



Archaeology of Death 5 Population Processes, DNA & Demography

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Ancient DNA & Archeogenetics

Archaeogenetics is the study of Ancient DNA using various molecular genetic methods and DNA resources. This form of genetic analysis can be applied to human, animal, and plant specimens. Ancient DNA can be extracted from various fossilized specimens including bones, eggshells, and artificially preserved tissues in human and animal specimens. In plants, Ancient DNA can be extracted from seeds, tissue, and in some cases, feces. Archaeogenetics provides us with genetic evidence of ancient population group migrations, domestication events, and plant and animal evolution. The ancient DNA cross referenced with the DNA of relative modern genetic populations allows researchers to run comparison studies that provide a more complete analysis when ancient DNA is compromised.

Genetic Analysis

Methods of Molecular Biology

The increasing availability of DNA sequencing since the late 1990s has allowed estimates on Paleolithic effective population sizes. Such models suggest a human effective population size of the order of 10,000 individuals for the Late Pleistocene. This includes only the breeding population that produced descendants over the long term, and the actual population may have been substantially larger (in the six digits). Sherry et al. (1997) based on Alu elements estimated a roughly constant effective population size of the order of 18,000 individuals for the population of *Homo* ancestral to modern humans over the past one to two million years. For the time of speciation of *Homo sapiens*, ca. 130,000 years ago, Sjödin et al. (2012) estimate an effective population size of the order of 10,000 to 30,000 individuals, and infer an actual "census population" of early *Homo sapiens* of roughly 100,000 to 300,000 individuals. The authors also note that their model disfavors the assumption of an early (pre-*Out-of-Africa*) population bottleneck affecting all of *Homo sapiens*.

Ancient DNA

Sources

Due to the morphological preservation in mummies, many studies from the 1990s and 2000s used mummified tissue as a source of ancient human DNA. Examples include both naturally preserved specimens, for example, those preserved in ice, such as the Ötzi the Iceman, or through rapid desiccation, such as high-altitude mummies from the Andes, as well as various sources of artificially preserved tissue (such as the chemically treated mummies of ancient Egypt). However, mummified remains are a limited resource. The majority of human aDNA studies have focused on extracting DNA from two sources that are much more common in the archaeological record – bone and teeth. Several other sources have also yielded DNA, including paleofaeces, and hair. Contamination remains a major problem when working on ancient human material.

Ancient pathogen DNA has been successfully retrieved from samples dating to more than 5,000 years old in humans and as long as 17,000 years ago in other species. In addition to the usual sources of mummified tissue, bones and teeth, such studies have also examined a range of other tissue samples, including calcified pleura, tissue embedded in paraffin, and formalin-fixed tissue. Efficient computational tools have been developed for pathogen and microorganism aDNA analyses in a small (QIIME) and large scale (FALCON).

Results

Taking preventative measures in their procedure against such contamination though, a 2012 study analyzed bone samples of a Neanderthal group in the El Sidrón cave, finding new insights on potential kinship and genetic diversity from the aDNA. In November 2015, scientists reported finding a 110,000-year-old tooth containing DNA from the Denisovan hominin, an extinct species of human in the genus *Homo*.

The research has added new complexity to the peopling of Eurasia. It has also revealed new information about links between the ancestors of Central Asians and the indigenous peoples of the Americas. In Africa, older DNA degrades quickly due to the warmer tropical climate, although, in September 2017, ancient DNA samples, as old as 8,100 years old, have been reported.

Degradation processes

Due to degradation processes (including cross-linking, deamination and fragmentation) ancient DNA is of lower quality in comparison with modern genetic material. The damage characteristics and ability of aDNA to survive through time restricts possible analyses and places an upper limit on the age of successful samples Allentoft et al. (2012). There is a theoretical correlation between time and DNA degradation, although differences in environmental conditions complicates things. Samples subjected to different conditions are unlikely to predictably align to a uniform age-degradation relationship. The environmental effects may even matter after excavation, as DNA decay rates may increase, particularly under fluctuating storage conditions. Even under the best preservation conditions, there is an upper boundary of 0.4–1.5 million years for a sample to contain sufficient DNA for contemporary sequencing technologies.

Research into the decay of mitochondrial and nuclear DNA in Moa bones has modelled mitochondrial DNA degradation to an average length of 1 base pair after 6,830,000 years at -5°C . The decay kinetics have been measured by accelerated aging experiments further displaying the strong influence of storage temperature and humidity on DNA decay. Nuclear DNA degrades at least twice as fast as mitochondrial DNA. As such, early studies that reported recovery of much older DNA, for example from Cretaceous dinosaur remains, may have stemmed from contamination of the sample.

Age limit

A critical review of ancient DNA literature through the development of the field highlights that few studies after about 2002 have succeeded in amplifying DNA from remains older than several hundred thousand years. A greater appreciation for the risks of environmental contamination and studies on the chemical stability of DNA have resulted in concerns being raised over previously reported results. The dinosaur DNA was later revealed to be human Y-chromosome, while the DNA reported from encapsulated halobacteria has been criticized based on its similarity to modern bacteria, which hints at contamination. A 2007 study also suggests that these bacterial DNA samples may not have survived from ancient times, but may instead be the product of long-term, low-level metabolic activity.

aDNA may contain a large number of postmortem mutations, increasing with time. Some regions of polynucleotide are more susceptible to this degradation, so sequence data can bypass statistical filters used to check the validity of data. Due to sequencing errors, great caution should be applied to interpretation of population size. Substitutions resulting from deamination of cytosine residues are vastly over-represented in the ancient DNA sequences. Miscoding of C to T and G to A accounts for the majority of errors.

Contamination

Another problem with ancient DNA samples is contamination by modern human DNA and by microbial DNA (most of which is also ancient). New methods have emerged in recent years to prevent possible contamination of aDNA samples, including conducting extractions under extreme sterile conditions, using special adapters to identify endogenous molecules of the sample (over ones that may have been introduced during analysis), and applying bioinformatics to resulting sequences based on known reads in order approximate rates of contamination.

Methods of DNA analysis

DNA extracted from fossil remains is primarily sequenced using Massive parallel sequencing, which allows simultaneous amplification and sequencing of all DNA segments in a sample, even when it is highly fragmented and of low concentration. It involves attaching a generic sequence to every single strand that generic primers can bond to, and thus all of the DNA present is amplified. This is generally more costly and time intensive than PCR but due to the difficulties involved in ancient DNA amplification it is cheaper and more efficient. One method of massive parallel sequencing, developed by Margulies et al., employs bead-based emulsion PCR and pyrosequencing, and was found to be powerful in analyses of aDNA because it avoids potential loss of sample, substrate competition for templates, and error propagation in replication. The most common way to analyze aDNA sequence is to compare it with a known sequence from other sources, and this could be done in different ways for different purposes.

The identity of the fossil remain can be uncovered by comparing its DNA sequence with those of known species using software such as BLASTN. This archaeogenetic approach is especially helpful when the morphology of the fossil is ambiguous. Apart from that, species identification can also be done by finding specific genetic markers in an aDNA sequence. For example, the American indigenous population is characterized by specific mitochondrial RFLPs and deletions defined by Wallace et al.

aDNA comparison study can also reveal the evolutionary relationship between two species. The number of base differences between DNA of an ancient species and that of a closely related extant species can be used to estimate the divergence time of those two species from their last common ancestor.

The phylogeny of some extinct species, such as Australian marsupial wolves and American ground sloths, has been constructed by this method. Mitochondrial DNA in animals and chloroplast DNA in plants are usually used for this purpose because they have hundreds of copies per cell and thus are more easily accessible in ancient fossils.

Another method to investigate relationship between two species is through DNA hybridization. Single-stranded DNA segments of both species are allowed to form complementary pair bonding with each other. More closely related species have a more similar genetic makeup, and thus a stronger hybridization signal. Scholz et al. conducted southern blot hybridization on Neanderthal aDNA (extracted from fossil remain W-NW and Krapina). The results showed weak ancient human-Neanderthal hybridization and strong ancient human-modern human hybridization. The human-chimpanzee and Neanderthal-chimpanzee hybridization are of similarly weak strength. This suggests that humans and Neanderthals are not as closely related as two individuals of the same species are, but they are more related to each other than to chimpanzees.

There have also been some attempts to decipher aDNA to provide valuable phenotypic information of ancient species. This is always done by mapping aDNA sequence onto the karyotype of a well-studied closely related species, which share a lot of similar phenotypic traits. For example, Green et al. compared the aDNA sequence from Neanderthal Vi-80 fossil with modern human X and Y chromosome sequence, and they found a similarity in 2.18 and 1.62 bases per 10,000 respectively, suggesting Vi-80 sample was from a male individual. Other similar studies include finding of a mutation associated with dwarfism in *Arabidopsis* in ancient Nubian cotton, and investigation on the bitter taste perception locus in Neanderthals.

aDNA Applications - Human archaeology

Africa

Modern humans are thought to have evolved in Africa at least 200 kya (thousand years ago), with some evidence suggesting a date of over 300 kya. Examination of mitochondrial DNA (mtDNA), Y-chromosome DNA, and X-chromosome DNA indicate that the earliest population to leave Africa consisted of approximately 1500 males and females. It has been suggested by various studies that populations were geographically “structured” to some degree prior to the expansion out of Africa; this is suggested by the antiquity of shared mtDNA lineages. One study of 121 populations from various places throughout the continent found 14 genetic and linguistic “clusters,” suggesting an ancient geographic structure to African populations. In general, genotypic and phenotypic analysis have shown “large and subdivided throughout much of their evolutionary history.”

