

Population, culture history, and the dynamics of change in European prehistory*

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Despite many attacks on its shortcomings, culture history has remained in practice the dominant framework for describing and interpreting European prehistory. It has gained even more salience in recent years because the new information coming from ancient DNA about the genetic ancestry of individuals in prehistory seems to show that this correlates closely with the cultural affiliation of the archaeological material with which they are found, raising concerns that old and discredited links between biological and cultural identity are being revived. This article argues that exploring the links between cultural and genetic ancestry does not need to fall into these errors if it takes its theory and methods from the discipline of cultural evolution and rejects characterization of the relationship in terms of 'ethnic groups'. This involves describing the archaeological record in more fine-grained, less essentialist ways and at the same time linking the archaeological and genetic patterns to histories of the rise and decline of populations and the interactions between them.

In this article, I will argue that identifying, dissecting, and explaining the kinds of culture historical patterns that archaeologists have been characterizing for the best part of the last 150 years is a legitimate and even fundamental endeavour for archaeologists in the twenty-first century. The ancient DNA (aDNA) information and the archaeological population proxies that have become available in recent years show the fundamental role of demography in understanding culture historical patterns and the dynamics of cultural change. However, to assume that the link between population patterns and cultural ones should be seen in terms of ethnic groups or other homogeneous entities is unhelpful and misleading. The models of cultural change that have been developed in the rapidly growing discipline of cultural evolution provide the tools to take a more analytical approach, by examining the extent to which cultural traditions in different spheres of life are transmitted and change in parallel with genomes. However, research to operationalize this approach archaeologically has barely begun and the models do not by themselves tell us much about macro-level change,

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where archaeology has a major contribution to make. Making that contribution requires us to integrate the newly available aDNA information, which tells us about the history of biological populations, or mating networks (Anthony *et al.* 2022), with chronologically high-resolution data on the specifics of individual cultural traditions at a high level of granularity, in the light of information about demographic dynamics and the factors that affect them.

In what follows, I will therefore briefly outline the historical background to the debates on culture history, critiquing the interpretation of cultures as ethnic groups and examining the renewed debates on these topics resulting from the results of aDNA analysis. I will go on to argue that we can escape the current impasse by making use of models from dual inheritance theory (Boyd & Richerson 1985; Cavalli-Sforza & Feldman 1981), which sees genetic and cultural transmission as parallel processes with different dynamics. However, these models work at the micro scale, and to understand the cultural patterns recovered by archaeology we need to take account of demographic patterns and processes at a larger scale; this has become possible thanks to recent methodological developments. These topics are brought together in a proposal for a research agenda for identifying the connections between genetic, cultural, and demographic patterns. The very different linkages between them in different cases are illustrated by two case studies: the spread of farming into Europe in the late seventh and sixth millennium BCE; and the spread of Corded Ware cultural traits across the northern half of Europe in the third millennium BCE. A brief conclusion summarizes the argument for taking a cultural evolutionary approach that escapes the dichotomy between biological ancestry and cultural groups and integrates cultural evolutionary models with the study of the scale of spatial interaction and demographic processes to address large-scale change.

Historical background

For prehistorians of Europe, and indeed of many other parts of the world, the culture history legacy of Gustaf Kossinna and Gordon Childe is still with us, theoretically despised but indispensable in practice. Its influence is visible to this day in the distribution maps and chronological charts of cultures that always accompany synthetic regional studies (e.g. Müller & Peterson 2015), which implicitly or explicitly start from the assumption that cultures are real entities, following Childe's famous definition:

We find certain types of remains – pots, implements, ornaments, burial rites and house forms – constantly recurring together. Such a complex of associated traits we shall call a 'cultural group' or just a 'culture'. We assume that such a complex is the material expression of what today we would call 'a people' (Childe 1929: v-vi).

It seems that despite the major theoretical shifts of the past sixty years, which have largely either rejected or ignored them, archaeological cultures provide organizing principles that we still need even if we have not been sure what they are and what to do with them (cf. Neves 2022: 44–51, for Amazonia; see Roberts & Vander Linden 2011 and Vander Linden & Roberts 2011 for an extensive review of the debates). This is despite the many demonstrations that when the distributions of individual elements of particular 'cultures' are plotted, they rarely, if ever, coincide, and there is no obvious criterion as to which we should choose to define the cultural boundary (e.g. Furrholt 2008a; 2020; Shennan 1978); or the ethnographic studies of domestic ceramic production showing that the spatial distributions of different attributes, such as decoration, fabric, and shape, stem from different kinds of interaction processes

(Gosselain 2000; Roux 2007). It is therefore unsurprising that the identification of cultures with other kinds of entities has been consistently problematical. Archaeologists have never been able to convincingly tie their patterns to the ethnic groups and boundaries that became the focus of ethnographically based anthropologists in the 1960s (discussed in, e.g., Jones 1997; Richard & MacDonald 2015). The same is true of political entities. Wotzka (1997) pointed out many years ago the enormous discrepancy in scale between the areas of the 'cultures' archaeologists identify and the size of political entities in non-industrial societies below the level of empires.

