

Genetics, archaeology and the far right: an unholy Trinity

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1 **Genetics, archaeology and the far right: an unholy Trinity**

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Genetics, archaeology and the far right: an unholy Trinity

Recent advances in archeogenetics have revived an interest in grand narratives in which ethnic groups are once again thought to be agents of historical change. New scientific developments are generating a sense of optimism that difficult questions in palaeodemography may at last be solved. However, genetic research often uncritically makes use of essentialist models of past populations, reifying genetic populations as ethnic groups. This paper explores how such views of the past may play into notions of racial purity and fears of non-European migrants stoked by adherents of far-right ideologies.

Keywords: archaeogenetics; culture history; migration; Far Right

Introduction

In June 2015, two papers were published that seemed to transform our understanding of the population history of Europe. Wolfgang Haak et al. (2015) and Morten Allentoft et al. (2015) undertook genomic analyses of 69 and 101 individuals, respectively, spanning a period of 5000 years, from 8000 to 3000 years ago. The studies showed a massive demographic change between 4500 and 3000 years ago when an earlier ancestral group which was described as a mixture of European hunter-gatherers and Near Eastern farmers was almost fully replaced by a third ancestral group deriving from the Eurasian steppe belt. This third ancestral group has been identified with the so-called Yamnaya culture characterised by distinctive burial practices (Allentoft et al. 2015, 167). The people who created this Yamnaya culture appear to have been engaged in nomadic-pastoralism. People associated with the late Neolithic Corded Ware culture subsequently traced 79 per cent of their ancestry to the Yamnaya (Haak et al. 2015, 210). Such massive demographic change has been linked to the plague, but also to the colonisation of western Europe by predatory males (Rasmussen et al. 2015; Kristiansen et al. 2017, 339).

1 These studies have had great significance, not only because they provide a further
2 dimension to our knowledge of the population history of Europe, but also because they re-
3 ignited an old debate about the origin of the Indo-European language family. The so-called
4 kurgan culture of the Bronze Age steppes north of the Caucasus was first proposed as the
5 homeland of proto-Indo-European (PIE) speakers by Marija Gimbutas (1965, 23).
6 Gimbutas's hypothesis was later countered by Colin Renfrew (1987, 159; 1992) who argued
7 that the spread of Indo-European languages was linked to the dispersal of agriculture in
8 Europe and that the origin of PIE therefore lay in Anatolia 9000 to 8000 years ago.
9 Nevertheless, the hypothesis of Bronze Age language dispersal from the steppes retained
10 currency; principally promoted by David Anthony (2013; 2007, 83). The new genetic studies
11 appeared to give strong support to the steppic origin of PIE. In one fell swoop two significant
12 problems in the population history of Europe appeared to have been solved: where did the
13 peoples of Europe come from? And where did their languages come from?

14 These, and other related studies of genomic population history, generated great
15 enthusiasm among some archaeologists and geneticists about the possibilities now offered by
16 ancient DNA studies to archaeological research (Der Sarkissian et al. 2015; Kristiansen 2014;
17 Kristiansen et al. 2017; Anthony and Brown 2017). In a discussion article in *Current Swedish*
18 *Archaeology* which stimulated spirited responses Kristian Kristiansen calls these
19 developments the 'third science revolution' in archaeology, which, he claims, follows the
20 systematising work of the mid-nineteenth century and the radiocarbon revolution of the mid-
21 twentieth century (Kristiansen 2014, 14). He suggests that the new methods will have a
22 transformational impact not only by generating new evidence about the past, but – crucially –
23 also by changing how we study and think about the past. He states that 'we are in a period of
24 theoretical and methodological experimentation and reorientations, where everything that was
25 "forbidden" research 10–15 years ago are now among the hottest themes: mobility, migration,

warfare, comparative analysis, evolution, and the return of grand narratives' (Kristiansen 2014, 14). He considers these changes to be part of 'a larger shift from postmodernity to a revised modernity' (Kristiansen 2014, 23). In the face of such exuberant optimism, it is worth looking in more detail at what Kristiansen might mean by such a reorientation.