Genetic analysis has supported archaeological hypotheses of a large-scale migrations of Bantu speakers into Southern Africa approximately 5 kya. Microsatellite DNA, single nucleotide polymorphisms (SNPs), and insertion/deletion polymorphisms (INDELS) have shown that Nilo-Saharan speaking populations originate from Sudan. Furthermore, there is genetic evidence that Chad-speaking descendants of Nilo-Saharan speakers migrated from Sudan to Lake Chad about 8 kya. Genetic evidence has also indicated that non-African populations made significant contributions to the African gene pool. For example, the Saharan African Beja people have high levels of Middle-Eastern as well as East African Cushitic DNA.

Europe

Analysis of mtDNA shows that Eurasia was occupied in a single migratory event between 60 and 70 kya. Genetic evidence shows that occupation of the Near East and Europe happened no earlier than 50 kya. Studying haplogroup U has shown separate dispersals from the Near East both into Europe and into North Africa. Much of the work done in archaeogenetics focuses on the Neolithic transition in Europe. Cavalli-Sforza's analysis of genetic-geographic patterns led him to conclude that there was a massive influx of Near Eastern populations into Europe at the start of the Neolithic. This view led him “to strongly emphasize the expanding early farmers at the expense of the indigenous Mesolithic foraging populations.” mtDNA analysis in the 1990s, however, contradicted this view. M.B. Richards estimated that 10–22% of extant European mtDNA's had come from Near Eastern populations during the Neolithic. Most mtDNA's were “already established” among existing Mesolithic and Paleolithic groups. Most “control-region lineages” of modern European mtDNA are traced to a founder event of reoccupying northern Europe towards the end of the Last Glacial Maximum (LGM). One study of extant European mtDNA's suggest this reoccupation occurred after the end of the LGM, although another suggests it occurred before. Analysis of haplogroups V, H, and U5 support a “pioneer colonization” model of European occupation, with incorporation of foraging populations into arriving Neolithic populations. Furthermore, analysis of ancient DNA, not just extant DNA, is shedding light on some issues. For instance, comparison of Neolithic and Mesolithic DNA has indicated that the development of dairying preceded widespread lactose tolerance.

South Asia

South Asia has served as the major early corridor for geographical dispersal of modern humans from out-of-Africa. Based on studies of mtDNA line M, some have suggested that the first occupants of India were Austro-Asiatic speakers who entered about 45–60 kya. The Indian gene pool has contributions from earliest settlers, as well as West Asian and Central Asian populations from migrations no earlier than 8 kya. The lack of variation in mtDNA lineages compared to the Y-chromosome lineages indicate that primarily males partook in these migrations. The discovery of two subbranches U2i and U2e of the U mtDNA lineage, which arose in Central Asia has “modulated” views of a large migration from Central Asia into India, as the two branches diverged 50 kya. Furthermore, U2e is found in large percentages in Europe but not India, and vice versa for U2i, implying U2i is native to India.

East Asia

Analysis of mtDNA and NRY (non-recombining region of Y chromosome) sequences have indicated that the first major dispersal out of Africa went through Saudi Arabia and the Indian coast 50–100 kya, and a second major dispersal occurred 15–50 kya north of the Himalayas.

Much work has been done to discover the extent of north-to-south and south-to-north migrations within Eastern Asia. Comparing the genetic diversity of northeastern groups with southeastern groups has allowed archaeologists to conclude many of the northeast Asian groups came from the southeast. The Pan-Asian SNP (single nucleotide polymorphism) study found “a strong and highly significant correlation between haplotype diversity and latitude,” which, when coupled with demographic analysis, supports the case for a primarily south-to-north occupation of East Asia. Archaeogenetics has also been used to study hunter-gatherer populations in the region, such as the Ainu from Japan and Negrito groups in the Philippines. For example, the Pan-Asian SNP study found that Negrito populations in Malaysia and the Negrito populations in the Philippines were more closely related to non-Negrito local populations than to each other, suggesting Negrito and non-Negrito populations are linked by one entry event into East Asia; although other Negrito groups do share affinities, including with Australian Aboriginies. A possible explanation of this is a recent admixture of some Negrito groups with their local populations.

Americas

Archaeogenetics has been used to better understand the populating of the Americas from Asia. Native American mtDNA haplogroups have been estimated to be between 15 and 20 kya, although there is some variation in these estimates. Genetic data has been used to propose various theories regarding how the Americas were colonized. Although the most widely held theory suggests “three waves” of migration after the LGM through the Bering Strait, genetic data have given rise to alternative hypotheses. For example, one hypothesis proposes a migration from Siberia to South America 20–15 kya and a second migration that occurred after glacial recession. Y-chromosome data has led some to hold that there was a single migration starting from the Altai Mountains of Siberia between 17.2–10.1 kya, after the LGM. Analysis of both mtDNA and Y-chromosome DNA reveals evidence of “small, founding populations.” Studying haplogroups has led some scientists to conclude that a southern migration into the Americas from one small population was impossible, although separate analysis has found that such a model is feasible if such a migration happened along the coasts.

Australia and New Guinea

Finally, archaeogenetics has been used to study the occupation of Australia and New Guinea. The aborigines of Australia and New Guinea are phenotypically very similar, but mtDNA has shown that this is due to convergence from living in similar conditions. Non-coding regions of mt-DNA have shown “no similarities” between the aboriginal populations of Australia and New Guinea. Furthermore, no major NRY lineages are shared between the two populations. The high frequency of a single NRY lineage unique to Australia coupled with “low diversity of lineage-associated Y-chromosomal short tandem repeat (Y-STR) haplotypes” provide evidence for a “recent founder or bottleneck” event in Australia. But there is relatively large variation in mtDNA, which would imply that the bottleneck effect impacted males primarily. Together, NRY and mtDNA studies show that the splitting event between the two groups was over 50kya, casting doubt on recent common ancestry between the two.

Methods of DNA extraction

Once a specimen is collected from an archaeological site, DNA can be extracted through a series of processes. One of the more common methods utilizes silica and takes advantage of polymerase chain reactions in order to collect ancient DNA from bone samples.

There are several challenges that add to the difficulty when attempting to extract ancient DNA from fossils and prepare it for analysis. DNA is continuously being split up. While the organism is alive these splits are repaired; however, once an organism has died, the DNA will begin to deteriorate without repair. This results in samples having strands of DNA measuring around 100 base pairs in length. Contamination is another significant challenge at multiple steps throughout the process. Often other DNA, such as bacterial DNA, will be present in the original sample. To avoid contamination it is necessary to take many precautions such as separate ventilation systems and workspaces for ancient DNA extraction work. The best samples to use are fresh fossils as careless washing can lead to mould growth. DNA coming from fossils also occasionally contains a compound that inhibits DNA replication. Coming to a consensus on which methods are best at mitigating challenges is also difficult due to the lack of repeatability caused by the uniqueness of specimens.

Silica-based DNA extraction is a method used as a purification step to extract DNA from archaeological bone artefacts and yield DNA that can be amplified using polymerase chain reaction (PCR) techniques. This process works by using silica as a means to bind DNA and separate it from other components of the fossil process that inhibit PCR amplification. However, silica itself is also a strong PCR inhibitor, so careful measures must be taken to ensure that silica is removed from the DNA after extraction.

The general process for extracting DNA using the silica-based method is outlined by the following:

1. Bone specimen is cleaned and the outer layer is scraped off
2. Sample is collected from preferably compact section
3. Sample is ground to fine powder and added to an extraction solution to release DNA
4. Silica solution is added and centrifuged to facilitate DNA binding
5. Binding solution is removed and a buffer is added to the solution to release the DNA from the silica