In recent years, however, the long-standing debates about culture historical entities have been revived and given a new significance by the results of the whole genome aDNA studies of prehistoric populations that have appeared, many of them focused on populations of the last ten thousand years in Europe that have been central to culture historical studies (e.g. Allentoft *et al.* 2015; Haak *et al.* 2015; Hofmanová *et al.* 2016; Lazaridis *et al.* 2016). The reason for the controversy is that the findings seem to support some of the classic culture history claims that archaeological cultures correspond to biological populations (Frieman & Hofmann 2019; Furholt 2018; Kristiansen 2022). Thus, it turned out that the genomic ancestry of individuals associated with the Corded Ware 'culture', which appeared widely across northern, eastern, and central Europe in the first half of the third millennium BCE, included a large element suggesting descent from the Pit Grave (Yamnaya) culture of the Russian steppe (Allentoft *et al.* 2015; Haak *et al.* 2015). This was seen as supporting the long-standing and controversial proposal of the twentieth-century US-Lithuanian archaeologist Marija Gimbutas (1956) that invasions from the steppe introduced Indo-European languages to Europe. Moreover, she had characterized these people as patriarchal warrior pastoralists, and the genomic evidence indicated that expansion of people archaeologically associated with Corded Ware material culture seems to have been male-biased (Goldberg, Günther, Rosenberg & Jakobsson 2017; Saag *et al.* 2017; Scorrano, Yediay, Pinzotti, Feizabadifarahani & Kristiansen 2021). The debates have become all the more fraught because of the exploitation of these (and other) genetic results by right-wing nativist political groups whose agendas are similar to those of the Nazis and their use of Kossinna (see, e.g., Hakenbeck 2019).

(Un)linking aDNA and culture histories

To escape the historical baggage associated with making an equivalence between the genomic groups resulting from aDNA studies and the long-established culture historical categories, it has been suggested that the former should be described in terms of taxonomies that disregard archaeological information altogether (Eisenmann *et al.* 2018). However, this does not solve the problem. The proposal is a superficial one that fails to come to grips with the substantive processes that can result *in some cases* in genomic and cultural patterns being aligned and in other cases not (Riede, Hoggard & Shennan 2019).

To explain the relations between them, there are two requirements. First, we have to distinguish between demographic histories of populations and their genomes, on the one hand, and histories of the cultural traditions with respect to different practices for which we have evidence, on the other. Do we see changes in the genomic patterns in a given region at the same time as we see changes in cultural traditions, and vice versa? It is fair to say that on this there is a general agreement. But, second, we need a theoretical framework that specifies processes that may connect the two, potentially resulting in

close correlations in some cases but not in others. We can make this connection if we see them both as a result of information transmission processes, making use of the foundational work on dual inheritance theory and the mechanisms of cultural evolution by Boyd and Richerson (1985), Cavalli-Sforza and Feldman (1981), and others.

In the case of genetic transmission, the process is obviously biological reproduction, 'vertical transmission' from parents to offspring. The processes involved in the transmission of cultural traditions, based as they are on social learning, are much more complex. Work on dual inheritance theory showed that what is transmitted may be affected by a wide range of different factors, such as a tendency to conformist learning or to preferring prestigious models, or whether the model-to-learner ratio is one-to-one, one-to-many, or many-to-one (Boyd & Richerson 1985; Cavalli-Sforza & Feldman 1981; for archaeological examples, see, e.g., Bettinger & Eerkens 1999; Crema, Kandler & Shennan 2016). These factors will affect the extent to which people are open to novelty, whether local or introduced from outside.