Migrations

Migration is one of the areas of 'forbidden' research mentioned by Kristiansen and it serves as a useful prism for tracking changes in archaeological thought over time. Throughout the nineteenth and early twentieth centuries, scholars had assumed that achievements of civilisation had spread westwards from the Near East and Egypt either through the diffusion of ideas or with the migration of people (Trigger 1997, 148; Adams, Von Gerven, and Levy 1978, 487). The primary method by which such migrations were traced in prehistory, and indeed in historic periods too, was by tracing the movement of 'cultures' or 'culture groups' (Childe 1925, 1950). Crucially, this notion of archaeological cultures assumes that ethnic groups are uncomplicated categories, clearly bounded and with a material record that is uniquely distinctive to them. The movement of these material attributes then becomes a proxy for the movement of people.

In British archaeology, the dominant perspective up to the 1960s was that all cultural innovations had come to the British Isles from continental Europe, either through the movement of people or through the diffusion of ideas. This was so universally accepted that Grahame Clark diagnosed British archaeologists in 1966 with an invasion neurosis, suggesting that 'they went out of their way to ascribe every good thing about their early past to foreign influences, if not indeed to foreign conquerors' (Clark 1966, 173).

The major theoretical critiques of the 1960s and again in the 1980s completely overturned this and shifted the focus towards local developments, initially from an evolutionary perspective and later with a turn towards theoretical approaches that

1 foregrounded local and small-scale developments and which focused on identities over
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6 2 externally ascribed ethnic identifiers. Migration was largely rejected as an explanatory device
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8 3 (Adams, Von Gerven, and Levy 1978, 503). Instead, social change was explained primarily
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10 4 with indigenous developments and, more specifically, with the notion that shifting ideas and
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12 5 identities bring about change in material culture. These approaches have latterly been
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14 6 criticised as ‘local, ‘indigenist’” or “immobilist” theorizing’ (Hawkes 1987, 203; Chapman
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16 7 and Hamerow 1997, 1).

19 8 When Kristiansen speaks of a coming paradigm shift in archaeology, in the wake of
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21 9 new scientific advances, and of a shift from ‘postmodernity to a revised modernity’, he means
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23 10 a turn away from these ‘immobilist’ approaches. However, he also implies a turn away from
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25 11 the notion that the subject and his or her subjective experiences of identity have primacy over
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27 12 external material signs of ethnicity or over genetic attributes of ancestry. Scientific
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29 13 approaches seem now to provide certainty and clarity in the formerly confused mixture of
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31 14 people and things. Yet, does this really herald a new way of thinking about the past? A closer
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33 15 look at the assumptions inherent in many genomic studies should raise doubts. The paper by
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35 16 Allentoft et al. (2015) was the more extensive of the two studies, involving a sample of 101
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37 17 individuals across Eurasia, spanning a date range of about 3000 years and a distance from
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39 18 east to west of about 5000 kilometres (3000 miles). Samples were chosen to represent
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41 19 different archaeological cultures, the clusters still matching Gordon Childe’s map of early
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43 20 Bronze Age cultures from 1925 very well (Childe 1925, 343) (Fig. 1). The genetic samples –
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45 21 teeth from specific individuals picked out from cemeteries – stand in for entire archaeological
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47 22 cultures which, in turn, represent ethnic groups. The implication of this sampling
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49 23 methodology is that each individual is representative of their ethnic group. There is no
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51 24 consideration of the particular social, economic and environmental contexts of the burials,
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53 25 nor of multiple ways by which social factors might influence population structure.
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Work since 2015 has focused on the nature and process of these migrations into western Europe. A study of Y-chromosome sequences, for example, noted an expansion of male lineages in Europe that coincided with the origin of the Yamnaya culture and two other significant archaeological cultures (Corded Ware and Bell–Beaker cultures) (Poznik et al. 2016, 597). Choosing selectively to focus on this evidence over other studies that detected evidence for high levels of female mobility and patrilocality, Kristiansen et al. (2017, 339) interpreted this pattern as being caused by war-bands of young men who migrated from the steppes to marry, or perhaps abduct, local women (contra Knipper et al. 2017; Sjögren, Price, and Kristiansen 2016).

They based this interpretation on work undertaken by scholars of Indo-European linguistics. Drawing on words and texts from the vast corpus of Indo-European languages, these scholars paint a picture of groups of roving, predatory young men that were thought to be a part of the social organisation of all Indo-European societies, from the earliest PIE-speakers to the Vrātyas of the Indian subcontinent and such groups among early medieval populations (Kershaw 2000; Petrosyan 2011). The assumption is that all societies sharing Indo-European languages must therefore also share a common social organisation.

