüze Türk Tarih Tezi*, 164-177.

184 Eligür, *Mobilization of Political Islam in Turkey*, 96.

The proximity of research questions to trends in Turkish historiography and in Turkish politics, therefore, was the reason for the detailed analysis of funding sources and the composition of research teams. Although the contiguity between research questions and Turkish historiography seems striking at the first glance, funding and the composition of research teams do not prove any intended political agenda of the genetic studies at hand. As a matter of fact, though, results are often presented in a rather catchy and subjective manner in public media as well as in websites and forums operated by private individuals and associations.

Concerning the Central Asian origin, I would like to pose the question Rudi Paul Linder asked in 1982: »What was a nomadic tribe?« In early anthropological research, tribes were traditionally construed as a group or community sharing a common territory, speaking a common language or dialect, sharing a culture and religious tradition, united under a single political organization, and having a common economic pursuit. Additionally, the terms »tribe« and »ethnic group« were often used interchangeably. Geoff Emberling discussed several items that do not allow for the determination of a tribe: tribal names (self-assigned or not), language(s), political system(s), physical variation or race.¹⁸⁵ As early as 1969, Fredrik Barth rejected the equation of race, culture and language that were entailed in early perceptions of ethnic groups. Instead he suggested that »ethnic groups are categories of ascription and identification by the actors themselves«. ¹⁸⁶ This definition implies that ethnic identity was part of a dynamic social process and it introduced the possibility of change in actor's group membership.¹⁸⁷

The same has to be stated for tribes: nomadic tribes were of hybrid and dynamic natures; shared concerns – such as pastures, raids and the will to expand – played a much greater role in medieval tribal formation than kinship did; external pressure – be it from sedentary societies or other nomadic tribes – was the major factor in their formation.¹⁸⁸ Tribal organisation provided a simple and efficient means to channel and escalate conflict by involving additional groups according to an essentially binary logic of inclusion or exclusion. Finally, the common descent of a tribe does not necessarily describe a biological fact, but rather a genealogical and thus cultural construction.¹⁸⁹ These tribal genealogies may serve as an idiom or charter that nomads use to explain their history and politics. Tribal genealogies are rearranged and a particular chief's lineage is ›discovered‹ to be the senior lineage. The utility of genealogies as political supports derives paradoxically from the inability of most steppe nomads to render a precise and complete account of their descent. Typically, tribal genealogy is quite clear for the fairly immediate antecedents, becomes hazy and often contradictory for a number of more distant generations, but finally emerges precise and unequivocal in describing the apical ancestor of the tribe and his sons.¹⁹⁰

185 Emberling, *Ethnicity in Complex Societies*, 297-298; see there for further literature.

186 Barth, Introduction, 10. For the context of ethnicity and genetic history see Renfrew, *Roots of Ethnicity*, 21-29.

187 Emberling, *Ethnicity in Complex Societies*, 299.

188 Linder, *What was a Nomadic Tribe?*, 698-699.

189 Emberling, *Ethnicity in Complex Societies*, 302; Pohl, *Archaeology of Identity*, 14.

190 Linder, *What was a Nomadic Tribe?*, 696-697.

Genealogies, however, provide the notion of a common ancestry. In the past, this common ancestry served predominantly to create kinship relations, in a mythic sense rather than biological, and to support social cohesion of group members.¹⁹¹ The »forefather-group« – a descent group who shared common patrilineal ancestors up to the seventh generation before their own – is a standard feature in the kinship society model of Turkic »nomads«. The ethnographic evidence for this is rather slight.¹⁹² For the Eurasian steppe in particular, David Sneath observed that the deployment of descent and genealogies serve as technologies of power and forms of government that administer political subjects. Thus descent groups are more likely to reflect contingent historical conditions and forms of government in the wider sense than the kinship structures supposed in earlier anthropological models.¹⁹³

In the present, though, the notion of common ancestry suggests a collective memory of a former unity, of a time when a group was geographically united. Often, in this past, the group was autonomous or held political control. A frequent, but not universal, concomitant of this memory of past togetherness is the hope of a political reunification in the future.¹⁹⁴

