# ISOTOPIC AND GENETIC EVIDENCE FOR MIGRATION IN MEDIEVAL ENGLAND

**Mark Jobling and Andrew Millard**

## Introduction

Scientific approaches to identifying past human movements and migrations have been developed over the last 60 years. Initial studies in genetics used blood groups and other measurable biochemical differences among living human populations to project back into the past and provide evidence for migrations.[1] In the 1980s and 1990s the focus of such work moved to DNA sequences rather than their protein products, and the rate of production of data since then has been exponentially increasing. Biochemical and geochemical analysis of skeletal remains from archaeological sites to study migration has also been developed over the last 30 years or so, starting with analyses of strontium isotopes[2] and the first extraction of ancient DNA (aDNA) from bone.[3] Many of the early applications were to prehistoric remains, but application to medieval remains soon followed.

Analysis of isotopes or aDNA from skeletal remains provides information directly about that individual. Isotopes incorporated in the skeleton inform us about the geographical

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[1] L. L. Cavalli-Sforza, P. Menozzi, and A. Piazza, *The History and Geography of Human Genes* (Princeton, NJ, Princeton University Press, 1994).

[2] J. E. Ericson, ‘Strontium Isotope Characterisation in the Study of Human Prehistory’, *Journal of Human Evolution*, 14 (1985), 503–14.

[3] E. Hagelberg, B. Sykes, and R. E. M. Hedges, ‘Ancient Bone DNA Amplified’, *Nature*, 342 (1989), 485.

sources of their foods, and thus their locations during their lifetimes. On the other hand, both ancient and modern genetics not only provide information about an individual's phenotype, such as sex or hair colour, but also reflect their relationships with others, and the population or populations that they descend from. Published isotope studies are rarely of a scale that enables population-level inferences to be made, but the totality of data currently available (over 400 analyses are reviewed below) now means that we can start to think about such questions, for example, whether overall migration and mobility patterns change through time in the medieval period in England.

Isotope and aDNA analyses are restricted to excavated human remains, and this leads to temporal and geographical biases. Early medieval England has some regions where cremation was the primary funerary rite. Survival of DNA depends on the temperature reached during cremation: under experimental conditions DNA is recoverable from samples heated up to 600°C,[4] but reliable data from archaeological cremations are currently lacking. Oxygen isotope signals are also erased by cremation, and it is only recently that strontium isotope analysis has been extended to cremated individuals.[5] In regions with acidic soils,

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[4] M. Harbeck *et al.*, 'Research Potential and Limitations of Trace Analyses of Cremated Remains', *Forensic Science International*, 204 (2011), 191–200.

[5] C. Snoeck *et al.*, 'Mobility During the Neolithic and Bronze Age in Northern Ireland Explored Using Strontium Isotope Analysis of Cremated Human Bone', *American Journal of Physical Anthropology*, 160 (2016), 397–413.

bones and teeth are poorly preserved, if at all,[6] leaving us with much less intact skeletal evidence from upland and western parts of England.

The richness of interpretation and understanding produced by isotope and aDNA analyses are dependent on information from the archaeological context. From the mid-seventh century the use of grave-goods in burials declines and is rare after *c*. 700,[7] thus cultural dating evidence can be imprecise. Radiocarbon dating is therefore of great importance to verify the age of the samples, as illustrated by the isotopic investigations of mobility at Riccall and Carlisle Cathedral discussed below. Comparisons of isotopic results with grave goods, body positions, and location within a cemetery can all add to the interpretation of migration. Osteological analyses are also a key part of mobility studies. Interpretations of both isotope and aDNA analyses depend on osteological estimates of age, and may incorporate identification of other features such as diseases or injuries. Osteological sexing is frequently used in isotope studies; in contrast, in recent aDNA studies, sex is usually independently estimated via the detection and analysis of sex chromosomes in whole genome sequencing.

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[6] M. Kibblewhite, G. Tóth, and T. Hermann, 'Predicting the Preservation of Cultural Artefacts and Buried Materials in Soil', *Science of The Total Environment*, 529 (2015), 249–63.

[7] A. Bayliss *et al*., *Anglo-Saxon Graves and Grave Goods of the 6th and 7th Centuries AD: A Chronological Framework*, Society for Medieval Archaeology Monographs, 33 (London, Society for Medieval Archaeology, 2013); H. Geake, *The Use of Grave Goods in Conversion-Period England c.600–c.850*, BAR, British Series, 261 (Oxford, BAR, 1997).

DNA studies of modern individuals usually select individuals based on their known ancestry. In so doing, investigators are trying to control for the extensive movement and mixing of people that has occurred since the advent of railways and motor vehicles, and from twentieth-century immigration. Such a recruitment strategy assumes that, prior to modern times, most mobility in the past was limited in distance, except for a few larger-scale and longer-distance migrations.