Rather than being a dawn of new ways of thinking about the past, this is a throw-back to archaeological and linguistic methods of the early twentieth century, by-passing developments that have led to a more critical and nuanced way of thinking about ethnicity, gender and migrations. Instead, we see a return to notions of bounded ethnic groups equivalent to archaeological cultures and of a shared Indo-European social organisation based on common linguistic fragments. Both angles are essentialist and carry a deeply problematic ideological baggage. We are being offered an appealingly simple narrative of a past shaped by virile young men going out to conquer a continent, given apparent legitimacy by the scientific method.

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Archaeology, genetics and the public

The results of these studies were disseminated to news media through university press releases ("When modern Eurasia was born" 2015; "A massive migration from the steppe brought Indo-European languages to Europe" 2015). The publications on the genetic impact of the Yamnaya culture were picked up enthusiastically, with headlines particularly focusing on a narrative of migrations and the origins of Europeans (e.g. Jakobsen 2015; Griffiths and Newton 2015; "Wir sind Erben der Steppenreiter" 2015). Similarly, the highly gendered elements of the subsequent papers was directly promoted by the scholars in a press release and reworked into exciting headlines by journalists (Liberatore 2017; "Steppe migrant thugs pacified by Stone Age farming women" 2017). In a recent story in the *New Scientist*, Kristian Kristiansen again emphasised the apparently violent impact of the Yamnaya: "I've become increasingly convinced there must have been a kind of genocide," says Kristian Kristiansen at the University of Gothenburg, Sweden (Barras 2019).

It is therefore not surprising that far-right and white supremacist groups also considered the results of these studies. Far-right groups have had an interest in genetics that can be traced back to the racial anthropology of the nineteenth century and to the eugenics movement (Levine 2010; Marks 2012). The increasing commercial availability of genomic ancestry tests over the last decade have reignited this interest, making it possible for members of these groups to examine their own whiteness genetically. While these tests have at times had destabilising effects on white nationalists' notions of their own racial identity, there is nevertheless a widespread consensus that race is a genetic reality. Sociologists Aaron Panofsky and Joan Donovan (2017) carried out a study of the engagement of white nationalists with genetics on the webforum Stormfront. This forum has existed since 1995 when it was launched by a former Grand Wizard of the Ku Klux Klan, Don Black. It receives several million page views per month (Panofsky and Donovan 2017, 13). Due to its size, it

provides a useful sounding board for discussions about race and genetics among white supremacists online. Panofsky's and Donovan's study revealed a preoccupation with population history, especially in the context of the results of forum users' own genetic ancestry tests.

My own examination of discussion threads on Stormfront revealed that the main interest of members was in Y-chromosome haplotypes that they believe to identify the white race. However, there were also 250 mentions of 'Yamnaya', 346 of 'Corded Ware' and 87 of 'Bell Beakers' (last accessed on 2 April 2019). A number of these make direct reference to recent genomic studies. In a thread entitled 'West-Europeans not the original Indo-Europeans' forum members discussed the results of the studies by Haak et al. (2015) and Allentoft et al. (2015). User PolishSlavAryan came to the conclusion that the Yamnaya culture represented the Aryans they were looking for as the ancestors of Europeans. Another user, Everdred, writes: 'A primarily male migration of Yamnaya herders westward into Central and Northern Europe took up wives from the Neolithic farming cultures and gradually formed the new Corded Ware Culture, which likely represented the Proto-Germanic community (Thread: New study on the formation of Corded Ware Culture; 04-06-2017, 05:29 AM)'.

Responding rapidly to a story in the *New Scientist* ('Story of the most murderous people of all time revealed in ancient DNA', 27 March 2019) the same user comments, using anti-semitic code: 'Looks like ((([REDACTED]))) and others are starting an "academic" attempt to demonize the Yamnaya (Proto-Indo-Europeans) as evil, genocidal maniacs.' (Thread: Archaeology; 31-03-2019, 10:22 pm; redacted by author).

The great number of links to scientific publications and media reports of research on the Stormfront forum indicates that genomic research on population history are of great appeal to some members of racist and far-right groups since they believe that this research

will reveal objectively the origins of races. News reports on the Yamnaya are of particular interest since they seem to be providing clues to the origins of Aryans.