In the end, genetic research also reinforces this conclusion: Chaix *et al.* tested the hypothesis of common ancestry from the geneticists' perspective, examining genetically ethnographically assigned descent groups (lineages, clans and tribes) from Central Asia with the assumption that if patrilineally organised descent groups correspond to a genetic reality, there should be a correlation between Y-chromosome diversity and group affiliation.¹⁹⁵ However, the genetic kinship coefficients of people of the same tribe (but from different clans and lineages) were all slightly negative. Their genetic kinship was not significantly higher than the mean kinship of the whole population, and, in two populations, even significantly lower. Thus, Chaix *et al.* concluded, tribes do not correspond to a real genetic entity; their claimed common ancestry is likely to be socially constructed.¹⁹⁶

Furthermore, in their comparative analysis of genetic diversity (mtDNA and NRY) in pastoral and farming societies in Central Asia, Chaix *et al.* detected that the »molecular signature of pastoral social organisation disappears over a few centuries only after conversion to an agricultural way of life.«¹⁹⁷ They concluded the discussion of their results with an essential question: »To which extent could social organisation have modified the action of natural selection or the intensity of drift during recent human evolution?«¹⁹⁸

So, following Lindner – as well as Yardumian and Schurr¹⁹⁹ – the question remains: »What was a Turk?«

191 Weber, *Economy and Society*, 389. For the Islamic worlds see, i.e., Savant and de Felipe, *Genealogy and Knowledge*.

192 Sneath, *Headless State*, 226, n. 20.

193 Sneath, *Headless State*, 202-203. For Eurasia see also Gingrich, *Medieval Eurasian Communities by Comparison*, 485-489. For the early Ottomans, see Lindner, *Nomads and Ottomans in Medieval Anatolia*, 32-36.

194 Emberling, *Ethnicity in Complex Societies*, 303.

195 Chaix *et al.*, *Genetic or Mythical Ancestry*, 1113.

196 Chaix *et al.*, *Genetic or Mythical Ancestry*, 1114-1115.

197 Chaix *et al.*, *From Social to Genetic Structures in Central Asia*, 43.

198 Chaix *et al.*, *From Social to Genetic Structures in Central Asia*, 47.

199 Yardumian and Schurr, *Who Are the Anatolian Turks?*

Conclusion

In the introduction of his 1992 lecture on »The Roots of Ethnicity: Archaeology, Genetics and the Origins of Europe« Colin Renfrew emphasized its underlying topic: identity.²⁰⁰ And indeed, in this study the issue of identity was encountered on two different levels. One level concerned the sampling criteria, in the case of modern DNA, according to which the identity of donors was assigned as Turkish. In most of the cases, these sampling criteria consisted of geography or language or even both; this implies – intended or not – the assignment of ethnicity. The second level is related to the past identity of »the Turks« that comprises of an even a more fuzzy set of social and political components.

Discussing the topic of the Central Asian origin of the Turks, which was a major research objective in the studies at question, I showed the complexity of applied sampling criteria by illustrating settlement and language policies that had a great impact on who is considered to be Turkish today. Moreover, I traced the topic of the Central Asian origin of the Turks which, at the latest with the foundation of the Turkish Republic in 1923, became a state-induced idiom. In the first instance, the Central Asian origin served to create a Turkish identity by establishing a collective memory with the help of a continuous narrative of Turkish states since the fifth century, thus legitimising territorial claims in Anatolia and excluding the non-Muslim population. I ended my discussion with the initial question »what was a Turkish tribe« from a social-anthropological and historical view and illustrated the hybrid and dynamic nature of tribal formation that is least based on a common genetic ancestry. Ultimately, this conception has been confirmed by genetic research in Central Asia.

Thus, the past and the present identity of the »object of investigation«, i.e. »the Turks«, remains uncertain.

As I mentioned in my introduction, the results of this analysis are presented from an archaeologist and historian's perspective. History cannot resist being affected by the developments of genetic research as it opens new and important avenues for the study of human history, e.g. migration. Bearing in mind the ongoing and future development of aDNA studies, several of my arguments brought forward here will become obsolete. However, it seems evident to me that multidisciplinary research teams have already yielded with past and contemporary genetic methodology the most convincing and significant results. I do hope that future genetic studies will be arranged in similar ways. Furthermore, I hope that my discussion of the Turkish context has indicated the usefulness of interdisciplinary research in genetics, i.e. the involvement of the traditional disciplines in order to avoid some pitfalls in the initial research setting, to contextualise the genetic data and to gain a meaningful interpretation.

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²⁰⁰Renfrew, *Roots of Ethnicity*, 19-20.

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