Of course, this means that there is no *necessary* link between genetic patterns transmitted via biological reproduction and the cultural patterns transmitted by social learning, affected by the kinds of influences just mentioned. On the other hand, in cases where cultural features are passed on to children by parents, or other close relations of the senior generation within the household, we can expect genomic and cultural information to be transmitted significantly in parallel and therefore to show similar patterns in space and time: the cultural traits concerned will only be transmitted between people who are closely related. Thus, if people move, not only will their genomes move with them but so also will those vertically transmitted cultural traits. By the same token, there is also no necessary link between cultural patterns in different spheres of life: whether they are transmitted in parallel depends on whether the factors influencing them are similar or not. Kinship-related post-marital residence patterns are also relevant here: for example, predominantly female- or male-associated traits may be differentially distributed depending on whether residence is patrilocal or matrilineal. Cultural traditions and their elements can come in different packages with different histories affected by different forces (Boyd, Borgerhoff-Mulder & Richerson 1997). In the case of craft traditions, how such processes work at the micro scale is increasingly well understood as a result of the growing number of studies of apprenticeship in different crafts (e.g. Roux *et al.* 2017), which are effectively providing the micro foundations for evolutionary studies of cultural practices. In the light of these, there is no reason to believe that the factors affecting the transmission of domestic pottery styles are the same as those, for example, that affect the continuity or otherwise of burial practices in a community. Moreover, there is no basis for assuming that innovation rates in different domains will be the same.

Taking this perspective confirms the view that 'archaeological cultures' represent a very simplistic and misleading way of conceptualizing this kind of patterning, an error that is compounded by then asking how they relate to genomic patterns, producing the crisis described above. In effect, we need to create a very different kind of culture history, one based on the kinds of mechanisms proposed by cultural transmission theory. It is the different dynamics created by such mechanisms that produce the varying spatial distributions of different cultural attributes when they are frozen in a distribution map. Potentially, then, we can use the quantitative tools of cultural evolution to identify the outcomes of transmission processes in different domains and the factors affecting them (e.g. Crema *et al.* 2016; Shennan, Crema & Kerig 2015).

However, we cannot consider cultural patterns and processes or their links to genomic ones in isolation. They are inseparable from demographic ones, and exploring the links between them requires independent information on demographic patterns and processes.

Obviously, the starting point for this is the aDNA genomic revolution discussed above, because it tells us directly about changing spatial and temporal patterns of human mobility and their links to people's genomic ancestry. In doing so, it also provides us with an independent way to assess whether particular cultural traits were transmitted vertically in parallel with the genes or not. However, to make sense of these patterns, we need to consider demographic dynamics, and the growing availability of archaeological 'big data' and associated methods of analysis make it possible to do this.

Population patterns and processes

Population patterns play a major role in understanding genomic and cultural change, for two connected reasons. First, they represent the outcome of adaptive processes. When population increases in a region, it is an indication of the adaptive success of the culturally transmitted subsistence strategy of those who use it (Puleston & Winterhalder 2019). However, other things being equal, any strategy will eventually lead to a population equilibrium, with births and deaths balancing one another, following the well-known logistic curve of population growth (Wood 1998). Regional population decline, on the other hand, is likely to reflect adaptive failure of some kind, over-exploitation of resources, for example, or the effect of changing environmental conditions. Second, to the extent that the appearance and disappearance of a particular genomic ancestry pattern or the rise and demise of particular material culture traditions in specific domains is associated with demographic expansions and contractions, tracing the associated population trajectories is fundamental. From a spatio-temporal point of view, we can imagine the existence of a dynamic population 'surface', going up in some regions as it goes down in others, influenced by external factors like climate change, but also internal ones like subsistence innovations or the regional prevalence of warfare (cf. Kondor *et al.* 2023).

Of course, addressing questions about the effect of demographic processes on cultural and genomic distributions in space and time depends on having independent knowledge of population patterns. These attracted little interest in archaeological studies until recently (though see Hassan 1979; 1981). The Neolithic Revolution apart, it was assumed that populations grew extremely slowly but steadily through prehistory so were of little interest. In any case, it was believed that population patterns in prehistory were very difficult, if not impossible, to reconstruct.

Over the last two decades, the growing understanding of evolutionary demography (e.g. Hill & Kaplan 1999) and of the role of population processes in human adaptation, combined with the need to explain the patterns being revealed by aDNA, has led to a steadily increasing interest in the development of methods for creating reliable, widely applicable archaeologically based proxies for monitoring prehistoric population patterns, and it has turned out that these patterns have not been nearly as stable as previously assumed.