The gendered elements of the research, especially the focus on male war-bands, also resonate with masculine self-conceptions on many far-right websites. The Aryan Männerbund was promoted by the Nazis to be part of the natural order of German society and can be found again in modern fascist movements (Gottschewski 1934; Baeumler 1934; Weiser-Aall 1927). Over the course of the twentieth century far-right men in Scandinavia, Germany and the US have enduringly identified themselves with the ideal of the warrior hero, banded together in militias (Miller-Idriss 2017; Michael 2003).

Migrations and grand historical narratives

White nationalists do not exist in a social vacuum and their notions about race and migrations are extreme re-imaginings of widely shared popular ideas. The widespread use of commercial genetic ancestry testing has led to a ‘racialization of genetics and the molecularization of race’, according to Aaron Panofsky and Catherine Bliss (2017, 80), caused in part by geneticists’ frequent use of race- or geography-based population labelling in their studies which is in turn replicated by commercial companies. Catherine Nash (2015, 81) notes that population geneticists often hold the prior assumption ‘that sociocultural categories such as ethnic identities correspond with genetic distinctiveness’. While the impact of such tests on personal identities may be variable (Scully, Brown, and King 2016), we can nevertheless detect a broader social consensus that there is indeed a genetic basis to many common-sense conceptions of population difference. This ties in with a current popular concern with migration, brought on partly by the European refugee crisis beginning in 2014, but also more widely by the global labour-migrations of the last decades. News stories involving past migrations generate significant interest and these are invariably framed in ethnic terms. The infamous ‘Breaking Point’ poster of the Vote Leave campaign in front of

1 which the British far-right politician Nigel Farage was photographed in June 2016, just weeks
2 before the Brexit referendum in the UK, illustrates the clearly racial dimensions of this.

3 Scholars working on genomic population histories have so far not engaged enough
4 with the wider social context in which their work is received. The histories of archaeology
5 and anthropology are intertwined with the histories of nationalism, colonialism and racism,
6 and much important research has revealed past political appropriations of our disciplines (e.g.
7 Trigger 1984; Alfredo 2010; Gould 1996; Kohl and Fawcett 1995; Beck et al. 2004), but
8 there is a danger that this is considered a problem of the past that has been overcome. While
9 there is a lively scholarly debate both about the implication of the results of genomic studies
10 and about research methods and assumptions, this has largely been confined to scholars in the
11 field (Hofmann 2015; Furholt 2017; Vander Linden 2016; Vander Linden 2018; Heyd 2017;
12 "Forum: Genetic History" 2018). However, geneticists and archaeologists also need to
13 consider the outward-facing consequences of their genomic studies more critically.

15 **Nomenclature and sampling practices: top-down or bottom-up?**

16 What is to be done? There are two areas where more work is needed. First, the
17 research methodology of genomic studies must fully consider the complexities surrounding
18 ethnicity and migration that are coming out of theoretically-informed research in
19 archaeology, and it must do so before data collection, not after (Niklasson 2014, 59). A
20 central problem here is that biological populations are often implicitly assumed to be
21 congruent with ethnic groups. In a survey of archaeogenomic publications since 2014,
22 Stefanie Eisenmann et al. (2018) examined the nomenclature used to describe the relationship
23 between genetic clusters and archaeological evidence. They found that only one publication
24 (Fu et al. 2016) used an entirely neutral nomenclature, i.e. by simply naming genetic clusters
25 based on the name of the site from where the samples were taken. All others used labels

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1 based on subsistence strategies (e.g. hunter-gatherers) or archaeological cultures (e.g. Corded
2 Ware), or a combination of both. The authors are of the opinion that the use of such labels
3 nevertheless has value, since ‘convergences [between genetic clusters and archaeological
4 cultures] might help shed light on the nature of an archaeological culture, how it spread, and
5 what may lie hidden behind a group of similar objects and/or practices.’ (Eisenmann et al.
6 2018, 8).

7 Perhaps, but this sidesteps a more fundamental methodological problem. Taking small
8 numbers of samples of individuals as representative of social or culture groups introduces an
9 *a priori* assumption that social or culture groups must be genetically homogeneous and it
10 obscures any genetic heterogeneity that may be present. That this may be the case has already
11 been observed in some cases (Olalde et al. 2018; Gamba et al. 2014). To counter simplistic
12 notions of migration, Marc Vander Linden (2019) has called for explicit hypothesis testing
13 through a series of demographic simulations that would allow us to determine the most likely
14 causes of genetic admixture or replacement.