Inferring past migration events from modern genetic data requires the use of mathematical models devised for population genetics.[8] Although large-scale migrations can be detected, it is not always possible to distinguish single migration events from multiple and repeated population flows from the same place. Thus, the number and timing of migration events identified through these methods is often ambiguous.

Our review of the state-of-the-art in isotopic and genetic studies of medieval migration into and within England is shaped by the published literature. Past work using isotopes is composed of numerous small studies, although they have now reached a significant total in aggregate. Modern DNA studies are of much larger scale than those based on archaeological material, but they use an indirect form of evidence, and require complex and sometimes debatable processes of inference in order to yield reliable information about the past. Ancient DNA studies have the advantage of directness in analysing the genomes of individuals from the medieval period but have so far been limited to a few small-scale studies. In the following sections, we review in turn the evidence from isotopic and genetic data, and

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[8] J. G. Schraiber and J. M. Akey, 'Methods and Models for Unravelling Human Evolutionary History', *Nature Reviews Genetics*, 16 (2015), 727–40.

then draw these together with some observations about how these different scientific fields can best combine to provide information about medieval England.

## Isotope Analyses

Isotope analysis of human remains can be carried out on the three main skeletal tissues: tooth enamel, dentine, and bone. Enamel has the advantage of being almost entirely composed of mineral, thus making it the hardest tissue in the human body and giving greater resistance to alteration by the burial environment (a process known as diagenesis). Bone and dentine are composites; their primary components comprise approximately 70% biomineral and 20% the protein collagen. Due to their porosity and the attraction of protein as a food source for micro-organisms, bone and, to a lesser extent, dentine, are much more susceptible to diagenesis than enamel. Diagenesis of bone mineral is therefore almost universal.[9] Biomineral offers the opportunity for analysis of carbon, oxygen, strontium, and lead isotopes, while collagen can be analysed for hydrogen, carbon, nitrogen, oxygen, and sulfur isotopes. Enamel and dentine are laid down during childhood and do not renew during adult life, so their composition reflects diet and place of residence in childhood. The teeth most frequently used for analysis are the first, second, and third permanent molars, and the second premolar, whose enamel is formed at the ages of 0–3 years, 3–8 years, 9–13 years and 2–7 years

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[9] A. R. Millard, ‘Deterioration of Bone’, in D. R. Brothwell and A. M. Pollard (eds), *Handbook of Archaeological Sciences* (Chichester, Wiley, 2001), pp. 633–43.

respectively.[10] Bones are continuously renewed so their composition reflects average diet over a period of time before death, the length of the period varying from less than a year with infants to a few decades in older adults.[11] Enamel is therefore the tissue of choice for migration studies as it is resistant to diagenesis, with a composition reflecting childhood residence, which can be compared to that expected for the place of burial. The major assumption of this approach is that, prior to industrialisation, the majority of food and water was sourced locally, and thus that enamel composition reflects the local environment.

In past investigations of migration in medieval England, only strontium and oxygen in enamel have been of major importance, with multiple studies covering a wide temporal and spatial range. Lead isotopes have been measured in remains from a number of sites[12] but in this period human exposure to lead is primarily technological rather than natural,[13] and they have limited application in identifying movement. The other isotope systems have been less well researched and have seen very limited, if any, application to medieval England.

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[10] S. J. AlQahtani, M. P. Hector, and H. M. Liversidge, 'Brief Communication: The London Atlas of Human Tooth Development and Eruption', *American Journal of Physical Anthropology*, 142 (2010), 481–90.

[11] R. E. M. Hedges *et al*., 'Collagen Turnover in the Adult Femoral Mid-Shaft Modeled from Anthropogenic Radiocarbon Tracer Measurements', *American Journal of Physical Anthropology*, 133 (2007), 808–16.

[12] J. Montgomery *et al*., '"Gleaming, White and Deadly": Using Lead to Track Human Exposure and Geographic Origins in the Roman Period in Britain', *Journal of Roman Archaeology Supplement*, 78 (2010), 199–226.

[13] J. A. Lee-Thorp, 'On Isotopes and Old Bones', *Archaeometry*, 50 (2008), 925–50.