The most important of these methods has been the use of summed probabilities (and related measures) of radiocarbon dates (e.g. Shennan *et al.* 2013), because these are very widely available in increasingly large numbers and now provide relatively precise dating information. To a first order of approximation, especially if large numbers

of dates are available, there should be a relationship between the number of dates falling within a given time interval in a given region (or their summed probabilities or other derived measure) and the amount of human activity, which depends on the population size. In general, the more dates we have, the more reliable our conclusions are likely to be. However, because of the complexities of radiocarbon calibration, we need methods to establish whether the fluctuations we see are ‘real’ and not artefacts of the calibration curve. The validity of the summed radiocarbon probability method has been the subject of intense debate between proponents and critics, leading to progressive methodological developments in this area (Attenbrow & Hiscock 2015; Contreras & Meadows 2014; Crema 2022; Crema & Bevan 2020; Ramsey 2017; Shennan *et al.* 2013; Timpson, Ramiro, Thomas, Méndez & Manning 2021), combined with an increasing effort to cross-check them against other lines of evidence, for example the extent of forest clearance, visible in fossil pollen cores. These have consistently been shown to correlate with the radiocarbon proxy (e.g. Feeser, Dörfler, Kneisel, Hinz & Dreibrodt 2019; Kolář, Macek, Tkáč, Novák & Abraham 2022; Lechterbeck *et al.* 2014; Woodbridge *et al.* 2014). Most recently, methods have been developed to systematically integrate different proxies using Bayesian modelling (Hinz, Roe, Laabs, Heitz & Kolář 2022).

In fact, wherever they have been used, these methods have revealed the existence of regional population fluctuations (e.g. Arroyo-Kalin & Riris 2021 for South America; Crema & Shoda 2021 for Japan; Manning & Timpson 2014 for North Africa; Zahid, Robinson & Kelly 2016 for North America). As discussed below, they have revealed unexpected regional patterns of population boom and bust across Europe after the arrival of farming (Hinz, Feeser, Sjögren & Müller 2012; Hinz *et al.* 2022; Kolář *et al.* 2022; Parkinson, McLaughlin, Esposito, Stoddart & Malone 2021; Porčić, Blagojević, Pendić & Stefanović 2021; Shennan *et al.* 2013).

A research agenda

In the light of the various considerations outlined above, we can propose a set of questions that define a general research agenda for examining the relations between demography and space-time patterns in genomic variation and cultural traditions in particular times and places.

- Do we have radiocarbon and/or related evidence of population expansions and/or contractions?
- Do we see changes in the spatial-temporal distribution of genomic variation?
- Do population fluctuations or changes in the distribution of genomic variation correlate with changes in cultural traditions or their distribution?
- If so, do all cultural domains change or only some of them? Do any changes occur at the same rate or have the same origin?
- Conversely, do cultural traditions in some domains change (or remain stable) in their content or distribution regardless of population fluctuations or changes in genomic variation?
- What interaction and/or transmission processes underlie these various possibilities?

The next two sections of this article will address these questions by means of two contrasting case studies from Neolithic Europe: the initial spread of farming into

southeast and central Europe in the late seventh and sixth millennium BCE; and the spread of Corded Ware in central and northern Europe at the beginning of the third millennium BCE.

The initial spread of farming into southeast and central Europe: population dispersal and cultural change

Although the initial development of the southwest Asian Neolithic package of farming practices – combining cereals, pulses, and domestic animals with the knowledge to exploit them successfully and ensure their propagation – was not a rapid one, once it had come together it spread rapidly westwards from central Anatolia, starting in the early seventh millennium BCE (Brami 2015; Fort, Pujol & Vander Linden 2012). It reached the coastal zone of northern Greece by 6500 BCE (Maniatis & Adaktylou 2021), and by 6200 BCE, the farming frontier had reached the middle Danube (e.g. Whittle, Bartosiewicz, Borić & Pettit 2002).

The population increase in southeast Europe anticipated on the basis of the introduction of the agricultural subsistence system is seen in the summed radiocarbon probabilities for Greece and the Balkans (e.g. Porčić *et al.* 2021; Vander Linden & Silva 2021; Weiberg *et al.* 2019). The genomic evidence has shown that it was overwhelmingly an expansion of successive generations of descendants of farmers whose ancestry lay in the Aegean-Anatolian region, with very little reproductive intermixing, except for the site of Lepenski Vir (Brami *et al.* 2022; Gelabert *et al.* 2023; Mathieson *et al.* 2018).