15 Instead of presupposing that genetic ancestry and patterns in material culture must
16 overlap, we should therefore ask ourselves, do burial identity, ancestry and migration form a
17 coherent package? If not, what does this mean for the past societies that we study? A number
18 of fine-grained genomic studies of individual cemetery populations are beginning to provide
19 fascinating insights here (Amorim et al. 2018; Knipper et al. 2017; Schiffels et al. 2016).
20 Krishna Veeramah (2018, 87) rightly calls for the need for a ‘bottom up’ approach to
21 genomic sampling as the only way that will allow us to understand past social processes such
22 as migrations.

23 **Communicating with the public**

Second, scholars need to reflect more critically on how their research and the processes by which it is communicated to the public may further problematic political and social agendas. Journalists and popular authors are beginning to show the way. Two recent books written for a more general audience have tried to emphasise the complexity of human ancestry and have also referred to the dangers of racist interpretations of genomic data (Bojs 2017, 340; Reich 2018, 247). In an article in the *New York Times Magazine*, Gideon Lewis Kraus drew attention to the complex web of personal relationships, laboratory infrastructures, sampling strategies and journals' peer review practices that characterises contemporary archaeogenetics and which may facilitate researchers' emphasising exciting stories over nuance (Lewis-Kraus 2019).

Yet, such critical reflection should not be left to outside observers. Archaeologists and geneticists need to do the intellectual work themselves. We have to be more aware of the public impact of our work, but, more importantly, we should also make efforts to shape the public discourse ourselves.

Press releases are the main route by which academics can disseminate their work to the media. University press offices generally work closely with academics to make sure that the text is both scientifically accurate and engaging for a journalistic audience, since journalists often quote directly from the releases or rewrite them only in a minor way. Press releases are therefore key to shaping how research news is presented in the media. Rather than aiming to tell a simple, exciting story about ethnic groups and migrations, there is great value in being transparent about the complexities and difficulties that scholars encounter when they go about their work and there many are examples that show that such news stories can be just as engaging (e.g. Greshko 2017; Ward 2017).

This is particularly important in cases where research results are controversial or easily slotted into a Far Right or racist discourse. The demographics of Roman Britain have

1 been one such area of controversy. In July 2017, an educational video produced by the BBC
2 which showed a brown-skinned centurion generated an intense (and sometimes vicious)
3 discussion on Twitter, with many contributors questioning the genetic and archaeological
4 evidence for such ethnic diversity in Roman Britain. Subsequently, a number of academics
5 contributed in nuanced and informative ways to the public debate, explaining the scientific
6 methods and countering misinformation (e.g. Raff 2017; Redfern 2018).

7 Public engagement can and should go beyond simply generating scientific news
8 content. As researchers we should be transparent about the complexities of the research
9 process and the limits of our interpretations, but we should also aim to intervene critically in
10 public debates and to respond proactively when our research is used for problematic political
11 and ideological ends.

12
13 **Conclusion**

14 Scientific advances in sequencing ancient DNA over the last decade have opened up
15 new areas of research. It is now possible to create genomic population maps for different
16 periods in the human past and to discover information about past populations that was
17 previously entirely inaccessible to us. However, much of genomic research so far has
18 employed assumptions about past populations as static bounded units, characterised by
19 distinct material culture. These assumptions have much more in common with conceptual
20 approaches in the archaeology of the early twentieth century than of the early twenty-first. As
21 a result, the past few years have seen a reification of race and ethnicity under the banner of
22 scientific progress, and this has been communicated to a public already very interested in
23 narratives about origins and ancestry. Notions of a biological basis of race have also been
24 taken up enthusiastically by white supremacists interested in the ancestry of the ‘white race’.
25 Recent genomic research on population histories has therefore provided scientific

1 legitimization of pre-existing racialized and even racist ideas. There is little evidence that
2 scholars engaged in genomic research are trying to communicate the complexity of their
3 work; instead exciting but simplistic narratives abound. There is an urgent need for much
4 more critical rigour in genomic population studies, both in terms of the kinds of questions
5 that are being asked and in terms of how results are being communicated to the public.

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12 Figure 1. Sampling locations and classification according to period and/or archaeological
13 culture from the study by Allentoft et al. (2015: 168) superimposed on Gordon Childe's map
14 in *Dawn of European Civilization* (1925: 343-4).