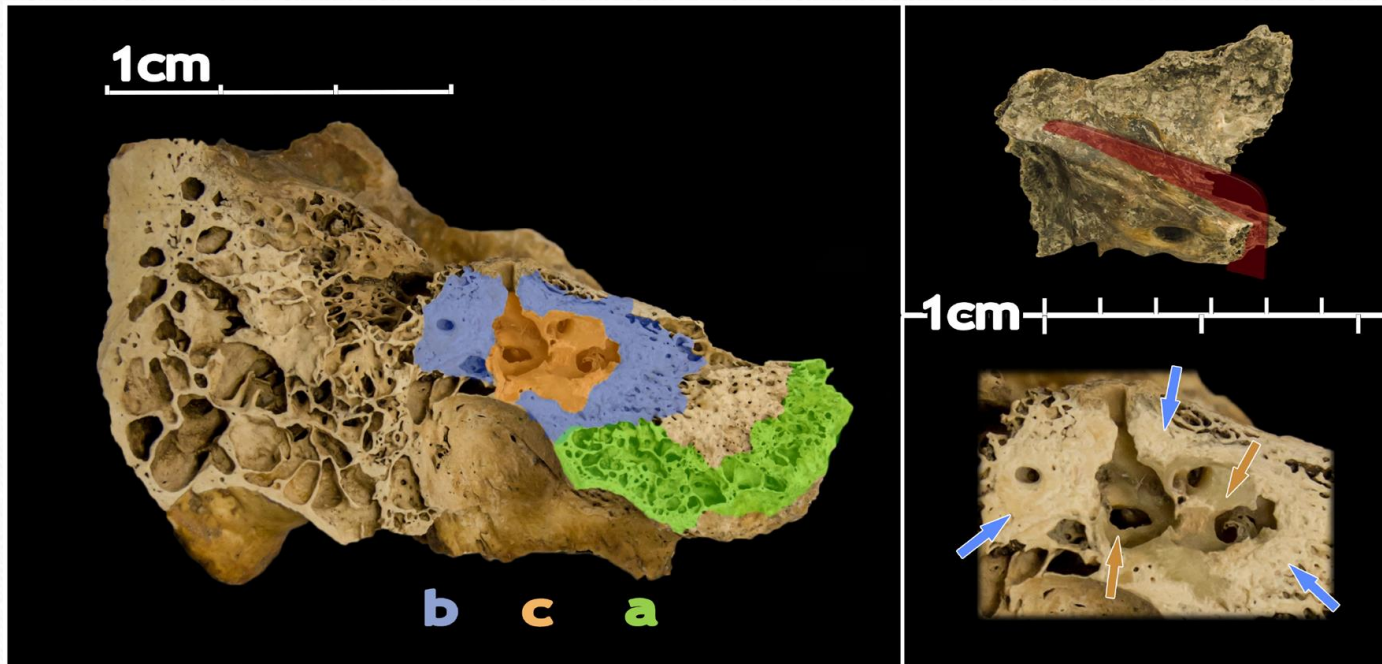
One of the main advantages of silica-based DNA extraction is that it is relatively quick and efficient, requiring only a basic laboratory setup and chemicals. It is also independent of sample size, as the process can be scaled to accommodate larger or smaller quantities. Another benefit is that the process can be executed at room temperature. However, this method does contain some drawbacks. Mainly, silica-based DNA extraction can only be applied to bone and teeth samples; they cannot be used on soft tissue. While they work well with a variety of different fossils, they may be less effective in fossils that are not fresh (e.g. treated fossils for museums). Also, contamination poses a risk for all DNA replication in general, and this method may result in misleading results if applied to contaminated material.

Extraction of DNA sample in field - contamination protection



The invention and development of next or second generation sequencing methods has resulted in a dramatic transformation of ancient DNA research and allowed shotgun sequencing of entire genomes from fossil specimens. However, although there are exceptions, most fossil specimens contain only low ($\sim 1\%$ or less) percentages of endogenous DNA. The only skeletal element for which a systematically higher endogenous DNA content compared to other skeletal elements has been shown is the petrous part of the temporal bone. In this study we investigate whether (a) different parts of the petrous bone of archaeological human specimens give different percentages of endogenous DNA yields, (b) there are significant differences in average DNA read lengths, damage patterns and total DNA concentration, and (c) it is possible to obtain endogenous ancient DNA from petrous bones from hot environments. We carried out intra-petrous comparisons for ten petrous bones from specimens from Holocene archaeological contexts across Eurasia dated between 10,000-1,800 calibrated years before present (cal. BP). We obtained shotgun DNA sequences from three distinct areas within the petrous: a spongy part of trabecular bone (part A), the dense part of cortical bone encircling the osseous inner ear, or otic capsule (part B), and the dense part within the otic capsule (part C).

Our results confirm that dense bone parts of the petrous bone can provide high endogenous aDNA yields and indicate that endogenous DNA fractions for part C can exceed those obtained for part B by up to 65-fold and those from part A by up to 177-fold, while total endogenous DNA concentrations are up to 126-fold and 109-fold higher for these comparisons. Our results also show that while endogenous yields from part C were lower than 1% for samples from hot (both arid and humid) parts, the DNA damage patterns indicate that at least some of the reads originate from ancient DNA molecules, potentially enabling ancient DNA analyses of samples from hot regions that are otherwise not amenable to ancient DNA analyses.



Medial view of a cut of a left petrous bone. The main image shows the location of the different areas targeted in this study (parts A, B and C) with different colours. The top box shows the direction of the cut. The lower box shows the area comprising parts B and C in detail and non-coloured. Blue and orange arrows point to areas of B and C, respectively.

aDNA Analysis – Case Studies



Alissa Mittnik, Chuan-Chao Wang, Jiří Svoboda, Johannes Krause

A Molecular Approach to the Sexing of the Triple Burial at the Upper Paleolithic Site of Dolní Věstonice <https://doi.org/10.1371/journal.pone.0163019>

In the past decades ancient DNA research has brought numerous insights to archaeological research where traditional approaches were limited. The determination of sex in human skeletal remains is often challenging for physical anthropologists when dealing with incomplete, juvenile or pathological specimens. Molecular approaches allow sexing on the basis of sex-specific markers or by calculating the ratio of DNA derived from different chromosomes. Here we propose a novel approach that relies on the ratio of X chromosome-derived shotgun sequencing data to the autosomal coverage, thus establishing the probability of an XX or XY karyotype. Applying this approach to the individuals of the Upper Paleolithic (Gravettien 31,000 BP) triple burial of Dolní Věstonice reveals that all three skeletons, including the individual DV 15, whose sex has long been debated due to a pathological condition, were male.



[Hannes Schroeder](#) et al 2019: Unraveling ancestry, kinship, and violence in a Late Neolithic mass grave. *Proceedings of the National Academy of Sciences* 116(22)
DOI: [10.1073/pnas.1820210116](#)

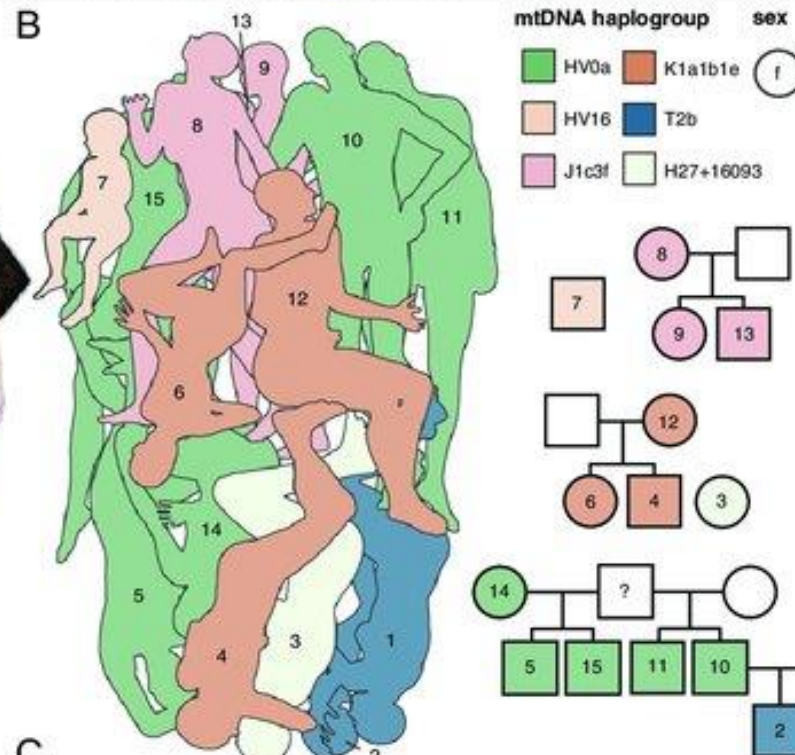
The third millennium BCE was a period of major cultural and demographic changes in Europe that signaled the beginning of the Bronze Age. People from the Pontic steppe expanded westward, leading to the formation of the Corded Ware complex and transforming the genetic landscape of Europe. At the time, the Globular Amphora culture (3300–2700 BCE) existed over large parts of Central and Eastern Europe, but little is known about their interaction with neighboring Corded Ware groups and steppe societies. Here we present a detailed study of a Late Neolithic mass grave from southern Poland belonging to the Globular Amphora culture and containing the remains of 15 men, women, and children, all killed by blows to the head. We sequenced their genomes to between 1.1- and 3.9-fold coverage and performed kinship analyses that demonstrate that the individuals belonged to a large extended family. The bodies had been carefully laid out according to kin relationships by someone who evidently knew the deceased. From a population genetic viewpoint, the people from Koszyce are clearly distinct from neighboring Corded Ware groups because of their lack of steppe-related ancestry. Although the reason for the massacre is unknown, it is possible that it was connected with the expansion of Corded Ware groups, which may have resulted in competition for resources and violent conflict. Together with the archaeological evidence, these analyses provide an unprecedented level of insight into the kinship structure and social behavior of a Late Neolithic community.