Since the Balkan farmers were immigrants into a region only thinly occupied by hunter-gatherers with a very different way of life, in addition to their subsistence system they must have brought with them *all* the features of the new way of life, including their social norms and institutions, the new subsistence system, their pottery (characterized by a similar set of fabrics, manufacturing techniques, and decorative styles), as well as their novel forms of architecture, which therefore must have been transmitted broadly in parallel with one another and also with their genomic signature. However, there were several routes north from the Aegean coast (Krauss, Marinova, De Brue & Weninger 2018: fig. 5) and it is likely that the dispersal took place in small groups that would not have been completely identical in their cultural attributes, while innovation rates would also have varied in different domains and some would have been more prone to horizontal between-group transmission than others. Thus, the results of Gaastra, de Vareilles, and Vander Linden (2022) show variation in subsistence patterns, responding to local environmental conditions. De Groot (2016: chap. 6) demonstrates spatial and temporal stylistic variation in pottery, but ceramic fabric recipes were more stable, as we would expect from the ethnoarchaeological work on ceramic attribute transmission discussed above (Spataro 2010).

So far, then, we can answer the first four of the questions above in the affirmative. There was a demographic expansion. It correlated with an expansion of the distribution of a characteristic genomic pattern originating in the Aegean-Anatolian area. These changes were associated with an expansion in the distribution of a broad range of cultural traditions, in addition to subsistence practices, but these were not immutable and underwent change in the course of the expansion.

However, the northwards demographic expansion was not sustained. The central Balkans saw a shift from boom to bust c.6000 BCE and then another boom-bust sequence from c.5800-5500 BCE (Porčić *et al.* 2021), paralleling a similar boom-bust pattern in the Carpathian Basin with the arrival there of farming and the characteristic

first farmer cultural traditions (Blagojević, Porčić, Penezić & Stefanović 2017). In fact, all the evidence points to a massive drop in population, if not an occupation gap, in the central Balkans and southern Carpathian Basin after 5500 BCE (Oross *et al.* 2020; Vander Linden & Silva 2021; Weninger 2020).

Thus, after arriving at a latitude of $\sim 45^\circ$ north at ~ 6000 BCE, the northern farming frontier remained largely static in the Carpathian Basin (Bocquet-Appel, Naji, Vander Linden & Kozłowski 2009; Oross *et al.* 2020) and population declined. A new phase of northwestwards expansion only began after 5500 BCE, probably ~ 5350 BCE (Oross *et al.* 2020). It is likely that this frontier corresponds to the limit of the Mediterranean seasonality conditions to which the wild ancestors of the crops and their domestic descendants were genetically adapted, and the ensuing delay reflected the time required for the evolution of crop varieties that would be successful at latitudes with a lower number of growing-degree days (Ivanova-Bieg 2020).

It is during this static phase of apparently low population that we see the Formative Linear Pottery Culture (LBK, from its German name) developing, so far known from only two sites on the western edge of the Carpathian Basin (see, e.g., Jakucs 2020). The formation of new cultural patterns is more likely to occur in small groups physically separated to some degree from their parent population, for a variety of reasons: the sanctions that help to maintain the existing pattern may be weaker, for example, allowing social innovations. Moreover, the new pattern that emerges may have a considerable chance element to it, especially in the presence of founder effects and drift arising from transmission in small populations, though there is little sign of this in the genomes (Gelabert *et al.* 2023).

From ~ 5350 BCE, we see another massive demographic expansion. On the basis of an extrapolation from local survey data, Oross *et al.* (2020) estimate that there were already ~ 285 LBK sites in the western Carpathian Basin in the fifty-fourth century BCE, increasing to nearly 2,400 by the late sixth millennium BCE. But this is not just a local increase. At the same time, there is a very rapid demographic expansion westwards across central Europe as far as the Rhineland, evidenced by the booms visible in the summed radiocarbon probability distributions in the regions that were occupied (Shennan 2018: chap. 4), based on the apparently paradoxical combination that had emerged of, on the one hand, a sedentary lifestyle, evidenced by the large investment in longhouses, and, on the other, very high mobility (Petrasch 2020).

This is another population dispersal of genetic descendants of Aegean-Anatolian farmers with continuing very low levels of hunter-gatherer genetic admixture, which had probably already occurred not long after 6000 BCE (Gelabert *et al.* 2023; Lipson *et al.* 2017). However, in the obscure phase in the northern Balkans and the Carpathian Basin in the mid-sixth millennium BCE, a major cultural transformation takes place. In fact, there are two. The Early Neolithic Starčevo tradition splits into the LBK to the north and the Vinča culture to the south, in a process of cultural phylogenesis (Bánffy & Höhler-Brockmann 2020; Jakucs 2020; Oross *et al.* 2020), with very distinct traditions in ceramics and figurines but the common appearance of longhouses.