15 Childe's legend: 'Europe in period IV c. 1400 B.C.: I Minoan-Mycenaean civilization; II
16 Civilization of Troy VI.; VII Perjámos culture; VIII Unětician culture; IX Glina III culture; X
17 Pontic Copper Age; XII Northern culture; XIIa Globular amphorae; XIII Siculan II culture;
18 XIV Terremare and allied cultures; XV El Agrar culture; XVI Mondsee-Altheim culture;
19 XVIII Armorican Bronze Age; XVIII Wessex culture; XIX Food-vessel culture; Battle-axe
20 cultures: E Boat-axe, F Separate grave, G Oder.'

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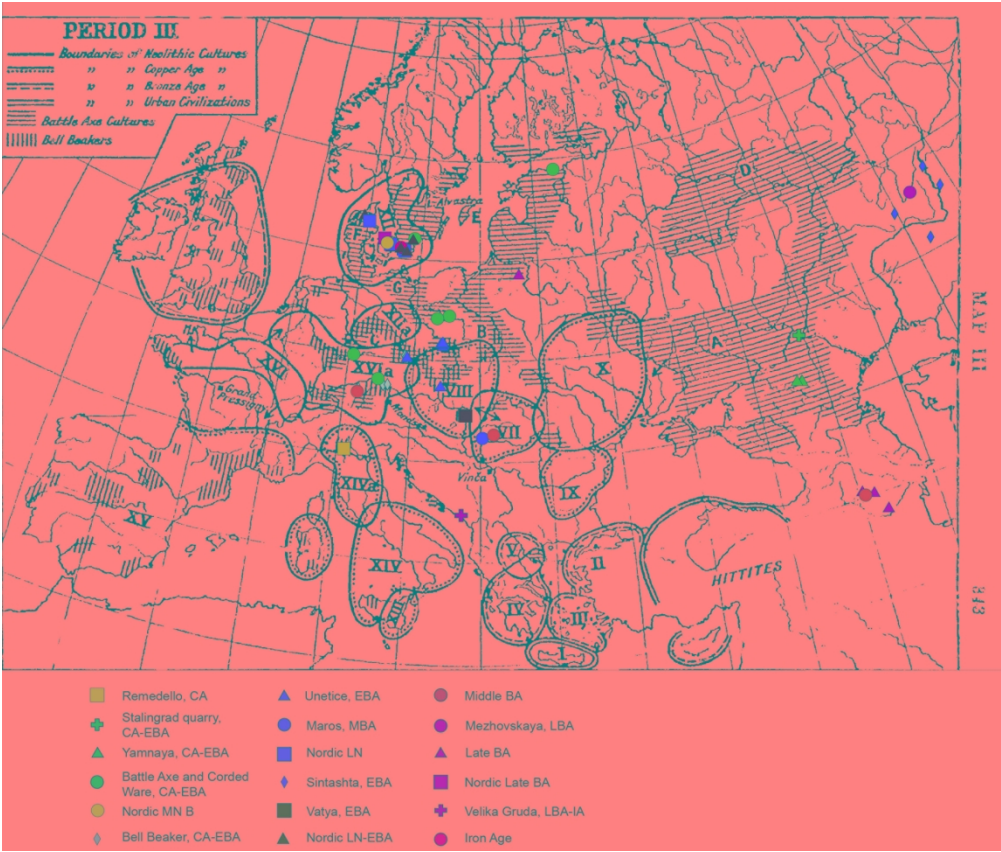


Figure 1. Sampling locations and classification according to period and/or archaeological culture from the study by Allentoft et al. (2015: 168) superimposed on Gordon Childe's map in Dawn of European Civilization (1925: 343-4).

Childe's legend: 'Europe in period IV c. 1400 B.C.: I Minoan-Mycenaean civilization; II Civilization of Troy VI.; VII Perjámos culture; VIII Uneticean culture; IX Glinia III culture; X Pontic Copper Age; XII Northern culture; XIIa Globular amphorae; XIII Siculan II culture; XIV Terremare and allied cultures; XV El Agrar culture; XVI Mondsee-Altheim culture; XVIII Armorican Bronze Age; XVIII Wessex culture; XIX Food-vessel culture; Battle-axe cultures: E Boat-axe, F Separate grave, G Oder.'