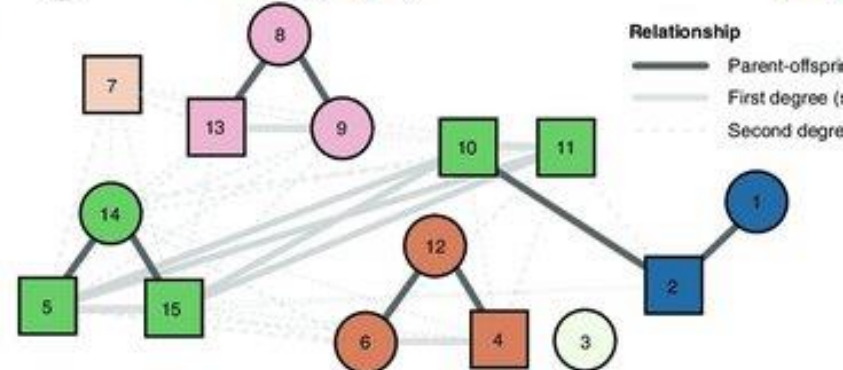
A



B

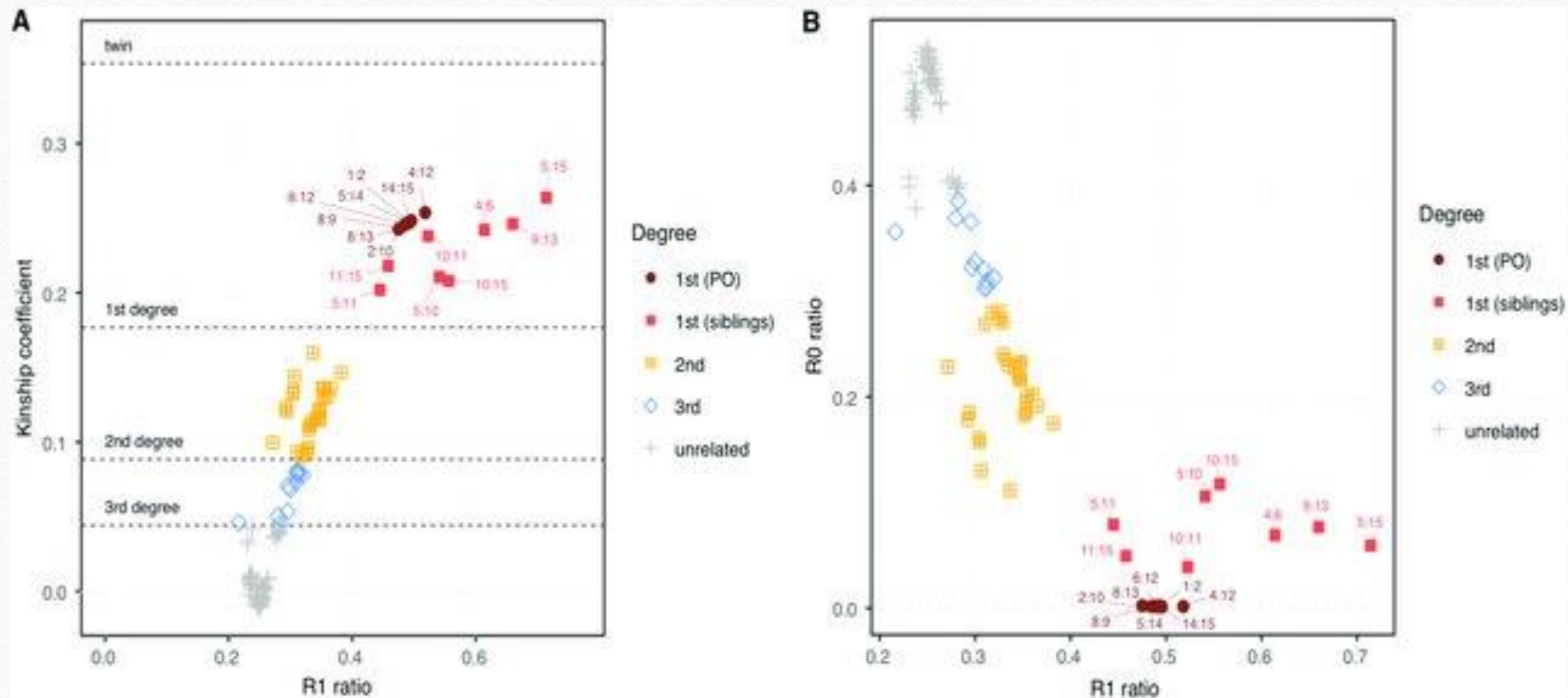


C

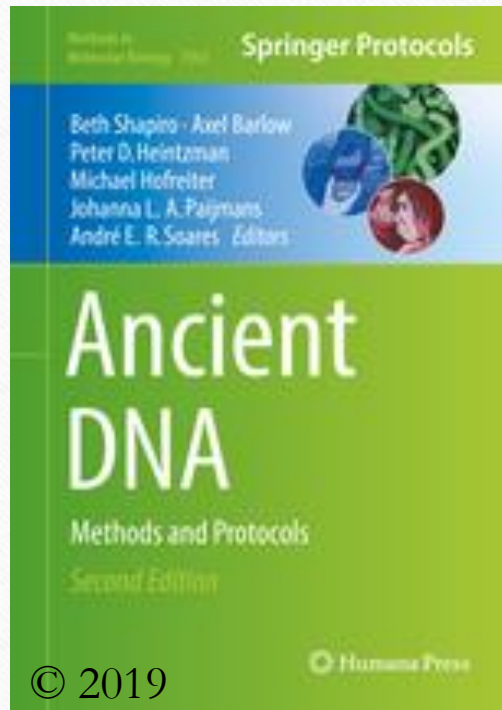


Kinship

- A) Artistic reconstruction of the Koszyce mass burial based partly on phenotypic traits inferred from the ancient genomes (reconstruction by M. Podsiadło)
- B) Schematic representation of the burial and pedigree plots showing kinship relations between the Koszyce individuals inferred from genetic data.
- C) kinship network based on kinship coefficients inferred from IBS scores for pairs of Koszyce individuals showing first- and second-degree relationships. Kinship coefficients and R scores are plotted in the following slide...



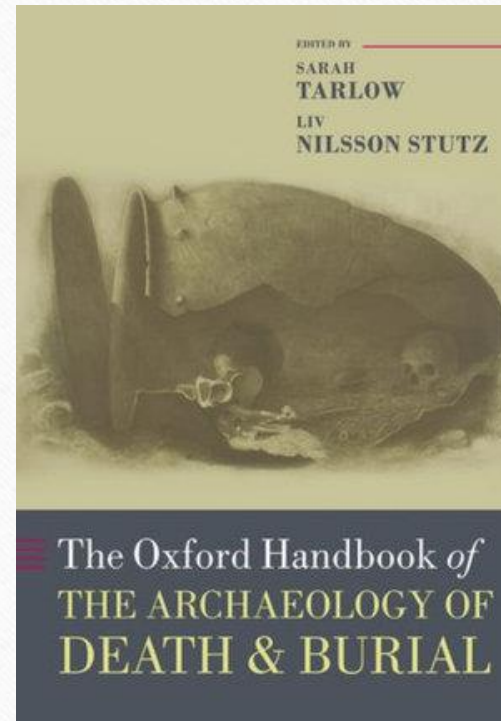
Relatedness among the Koszyce individuals. A) Kinship coefficients and R1 ratios inferred from IBS scores for pairs of Koszyce individuals. B) R0 and R1 ratios inferred from IBS scores for pairs of Koszyce individuals. For clarity pairs of individuals have only been marked with numbers for 1st degree relationships.



Ancient DNA

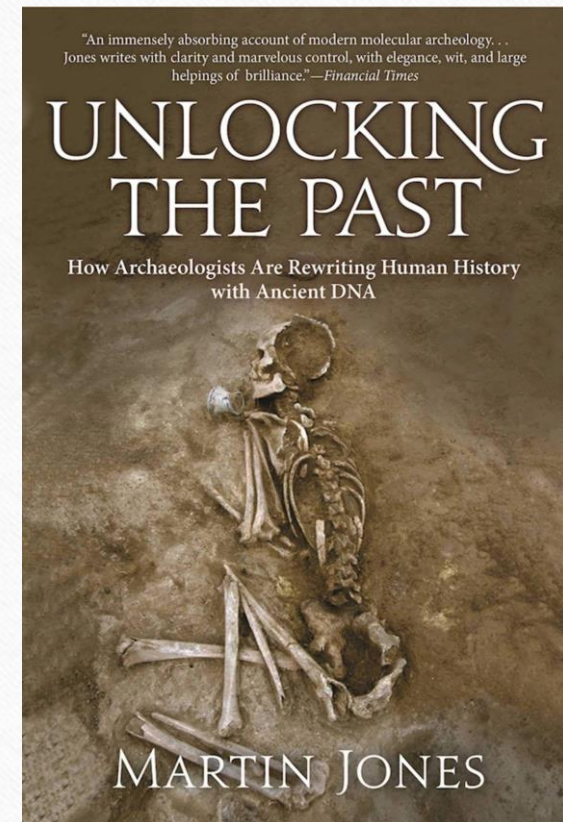
Methods and Protocols

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**Unlocking the Past: How
Archaeologists Are Rewriting
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Demography and Population Processes

Andrew Chamberlain 2009: Archaeological demography, [Hum Biol.](#) 2009 Apr;81(2-3):275-86. doi: 10.3378/027.081.0309.