In central Europe, then, as in the Balkans, we see a population expansion correlated with the spatial expansion of a specific set of genomic variation, in turn correlated with across-the-board cultural change. However, the key point is that, while genomically this population was essentially unchanged, culturally it had undergone a major transformation as it adapted to new conditions, though the specific reasons remain unclear.

The third millennium BCE: Yamnaya and Corded Ware cultural and genetic hybridization

As noted already, the most significant shift in the genomic composition of populations in many parts of Europe after the introduction of farming was revealed to have occurred in the third millennium BCE with evidence of a major new ancestry component originating in the Eurasian steppe (Allentoft *et al.* 2015; Haak *et al.* 2015), associated conventionally with a new archaeological culture, the Corded Ware, distributed across northern and central Europe from Russia to the Netherlands. As described above, it has also been the most controversial because it resurrected old images of warrior pastoralists sweeping violently across Europe, all the more so when it appeared that this expansion was male-biased: that is to say, females tended to be assimilated from local pre-existing farmer populations (Goldberg *et al.* 2017; Saag *et al.* 2017; Scorrano *et al.* 2021).

More recent work (Allentoft *et al.* 2022; Chintalapati, Patterson & Moorjani 2022; Pearson & Durbin 2023) has confirmed the initial claims of major changes in the genomic ancestry of European populations starting ~2900 BCE. It has also shown the great rapidity, within around two hundred years (Allentoft *et al.* 2022: fig. 3A), with which more mobile pastoralist people with genes of steppe origin moved into Europe, and that genetic admixture with relatively sedentary mixed-farming populations whose ancestors were the Neolithic farmer immigrants described in the previous section quickly followed. On the other hand, the formation of the genetic ancestry of the steppe people who migrated into Europe began to take place ~4400-4000, a millennium earlier than the formation of the set of Yamnaya cultural practices and material. It can be seen, for example, at the Khvalynsk cemetery in the Volga region (Anthony *et al.* 2022).

The identification of identity-by-descent (IBD) genomic segments in aDNA (Allentoft *et al.* 2022; Ringbauer *et al.* 2024) has made it possible to bring a much sharper focus to the admixture described above between the genes of the local Neolithic farmers and the genes from mobile populations whose ancestry lies in the steppe. Thus, individuals associated with Corded Ware material in a number of different regions have large quantities of long IBD segments, implying recent ancestral connections, in common with each other, and also with individuals associated with Yamnaya cultural practices. Not only that, individuals from eastern Europe associated with material of the preceding Globular Amphora Culture (GAC) and with local Neolithic genomic ancestry derived from the initial farming immigrants also show close IBD genealogical links with Corded Ware-associated individuals from all regions that have been sampled, including geographically distant ones (Allentoft *et al.* 2022; Ringbauer *et al.* 2024). Thus, they are the specific source of the Neolithic farmer ancestry found in Corded Ware-associated individuals. Moreover, that farmer genetic ancestry is female-biased (e.g. Saag *et al.* 2021). In other words, this part of eastern Europe must have been a core area where initial admixture between local people, mainly women, and immigrants, mainly male, took place and which then led to a rapid spatial expansion of communities with an admixed steppe and GAC Neolithic farmer genomic ancestry.

In this core area where genetic admixture occurred, we can also see corresponding cultural changes, as cultural packages of different origins relating to different cultural domains become linked together. Ceramic traditions of the local GAC can be seen to change gradually into Corded Ware ones (Furholt 2008b) but the burial rite of a gender-specific crouched inhumation in an earth pit roughly oriented east-west, often under a mound, originates from Yamnaya (see, e.g., Dergachev 2023).

However, not all elements of the Corded Ware have the same origin or the same spatial distribution. Thus, Furholt (2014) argues that the widespread type-A battle-axe, another element regarded as characteristic of Corded Ware assemblages, originated in Denmark. It therefore represents yet another distinct package that becomes linked to the ceramic forms and the burial rite and is then transmitted with it. Furholt goes on to point out that there is considerable inter-regional variation in many aspects of the burial rite associated with Corded Ware material. Correspondence analysis (Furholt 2011: fig. 9) demonstrates a great range of inter-regional variation in the occurrence of different types of pottery decoration and of vessel types in Corded Ware ceramic assemblages, as well as of other artefact types like axes. When the results are used as the basis of a network analysis (Furholt 2011: fig. 10; 2014: fig. 7), it is apparent that the degree of similarity between different regions varies greatly, and high levels of similarity can link regions that are quite distant from one another. Moreover, the regional patterning of material culture similarity does not match that in burial practices (Furholt 2014: 78), which link different regions more closely together.