Archaeological demography investigates the structure and dynamics of past human populations using evidence from traces of human activities and remnants of material culture in the archaeological record. Research in this field is interdisciplinary, incorporating findings from anthropology, paleogenetics, and human ecology but with a remit that extends beyond the primarily biological focus of paleodemography. Important questions addressed by archaeological demography include the establishment of methods for inferring past population structure, the timing of the emergence of modern human demographic systems, the relative importance of attritional and catastrophic patterns of mortality, and the search for adaptive explanations for demographic transitions, colonization events, and population extinctions. Archaeological evidence, including the extent of settlements and site catchment areas as well as measures of the exploitation, consumption, and discard of materials and artifacts, have traditionally been used as proxies for estimating past population size and density. In recent years this evidence has been supplemented by increasingly large data sets compiled from radiocarbon dating programs. These data sets have been used to investigate demographic waves of advance during continental-scale periods of colonization and cultural change and to detect episodes of population decline, extinction, and hiatuses in settlement history. By considering studies of human genetic diversity that indicate temporary but drastic reductions in effective population size, I hypothesize that catastrophic mortality may have had an important role in long-term population processes and may have limited long-term rates of growth, particularly in prehistoric populations.

Palaeodemography PREHISTORIC DEMOGRAPHY

by Evžen Neustupný*

- * As the best available review of Prehistoric Demography in Central Europe was comprehensively published by Professor Evžen Neustupný in this lecture we follow his work from: Exploratory Workshop on "Archaeology and Genetics" Toulouse, May 2004

https://www.kar.zcu.cz/texty/Neustupny_PrehistoricDemographyToulouse.pdf

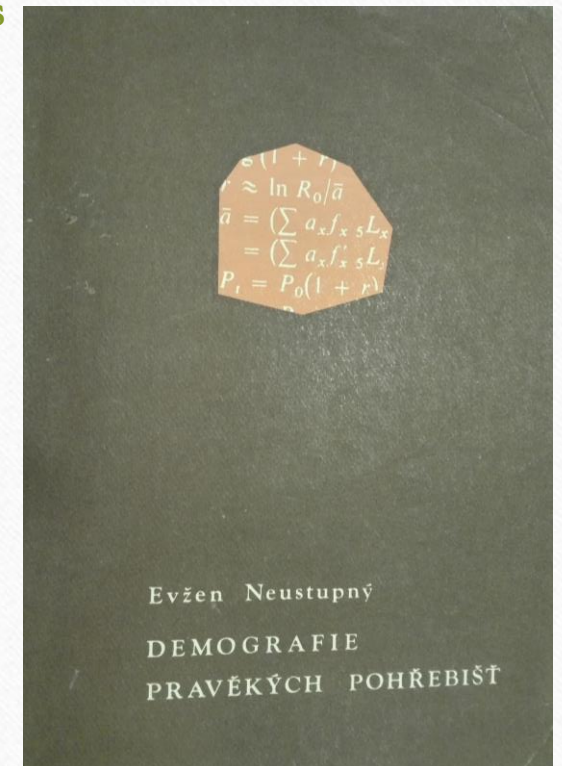
- Recommending also following publications:

Neustupný, E. 1982: Prehistoric migrations by infiltration. Archeologické rozhledy 34, 278-293

Neustupný, E. 1983a: Demografie pravěkých pohřebišť - The demography of prehistoric cemeteries. Praha: Archeologický ústav, 171 p.

Neustupný, E. 1983b: The demography of prehistoric cemeteries. Památky archeologické 74, 7-34

Neustupný E. 1998: Otherness in prehistoric times. In: L.Larsson, The World View of Prehistoric Man. Lund: The University.



Prehistoric demography is central to the solution of many problems of the past. It studies the conditions in which prehistoric people reproduced themselves, and in this sense it is crucial for an understanding of how genetic mechanisms worked in particular situations. I am going to explain prehistoric demography putting much weight upon archaeology, i.e. the study of artefacts. As I try to make my presentation fairly exhaustive, I have to abstain from going into details and using examples. As demography is largely a product of what is often termed culture, it varies from region to region and from period to period. There is nothing such as "prehistoric" demography, for there are many prehistoric demographies. This must be always kept in mind. My personal interest is in the prehistory of Central Europe that is unusually rich in the archaeological record. There are thousands of sites consisting mostly of the remains of graveyards, villages and/or other activity areas, many of them containing a wealth of finds that can be classified with the chronological accuracy of something like a century. Archaeological remains are densely distributed in space. Two contemporaneous sites frequently lie at a distance of less than 3 kilometres. This is unusual elsewhere.

In my view most questions of prehistoric demography can be solved in principle. However, many archaeologists have not yet paid enough attention to the methodological aspects of the problem that renders their work very difficult to use. Studies identifying the number of houses found in a village with the number of families living in the village in the past are still common. Therefore, I shall pay much attention to methodological and theoretical questions.

Prehistoric demography develops according to two lines of research. The first line is occupied with the structure of prehistoric populations, for example with the relationships between the number of men and women in their reproductive period, their life expectancy, the index of masculinity etc. Nearly all this can be derived from the so-called life tables. The role of biological (physical) anthropology in the solution of these questions is very important. The second line of research in prehistoric demography concerns the problems of the reproduction of prehistoric people. This field of demographic concern covers for example the questions of population increase or decrease, of the size of population groups, and of a possible non-biological intervention into human reproduction. The role of prehistoric archaeology is crucial for this kind of enquiry. There are two research strategies by means of which prehistoric demography can be reconstructed on the basis of the archaeological evidence:

1. by considering the evidence contained in human skeletons excavated by archaeologists
2. by considering the artefacts created by ancient people.

I shall now briefly discuss the two methods.

1 The evidence of skeletons

Skeletons are usually excavated, spatially documented and dated by archaeologists, but the expertise that leads to demographic knowledge cannot be realised without physical (biological) anthropology. The logic of the method used is simple: one can reconstruct most demographic parameters of any population simply by determining the sex and age of individual skeletons from a cemetery. The formulae needed for this purpose were derived in the 17th century by the English astronomer Halley during his visit of Wrocław in Silesia. Halley's method can be easily applied to archaeological finds once anthropologists classify the skeletons as to their age and sex.

The result is life tables consisting of demographic functions such as the probability of death at age x , the relative number of survivals at age x , and the life expectancy at age x . However, Halley's calculations cannot reveal any measure of natural increase and there is no simple way to determine the rate of natural increase on the basis of skeletons themselves.

There are several obstacles to a straightforward application of the Halley method:

1.1.1. The problem of stationarity

The first of them is the problem of stationarity that is often supposed to be the most severe limitation of the application of the method in archaeology. The main cause of complications is supposed to be the fact that ancient populations may not have been stationary, i.e. their natural increase was possibly not zero. This might be a major problem, because Halley's method for the calculation of life tables is based on the supposition of stationarity. It can be demonstrated on other grounds, however, that prehistoric populations were stationary on the average while the actual rate of increase could have been slightly positive or negative. It can also be demonstrated that even if strict stationarity were not met, minor rates of natural increase would hardly disturb the life tables calculated by the Halley method to a major degree.

1.1.2. The problem of completeness

The second obstacle is the fact that prehistoric burial grounds are mostly incomplete in the sense that large groups of population may have been interred elsewhere than in the formal cemeteries from which the Halley life tables are calculated.

We now have enough evidence in Central Europe, for example, that all prehistoric groups beginning with the Neolithic period buried some of their dead in deserted or half-deserted villages. This habit, for which we have so far no explanation, was widespread, but difficult to quantify. We do not know how many persons are missing from the regular cemeteries and how people were selected for this or that kind of burial.

What is even worse, children up to the age of 3 are missing almost entirely everywhere despite the fact that the mortality in this age group must have been considerable. This makes it very difficult to calculate some of the functions of the life tables. If full scale life-tables are needed, some of the values must be reconstructed. The incompleteness of the archaeological record is certainly more important for the evaluation of prehistoric demography than the possible, but probably not very real, problem of stationarity.

1.1.3. The age of skeletons

One of the most severe limitations is the fact that physical anthropologists cannot determine the age of skeletons with sufficient accuracy. The sex of the deceased can be sometimes decided on the basis of archaeological consideration and recently also by means of molecular methods, but the age remains quite a problem. Several decades ago physical anthropologists were still more optimistic about determining the age of adult skeletons setting them to 5 year or 10 year intervals, but nowadays many are more sceptical. Some anthropologists replace the empirically observed values by means of theoretical constructions of a dubious nature.

As an archaeologist I cannot discuss this in any detail, but I can point to the fact that □ the raw empirical data mostly generate fully acceptable life tables. They are acceptable in the sense that individual age groups are in the proportion expected by independent evidence such as the medieval series. □ Also, the life tables reconstructed for the prehistoric period by the Halley method show somewhat worse demographic parameters, such as lower values for the life expectancy function, than life tables reconstructed for the medieval period on the basis of the written record. This shows that our knowledge of the ageing of skeletons may not be so bad after all and that the life tables based on it need not lack sense.