Furholt's pre-aDNA conclusion is understandable: 'It seems more appropriate to think of the Corded Ware elements as symbols that were exchanged through several supra-regional networks without assuming that they had the same meaning and significance to all people involved' (2014: 80). In the light of the genomic evidence for the rapid spread of a genetically admixed steppe-farmer population, however, we have to look elsewhere and ask, what interaction and cultural transmission processes could lead to the generation of so much variation in different domains in a situation of large-scale immigration? We have already seen that cultural traditions and their elements can come in different packages with different histories affected by different forces (Boyd *et al.* 1997). There is no reason in principle why the social factors affecting burial rituals should correspond to those affecting changing ceramic styles or why innovation rates in one should correspond to those in the other. Moreover, assuming that in many, if not most, regions we are *not* dealing with a rapid and complete population replacement, the question arises of competition between existing and incoming traditions in different domains. This could be resolved by the demise of the existing local tradition, rejection of the incoming one, or the creation of some hybrid version of the two. The outcomes in any given domain might be affected by prestige, by weight of relative numbers and proximity, or by whether the domain relates to a male- or female-associated cultural practice.

Specific examples illustrate the possibilities. Thus, in the early Corded Ware phase in Bohemia, both females of mixed steppe-farmer ancestry and those of entirely GAC farmer ancestry were buried according to the Corded Ware rite (Papac *et al.* 2021). On the other hand, a cross-regional study of Corded Ware burials of male and female individuals indicated that patterning in female burial rituals was more localized than that of males (Bourgeois & Kroon 2017). Studies of Corded Ware ceramic technology indicate continuity in vessel-making techniques from previous local traditions in the Low Countries (Beckerman 2015; Kroon, Huisman, Bourgeois, Braekmans & Fokkens 2019). In the light of the ethnographic evidence that domestic pottery-making tends to be a female activity, this might point to female-biased local cultural transmission in communities where women were generally of more local descent. In the Baltic, on the other hand, evidence suggests that skilled Corded Ware potters crossed the sea from east to west with their pots (Holmqvist *et al.* 2018). However, on the Baltic island of Gotland, we can see a very different situation. Here the local Pitted Ware seal-hunters,

a genetically homogeneous group of Scandinavian Mesolithic descent with a small element of Neolithic farmer ancestry, showed no evidence of Corded Ware genetic admixture, despite a long period of temporal overlap, and even though some Pitted Ware individuals adopted Corded Ware burial practices and material culture, such as battle-axes (Coutinho *et al.* 2020).

In the eastern Baltic and northwest Russia, we may be dealing with a situation more like the initial spread of farming into southeast Europe. Here the introduction of cereal agriculture and animal husbandry is associated with the immigration of individuals with hybrid steppe-farmer ancestry and, at least in northwest Russia, no evidence of genetic admixture with the local foragers (Mittnik *et al.* 2018; Saag *et al.* 2017; 2021). These changes co-occur with the appearance of the Corded Ware burial rite and ceramics (Nordqvist & Heyd 2020). Conversely, some Corded Ware groups in the eastern Baltic gave up agriculture and became hunter-gatherer-fishers but continued producing pottery similar to other Corded Ware assemblages in the region (Piličiauskas *et al.* 2020).

There is similarly mixed evidence that the immigration associated with the widespread genomic shift and the appearance of elements of Corded Ware material culture and practices led to regional population expansion in regions where it occurred. There is clear evidence for a major increase following a population trough in Czechia (Kolář *et al.* 2022) and also in northern Germany (Feeser *et al.* 2019), but in southern Sweden, which certainly saw a major decrease in settlement at the end of the fourth millennium BCE, any subsequent increase is relatively slight (Friman & Lagerås 2023). In Switzerland, a new population proxy based on combining site counts, radiocarbon dates, dendrochronological dates, and landscape openness derived from pollen analysis points to population increasing over several hundred years to a peak at ~2750 BCE, the date at which Corded Ware material appears locally, then declining (Hinz *et al.* 2022).