1.1.4. The size of sample populations

There is another limitation to demographic reconstructions based on ancient skeletons, which is rarely considered. This is the size of sample populations. While modern demography has mostly no problems of principle with overcoming random variations because it can easily observe thousands of people, prehistoric samples are mostly small: several dozen or several hundred skeletons, usually less than five hundred. Because the conservation of bone in graves is frequently unsatisfactory, many of them do not contain remains from which their age and sex could be determined. This makes the number of usable skeletons even smaller. Archaeologists cannot go and excavate larger cemeteries because they do not exist: prehistoric communities that left the cemeteries were small or medium sized. Another factor influencing the situation of the record is the fact that in many regions of the world prehistoric populations moved quite frequently (over the period of several decades, possibly remaining at one place for less than 200 years); usually they also moved their graveyards without leaving any indication where the next cemetery of the same community lies.

2 The evidence of artefacts

The logical basis for the use of artefacts in demographic research lies in the fact that the number of artefacts depends on the number of persons that produced and used them. The number of houses may be in a proportion to the number of families, and the number of "sites" in proportion to the number of communities. Moreover, a growing population produces a growing number of artefacts, and in this way artefacts reflect the rate of population growth. All this seems to be so obvious that a number of archaeologists take the testimony of artefacts at its face value believing, for example, that more houses in an archaeological context indicate a larger village of the past, and more sites imply a greater density of population. It is a common belief that if a later period produces more sites than the previous one, it means a population increased over time. However, all these assumptions can be demonstrated to be invalid in principle. I shall soon discuss the methodological problem of how the quantity of the archaeological record changes. To approach this issue critically, we have to realize that the archaeological record as found by archaeologists (the "dead" culture) substantially differs from the living culture of the past. It is sometimes believed that this difference can be reduced to the fact that, in contrast to the living past, the archaeologically recovered artefacts are static and some of them are missing; for example those made of perishable materials. The reality, however, is more complicated. A series of processes changes the living culture radically, transforming it into the archaeological record. I shall refer to these processes as transformations. Some of the transformations are purely qualitative (such as the disintegration of shape) while others influence the quantity of artefacts. Transformations represent the archaeological parallel of taphonomy.

I believe, however, that the theory of archaeological transformations can be defined more exactly. I shall pay attention to those transformations that change the quantity of artefacts, as only by fully realizing them can archaeologists properly draw consequences in the sphere of demography. The transformations are as follows: fragmentation, reduction, and accumulation. I am going to shortly discuss them mainly from the point of view of their impact upon the reconstruction of ancient demography.

2.1.1. Fragmentation

Most artefacts appear in the archaeological record in the form of fragments of which only a part is accessible to archaeological research. Typically, pottery vessels disintegrate into sherds each original vessel being usually represented by a few fragments. Another example of fragmented artefacts is a few houses (sometimes incomplete) that represent a prehistoric village. The remaining houses are not accessible because they have been either destroyed by erosion or not yet excavated. This kind of fragmentation has a direct effect upon demographic considerations.

2.1.2. Reduction

Most archaeological artefacts are dramatically reduced in their numbers. The measure of reduction is not the same for all kinds of artefacts; it depends on the material from which it is made as well as on the environment to which the artefacts get after their exit from the live culture. Some artefacts are reduced almost to zero (e.g. wooden objects or most textiles), while others survive almost one hundred percent (e.g. stone tools). Most rates of reduction lie in between zero and one hundred. There are reasons to believe that more than 95 per cent of prehistoric pottery sherds and/or animal bones are destroyed in the soil of Central Europe. It is important for demographic considerations to note that villages built entirely above the ground leave no traces, and barrows with interments deposited at the level of the surrounding terrain can be entirely erased from the record by subsequent ploughing.

2.1.3. Accumulation

Many archaeologists do not suspect the existence of this kind of transformation that can severely change the quantitative relations among artefacts. The essence of this transformation is connected with the concept of the life span of artefacts, i.e. the average duration of its use or "life". If the life span of a pottery plate is one year, and the life span of an amphora is ten years, the quantitative relation in the living culture may be one amphora to one plate at any moment, while the relationship of broken vessels in an archaeological site will be one hundred plates to ten amphorae after a century. Let us consider an excavated Bronze Age village, lasting 80 years, with 16 house plans recovered by excavations. If the life span of a house is 20 years on the average, it can be easily calculated that the average number of houses at the site at any moment was 4.

$$P=(R*z)/t \quad P=(16*20)/80=4$$

It is obvious that the number of house remains in nearly any archaeological site must be much higher than the number of houses used by the past living population at any point of the past. The same logic applies to all kinds of artefacts.

3 Some results

So far, some of you may have obtained the impression that the reconstruction of prehistoric demography is very difficult if not impossible. I tried to point out the many difficulties mainly to demonstrate that demography is not a matter of simple narration in present day archaeology. But notwithstanding the difficulties we can say much that is positive about the demography already now.

3.1 Population size in prehistoric times

One of the most frequently discussed problems of prehistoric demography is the number of inhabitants in a territory. If the size of the territory is known, absolute numbers change into relative values expressing the density. The standard method used in such cases consists of three steps:

- (1) the assessment of the number of people living in one average house
- (2) the assessment of the number of houses in one average village
- (3) the assessment of the number of villages in a region. If these parameters are known, the number of inhabitants of a region is simply obtained by multiplying the three values enumerated above with each other. This procedure, however, requires some comment.

3.1.1. The number of people living in one house

Most archaeologists assume that each house was inhabited by one nuclear family, with possibly a few other people joining temporarily. It can be assumed, mainly on the basis of the study of prehistoric life tables as well as on the basis of ethnographic models that nuclear families were often joined by single old people of the preceding generation who did not form any new family any more after widowing for the last time, and possibly by young people, mostly orphans, who have not yet married.

Families that expanded in this way can be termed households; on the average they may have added less than one average person to nuclear families.

It is often assumed, on the basis of parallels with biblical families, with the situation in modern Third World countries, and with European families of the 19th century, that prehistoric nuclear families must have been large, something like 6 people on the average, or even more. Some 20 years ago, I derived a formula for the approximation of the number of people per one nuclear family on the basis of life table parameters (this formula in fact calculates the number of people per one female in the reproductive age). Alternative calculations based on the function cx show almost identical results: prehistoric nuclear families could hardly have exceeded 4 persons on the average. In consequence of this households represented less (often much less) than 5 persons on the average. The assumption of something like 6 people per one average nuclear family can be shown to lead to a very fast overpopulation of any region. In consequence of this, archaeologists have to give up their intuitive guesses based on unreasonable parallels.

3.1.2. The number of houses in a village

The problem of counting houses of an archaeologically-uncovered site seems to be extremely simple to many archaeologists. They just count the house plans found per one typological period or one stratigraphic layer and then extrapolate the results to the whole site (as the site is rarely excavated in its completeness). One typological phase at a site – as well as one stratigraphic unit – may easily last several decades and possibly many decades. In contrast to this the mean life time of a prehistoric house is most probably less than the time span of the occupation of the site, possibly less than 20 years. This makes it clear that all the houses whose plans are found at a site could not have stood there at the same time.

Also, not all the houses that stood in a village at one time were permanently occupied by a family or a household. The number of houses derived from archaeological excavations represents a quantity accumulated over time. In addition to the technology used as well as with other factors such as the type of agriculture, the life span of a prehistoric house could also have been influenced by purely "irrational" reasons of symbolic nature. The average number of inhabitants of one village can also be calculated from the number of graves in a (complete) cemetery using the life tables, here again under the condition of the stationarity of the population. It can be obtained from a simple formula:

$$P = D \cdot e_0 / t$$

where P is the average number of inhabitants at any time, D is the number of skeletons in the cemetery, e_0 is the life expectancy of a new born, and t is the number of years over which the cemetery was used. If we take, as a model example, $D = 200$ (skeletons), $e_0 = 28$ years (which corresponds to the death rate of approximately 3.5 %) and $t = 350$ years, we get

$$P = 200 \cdot 28 / 350 = 16 \text{ persons.}$$

This means either 4 nuclear families or, more realistically, something like 3 households. The parameters used in this example correspond approximately to the largest cemetery of the Corded Ware (or Battle axe) culture in Central Europe and in this way it can serve as a standard for many other prehistoric culture groups.

Obviously, we can play with the equation. Accepting a higher death rate (which is the reciprocal of life expectancy), the resulting live population will shrink further. D and t are more or less observed values and they cannot be easily manipulated. However, D may in fact be larger because of a part of the population "missing" in the regular cemeteries. It is obvious that even in doubling D , it is unlikely to get anything like large population groups.

3.1.3. The number of villages in a region

It is well known that various culture groups occupying the same territory and lasting approximately the same number of years produce a radically different number of archaeological sites. This phenomenon is most frequently explained by the unequal number of inhabitants in those periods, i.e. by significant fluctuations in the population density over time. The number of sites from two succeeding periods of prehistory may easily differ by the factor of ten or more. There is no doubt that the variation in the density of sites can hardly be explained by changing densities of the prehistoric population, but rather by the transformation of the archaeological record. The large number of sites is usually caused by an accumulation of objects that have a very short life span (such as the late Bronze Age storage pits, for example) while the reduction transformation is responsible for the deficiency of sites.

There emerges the problem of some regions and some periods of prehistory that remain almost without any archaeologically visible record in spite of the fact that prehistoric people did live there at that time. Imagine a region (such as southern Bohemia, for example) where subsurface prehistoric features are rare and the average sloping of the terrain is high. In such a case the refuse areas that usually supply most finds will normally be carried away by erosion and there will be no or very few intrusions into later layers. To prove the presence of all culture groups would be very difficult indeed. This is even more so if no subsurface features were dug in some of the culture groups for symbolic reasons while others had no such limitations. In fact, methods for discovering components of prehistoric settlement areas missing for these reasons have not yet been developed. The measure of reduction is tremendous as can be demonstrated by means of so-called intrusions of individual artefacts, mostly fragments, in later subterranean objects: a whole eneolithic village representing several decades of life can be reduced to one or two sherds scattered in the fill of a late Bronze Age storage pit. Therefore, the study of intrusions is becoming one of the most powerful tools in considering prehistoric demography.

3.1.4. Conclusions

It remains to briefly discuss the results on the size of populations. I would like to point out, here again, that demographic issues cannot be studied in a way other than in a regional context. What I am going to present is valid for many parts of prehistoric central Europe and even for the rural population of the Middle Ages. The basic parameters can be summarized in the following table:

	persons	families/households
average family	<4	
average household	<5	
village	12 to 30	3 to 6
density*	3 to 5 persons per sq.km. of the community area	approximately 1

I have to briefly comment on the problem of the density of the prehistoric population which is often, even if misleadingly, calculated in relation to modern territorial units. Although some regions seem to have been occupied densely with almost no gaps in between the individual community areas, there were other regions, mainly mountainous, with virtually no prehistoric settlement. The number of people obviously cannot be related to the latter type of regions. Therefore I tentatively approximate the density of prehistoric population by relating the average number of persons per village to the average size of its community area. The preliminary result of such calculations is included in the table.

3.2 The settlement structure in prehistoric Central Europe

In prehistoric Central Europe we are in the happy situation that we have detailed evidence for the spatial distribution of at least some periods and some regions. This does not mean that we can reconstruct the full settlement network, but we assume that regional fragments of it are known in some cases. In all well documented situations, the picture is the same: small villages situated quite close to each other, usually spaced from one to three kilometers.

All archaeological sites of one culture group need not have been fully contemporaneous, but many of them certainly were. Adjusting for the former cases, the density would become less, but it would still remain high. Therefore, the general rule seems to be small villages densely distributed in small distances. There are exceptions to such rules.

3.3 The rate of increase

The biological potential of humans is tremendous. It is only slightly weakened by the generally high death rate that did not allow the whole reproductive period of women to be exploited for the purpose of reproduction. However, something like a yearly increase of 3% was fully realisable; there is no reason to believe that such values of natural increase could not be achieved in prehistoric times. However, these or even much smaller positive values of natural increase, if made real, would cause enormous overpopulation mainly due to the vast time depth of prehistoric times. The following table approximates the factor by which the original population multiplies in a given number of years:

years	growth rate		
	1%	2%	3%
50	1.6	2.7	4.5
100	2.7	7.4	20.1
200	7.4	54.6	403
300	20.1	403	8103

This table displays, for example, that the original population of 100 persons increases to more than 800 000 over 300 years if its growth rate is 3%.

There are three models according to which the situation of rapid growth can be explained. 1. One of them relies on the supposition of unlimited "natural" growth followed by the emigration of the excess population. 2. The second solution allows the population to fluctuate: to grow for some time (possibly up to the carrying capacity of the area) and then to be reduced either by emigration or by some violent event, disaster, famine etc. 3. The third method is the installation of measures for preventing any population growth. The first two models assume the existence of areas in which the population grows over time prior to its emigration. However, archaeology can document no such areas. All the examples of which I am aware are heavily influenced by the transformation of the archaeological record, mostly by reduction and accumulation. The observed increase or decrease of the number of graves, pits, or sites in general can be explained by ritual peculiarities, the digging of subsurface hollows or, conversely, by building everything above the ground, and/or by the differential life span of archaeological features. Also, there are no areas where the excessive population could go after growing to unbearable dimensions, because since the developed Neolithic period, prehistoric farmers densely occupied most regions in Europe. Around 4500 BC there was an unanticipated movement of the European population colonizing the southern part of Scandinavia and the British Isles, previously occupied by Mesolithic cultures, but this does not seem to be the consequence of an overpopulation prior to the advance of the colonization wave.

In consequence of this, the third solution gains credibility: the prehistoric people apparently knew how to limit their growth by manipulating their sexual behaviour by social and ideological means, and possibly by supplementing such measures by infanticide. Otherwise they would overpopulate periodically, rapidly and in many regions at the same time. Such an overpopulation could not escape the attention of archaeologists.

3.4 The problems of migrations

Migration is a recognized concept of traditional demography. Surprisingly, its opposite, i.e. the continuity of population is rarely studied, apparently because it is considered to be the rule. In fact, both the concepts are extremely important in prehistoric demography. 3.4.1. Migrations as population discontinuity Although the culture historical paradigm, ruling archaeology for most parts of the 20th century, proposed migrations to be one of the main causes of events in prehistoric times, its adherents never suggested any demographic instrument by means of which it could occur. The almost exclusive explanation was overpopulation in some selected regions ensuing from unspecified natural factors. Migrations, however, are conditioned by demographic processes and, at the same time, they deeply influence the biology of human populations. Migration has rarely the form of population movement in which the migrating groups simply transfer themselves to a new area, leaving the area of their origin empty. Thus migration is almost always connected with a measure of population increase and often also population decrease to balance it. Because the means by which people manipulate their reproduction are social and ideological, it is more or less easy to install them almost immediately. Therefore, it seems to be simple to migrate at any time. Similarly to stop the higher natural growth after the migration presents no difficulty in a situation when there is no more any necessity to fill new territories with population.

The generally accepted assumption that migration results from overpopulation leads to the widely accepted conclusion that the growth came first and the movement of the population followed. In theories such as the wave of advance, the growth might have occurred at the same time as the movement, but this obviously slows the process down. Some time ago I suggested that migration need not have taken place in this way. It can be imagined that the spread of the migrating population occurred before the natural growth. This possibility was not considered by those anthropologists who believed in the purely natural causation of population growth. Small groups consisting of individual families or very small groups of families would penetrate into the newly colonized territories, not keeping the usual pattern of distances between two neighbouring villages. This would allow for a much faster occupation of new territories, while the sparsely distributed population could grow subsequently in the next several decades. It can be calculated that the "normal" population density would be restored over a time interval that is shorter than what archaeological chronology is usually able to grasp. Thus, such demographic events would not be observed easily by archaeological means. It is obvious that this kind of migration would have an impact upon the genetics of the migrating population because the whole population would originate from a rather restricted set of persons. The model "movement first, growth later" could have taken place during the colonization of Europe by farmers at the beginning of the Neolithic period. Colonization takes place in territories with sparse or no previous settlement, and for this reason the local population, if there was any, would not represent any major obstacle for the migrants. Expansion, in contrast to colonization, is directed into regions that were previously fully settled. In that case the earlier local population would have to be removed. If this were done, for example by exterminating it, the situation would be the same as in the case of any colonization. However, I am not aware of any prehistoric example of such an expansion.

With the exception of the colonization by which the agricultural stage of prehistory begins, there are in my view few archaeological examples of large scale long distance population movements preceding the Iron Age. This may have been caused by the many difficulties that any migration of larger groups of population of the Bronze Age type brings about. The problems begin with practical issues such as how to till fields in the first year of migration, how to feed the stock of domestic animals, and goes on into the social sphere (how to restore the networks of trade through which bronze was supplied, how to restore the networks by which marriages were concluded etc.). Also, there must have been problems how to mentally appropriate the landscape, including the possibly dangerous objects such as graveyards of the earlier population. In the Eneolithic period and in the Bronze Age the prehistoric community still formed a unique body that could not easily separate. In the Iron Age, however, it seems that the leading layers of the population could break away from the community by going away to replace the leading layer of another community. This process created the form of movement that I describe as invasion; it was typical of population groups of the developed Iron Age and later.

The pre-processual archaeology recognized many instances of the mixing of the older, local population with the newcomers. This mixing was assumed in the shapes of vessels, in the form of pottery decoration, and in the formal attributes of various artefacts. It was later recognized that virtually all this mixing of artefacts never took place. It seems that the mixing has become fashionable again, this time on the basis of the genetic evidence.