In the Corded Ware case, then, we have a different set of answers to our questions. Radiocarbon evidence of population increase is mixed but we see a major change in the spatial distribution of genomic variation, indicating large-scale immigration. In the apparent source region, we see interaction between local farmer and incoming steppe groups leading to genomic admixture with a majority female local farmer component and majority male steppe component. There is a correlation here with change in cultural traditions but it involves the linkage of continuous local change in ceramics with externally induced changes in burial practices. It must also have involved the economic and social changes that enabled large-scale westwards and eastwards migration to take place. In other regions to which groups with steppe-farmer genomes spread, the cultural patterns are even more variable, with some more stable than others, and changes do not all have the same origin. The interaction processes involved must have been complex and the factors influencing the maintenance or rejection of existing practices and the adoption of new ones in different domains very variable.

Conclusion

The many recent studies that have shown correlations in time and space between long-standing entities in culture history and specific genomic ancestries in the populations associated with them have conceptualized the two sides of the equation in completely different terms: on one side is biological ancestry; on the other are more or less essentialist cultural, if not 'ethnic', groups. The cultural evolutionary

modelling approach outlined in the first part of this article provides a theoretical and methodological basis for escaping this dichotomy by conceptualizing the variation in material culture practices, 'as underwritten by a system of information transmission across generations that has similar structural properties to the genetic system of information transmission' (Riede *et al.* 2019). The aDNA information provides the direct evidence of gene flow against which cultural features can be mapped in time and space to assess the importance of vertical cultural transmission, but they can also be mapped in relation to one another to investigate the role of different transmission and selection processes (cf. Shennan *et al.* 2015). However, by themselves, comparative transmission studies are not enough and will not realize archaeology's unique potential to discover and explain macro-level change. Key to understanding this are the changing scale and intensity of mobility and spatial interaction, and the demographic expansion and contraction processes that underlie them, which by and large do not figure in the models.

In their different ways, both the LBK and Corded Ware examples described above show how the demographic and interaction processes that produce population genomic patterns and cultural traditions can and should be unlinked from one another before, in some cases, they can be linked again, *not* as ethnic identifiers of the kind critiqued above but as indicators of parallel transmission.

Where does this leave the archaeological culture? At one level, it is clear that it will continue to be a useful shorthand for broad patterns of material culture variation that are coherent in time and space, just as biologists continue to use the 'species' concept despite their awareness of its many shortcomings. But in a fundamental way its essentialism has prevented, or at the very least retarded, the development of the fine-grained description of variation in the archaeological record that is necessary to reveal how different elements of it relate to one another or to shifting patterns of genomic variation. Without that description, we inevitably fall back on the culture names.

Finally, it is important to insist that the issues the case studies presented here illuminate are by no means restricted to post-Mesolithic European prehistory. Indeed, wherever aDNA genomic studies have been carried out, they have revealed unanticipated patterns of movement and population change as well as changing cultural patterns that do not simply match them. For example, Charlton *et al.* (2022) recently showed that human populations of two distinct ancestries were present in Late Palaeolithic Britain at similar dates but their lithic assemblages include types that elsewhere in Europe are associated with only one or other of these ancestries. Moreover, as space and time are ever more closely sampled for aDNA, more local population turnover is revealed (e.g. Papac *et al.* 2021). Dynamic demographic and cultural processes go all the way down.

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Population, histoire culturelle et dynamiques de changement dans la préhistoire européenne

Résumé

Bien qu'elle soit souvent attaquée sur ses lacunes, l'histoire culturelle reste, en pratique, le cadre dominant de description et d'interprétation de la préhistoire européenne. Elle est même encore plus prégnante depuis quelques années, depuis que les nouvelles informations fournies par l'ADN ancien sur l'ascendance génétique d'individus préhistoriques semble montrer une étroite corrélation avec l'affiliation culturelle du matériel archéologique découvert, suscitant la crainte de voire reparaitre les liens anciens et discrédités entre identité biologique et identité culturelle. Pour l'auteur de cet article, l'exploration des liens entre ascendance culturelle et ascendance génétique peut ne pas retomber dans ces errements si elle emprunte sa théorie et ses méthodes à la discipline de l'évolution culturelle et refuse de caractériser les liens en termes de « groupes ethniques ». Il faut, pour cela, décrire les archives archéologiques de manière plus fine et moins essentialiste, tout en reliant les schémas archéologiques et génétiques à des histoires d'ascension et de déclin des populations et de leurs relations entre elles.

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