3.4.2. The continuity of artefacts

I shall very shortly explain why and how archaeologists are able to articulate their views on the continuity of populations on the basis of their own records, i.e. on the basis of artefacts. I would start with the generally accepted opinion that human groups reproduce not only genes but frequently also language. Without going into details, I would like to draw your attention to the fact that by creating artefacts people generate, in addition to language, yet another body of symbols and signs. We communicate by means of a particular aspects of our artefactual culture such as clothing, weapons, grave ritual etc., as nearly any artefact has some sort of symbolic significance which is able to convey information. Artefacts also have what I call their expressive aspect. It is composed of those formal attributes of artefacts that have neither a practical function nor a communicative significance, but the simply express something. For example, the way in which the surface of a pot is treated cannot be considered to have a practical function already in view of the many possibilities of how the task can be done. Also, it does not contain any message. People treat the surface of pots in the way that is usual, customary, and/or common in their culture, just to express regularity, consistency, stability and the like. If they did it otherwise, they would violate their own group identity, as any deviation from what is usual would be considered to be a symbol which communicates a message. Prehistoric artefacts contain lots of expressive properties that simply express the usual. It can be assumed that many attributes that originally had a symbolic significance later lost it almost entirely and became expressions of identity. For example, the spiral on Neolithic pottery may belong to this class.

3.4.3. Cultural versus biological continuity

Archaeologists, mainly those in Central Europe, were acutely aware of the importance of the stability of human culture especially since the end of the 19th century. It was mainly on the basis of the continuity in the communicative and the expressive aspect of culture that they divided prehistory into many archaeological cultures or culture groups. We should be aware of the fact that the groups are real and they become important when we study the dynamics of human populations. From the point of view of time changes, archaeological cultures become manifestations of continuity. I would like to draw attention to these facts especially in this session, as cultural continuity is often forgotten when considering the inheritance of ancient populations. Cultural continuity is not identical with genetic continuity, but it is still continuity, and the two frequently coincide in concrete instances. There is a number of reasons why they are not identical, but the main factor is undoubtedly the fact that by creating artefacts, human beings make themselves free of natural inheritance. From the point of view of artefacts, even people with completely different genes may become closest relatives. This is not to say that archaeologists are not eager to obtain detailed knowledge of biological heredity that helps solve a number of archaeological questions in addition to solving biological issues. It seems to me – but as an outsider in biology I may be mistaken – that natural science has frequently been about species or about at least groups of individuals. However, by means of molecular biology, natural scientists get a tool for considering individuals. Archaeology has much experience with the study of individual events, their observation, description, systemization and explanation; there is much danger in doing all this. Therefore we are looking to the point in time when there will be some genetic information about more individuals from each population to see the variability.

3.5 The non-biological intervention into demography

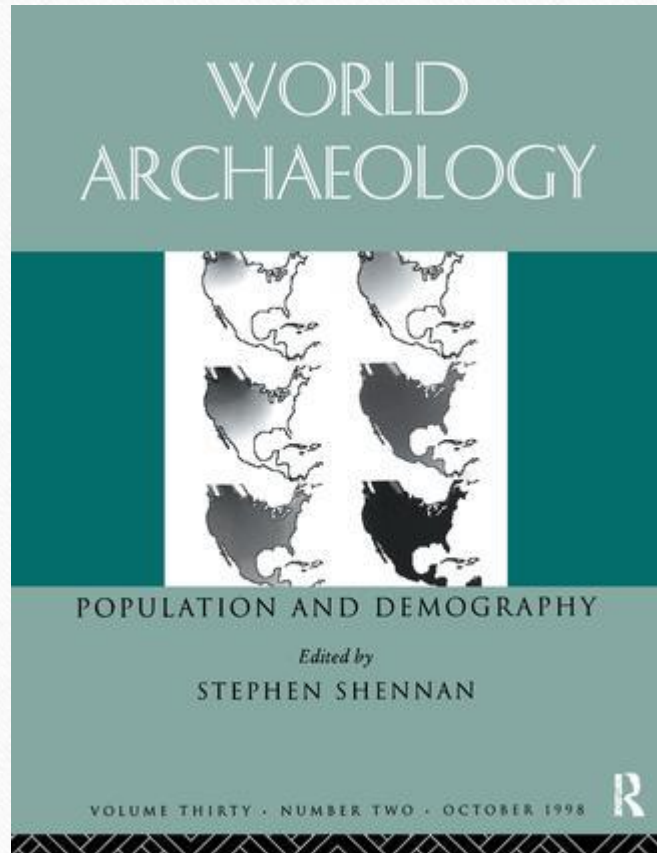
The case of population growth clearly demonstrates that prehistoric people were able to manipulate demographic processes with full success. In fact, any kind of migration was only feasible if people were able to release the rules imposing limits on their natural growth at the beginning of the migration and reintroduce it afterwards. The regional variability of the size of prehistoric communities occupying more or less the same ecological zone demonstrates that human demography was not a natural process. The same ensues from the fact that the size of populations settling the same region often differed in two subsequent periods. Also, the types of migrations are clearly socially determined. The rapid changes over time and space such as can be observed in the human world do not seem to have parallels in nature. The situation that human populations change their culture substantially over several decades or over the distance of several ten kilometres is common. We are unable to observe the causes of human incursions into the "natural" system of demographic relations in prehistoric times. It is almost certain that prehistoric people did not consider the demographic processes in terms of the discipline of demography, but their considerations had some ideological cover. Thus, demographic processes were cognitive but, for example, we cannot assume that we could come to the true reasons for the incompleteness of prehistoric cemeteries even if we had the possibility to ask ancient people. However, what archaeologists frequently can do is observe the results. In other cases we suspect that something went on that has no parallel in our modern life, but we are still unable to go into details.

3.5.1. The irregular behaviour

Irregularity in human behaviour can often be traced through the observation of cultural continuity and/or discontinuity. There are several large scale discontinuities in the archaeology of Central Europe. One of them, an almost absolute one, came at the beginning of the Neolithic period shortly after 5500 BC. The Mesolithic cultures, which up to that date occupied the region, developed into groups such as La Hoguette, found as far to the east as the Stuttgart region; this group is so much unlike the Linear Pottery culture of the colonists coming from the south-east that any inherent link between them is out of question. The character of the contacts between the two types of population remains unclear. Another discontinuity is between the middle Eneolithic period in Central Europe and the subsequent Corded Ware or Battle Axe culture. The middle Eneolithic period houses a number of formally divergent groups such as late Baden, Řivnáč, Cham, Horgen, Globular Amphora, Walternienburg-Bernburg and late phases of the TRB culture. All this diversity disappears some time between 2900 and 2800 BC, and is replaced by a rather uniform early phase of the Corded Ware culture. This represents a complete rupture with the past: pottery, stone tools, personal ornaments, types of weapons, and the burial rite are all new and typologically incomparable to the middle eneolithic culture groups. There are very few links between the two archaeological periods, most of them of a general nature. These empirically observed facts became known at the beginning of the 20th century and nearly everybody believed that they were a consequence of a demic expansion or invasion from outside Central Europe. It was believed that the Corded Ware had lived together with the earlier population of the middle Eneolithic type in the same landscapes. The assumed population movement was frequently connected with the arrival of the Indo-European speakers.

This explanation by means of large scale migration has now become difficult to support. Both absolute and relative chronologies demonstrate that what happened was a sudden replacement of culture over distances of thousands of kilometres. The long lasting contemporaneity of the Corded Ware with the middle Eneolithic period, as assumed earlier, could not take place on chronological grounds. But what is even more significant is the fact that detailed archaeological research in the surrounding countries showed that there was no region in Europe from which the Corded Ware culture could have come. There is no solution other than that the Corded Ware culture originated in Central Europe (plus possibly in southern Scandinavia), the change of culture being a point of discontinuity lasting not more than several decades. We have no theoretical model describing how this could have happened. We know, however, that the Corded Ware culture was extraordinary in many other respects. Its grave ritual was strict as to the position of the dead (depending on sex), to the position of artefact classes in graves, to the differential equipment of graves with artefacts in dependence on sex and age etc. While there are several hundred cemeteries in Bohemia, not a single storage pit or a dwelling dug under the surface has so far been recovered. There are some 1500 graves in Bohemia, but not a single one contained the large simple pot with a wavy ribbon under the rim that characterizes the places where Corded Ware people lived (apparently on the surface). Often I express the situation with the words that Corded Ware people were fundamentalists.

We still do not know what happened in Central Europe in the first half of the 3rd millennium BC. It is even more disquieting that a similar history repeats in the second half of the millennium with the Bell Beaker culture. This group does not reach into eastern Europe and Scandinavia, but it is found in western Europe and even in some places of northern Africa. This time the discontinuity of culture is matched by the discontinuity of biological attributes, as one part of Beaker skulls found in Central Europe are brachycephalic and there are also other peculiarities. Archaeologists feel that there is continuity between the Bell Beakers and the preceding Corded Ware but, here again, convincing evidence is missing. The presence of the Bell Beaker culture in many parts of western Europe remains a mystery – unless we accept the simplistic explanation that everything happened by means of migration. Looking at these two topics of archaeology in Central Europe from the demographic point of view, I have to state that the model "migration first, growth of population later" could possibly explain it. Better yet, I should say that it cannot be excluded on the basis of present day evidence. These people were undoubtedly our ancestors in the sense of cultural continuity. We are beginning to feel that their behaviour was not like ours. If their artefact production was unconventional, their demography, including reproduction, could also be likewise.



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Demography in Archaeology

Andrew Chamberlain



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