## Strontium isotopes

Strontium isotope ratios vary in nature because three of the four naturally occurring isotopes were formed early in the history of the solar system, but the fourth, strontium-87, is continuously formed by the radioactive decay of rubidium-87. The proportion of $^{87}$Sr in a rock, conventionally expressed as the ratio $^{87}$Sr/$^{86}$Sr, thus depends on its age and the initial ratio of rubidium to strontium. To a certain extent it is possible to predict local strontium isotope ratios, but the precise values observed in the biosphere depend on a series of additional factors. One important factor is that some minerals within a rock are preferentially weathered and thus release their strontium into the soil, where it is available to be absorbed by plants and passed along the food chain. In areas of high rainfall, such as the western Isles of Scotland, the input of strontium from rainwater can be significant. The $^{87}$Sr/$^{86}$Sr ratio in rain is the same as that of the ocean, which is uniform worldwide at 0.7092.[14]

The relationship between strontium isotope ratios in enamel and location of burial is more complex than a simple correlation. It is possible for local diet to mix foods from multiple geological formations with differing strontium isotope ratios.[15] The result in the enamel is a ratio intermediate between those of the formations involved, which may not

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[14] R. A. Bentley, 'Strontium Isotopes from the Earth to the Archaeological Skeleton: A Review', *Journal of Archaeological Method and Theory*, 13 (2006), 135–87; J. A. Evans *et al*., 'Spatial Variations in Biosphere $^{87}$sr/$^{86}$sr in Britain', *Journal of the Geological Society*, 167 (2010), 1–4.

[15] J. Montgomery, J. A. Evans, and R. E. Cooper, 'Resolving Archaeological Populations with Sr-Isotope Mixing Models', *Applied Geochemistry*, 22 (2007), 1502–14.

correspond to the ratio of any local geological formation. Marine foods, carrying the specific strontium isotope ratio of the ocean, may also contribute to this type of mixing. A map of strontium isotope ratios for Great Britain is available (Figure 2.1) based on environmental samples and extrapolation to similar geological formations.[16] This provides a rough guide to the variation across the country, but, as its authors note, the scale of the map can hide important local variations.

With strontium isotopes it is easy to identify an individual whose ratio is not local, but it is much more difficult to say where that person grew up. It is also the case that a person carrying the local ratio may not have acquired it locally. Both these limitations arise from the fact that there are many locations with the same strontium isotope ratio. For example, the entirety of the chalk of southern England yields narrow range of isotope ratios (0.7073–0.7078),[17] and within this wide area migration cannot be detected. Similar values are also expected from the chalk of northern France. A migrant from Arras in the Pas de Calais to Salisbury could not be detected via strontium analysis alone, but someone who moved from Cardiff to Salisbury could. Conversely, it is possible for there to be substantial variation in

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[16] J. A. Evans *et al.*, 'Spatial Variations in Biosphere $^{87}$sr/$^{86}$sr in Britain', *Journal of the Geological Society*, 167 (2010), 1–4.

[17] J. M. McArthur *et al.*, 'Strontium Isotope Stratigraphy for the Late Cretaceous: A New Curve, Based on the English Chalk', *Geological Society, London, Special Publications*, 70 (1993), 195–209.

strontium isotope ratios over a short distance,[18] in which case it may not be possible to say whether an individual had moved 10 miles or 200 miles from the place where they grew up.

## Oxygen isotopes

The oxygen in tooth enamel is present in three forms, as phosphate, carbonate, and hydroxyl ions. Both phosphate and carbonate have been analysed to study migration. Although some authors have expressed doubts about the resistance of carbonate oxygen to diagenesis,[19] more recent work has demonstrated that it can be reliable.[20] The oxygen in enamel derives from the water in the body at the time of tooth formation in childhood and adolescence, which itself derives from a combination of inhaled oxygen gas and oxygen present in drinking water and foods.[21] The two isotopes measured are oxygen-16 and oxygen-18. Their natural proportions vary because their different masses lead to slightly different rates of transfer in chemical reactions and physical processes: this is termed fractionation. The ratio of these isotopes is

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[18] For example, S. S. Hughes *et al.*, ‘Anglo-Saxon Migration Investigated by Isotopic Analysis of Burials from Berinsfield, Oxfordshire, UK’, *Journal of Archaeological Science*, 42 (2014), 81–92.

[19] S. Lucy *et al.*, ‘The Burial of a Princess? The Later Seventh-Century Cemetery at Westfield Farm, Ely’, *Antiquaries Journal*, 89 (2009), 81–141.

[20] C. A. Chenery *et al.*, ‘The Oxygen Isotope Relationship between the Phosphate and Structural Carbonate Fractions of Human Bioapatite’, *Rapid Communications in Mass Spectrometry*, 26 (2012), 309–19.

[21] M. J. Kohn, ‘Predicting Animal D$^{18}$o: Accounting for Diet and Physiological Adaptation’, *Geochimica Et Cosmochimica Acta*, 60 (1996), 4811–29.

expressed as fractional deviation from a standard, $\delta^{18}O$, using units of parts per thousand (permille, symbol ‰). Confusingly there are two standards in use, abbreviated VSMOW and VPDB,[22] but almost all work on tooth enamel phosphate uses VSMOW. Atmospheric oxygen has a constant composition, so does not contribute to variation in enamel $\delta^{18}O$. The main driver of geographic variation is the composition of precipitation, which is reflected in surface waters and the plants and animals that take them in.[23] Maps based on measurements of precipitation, groundwaters, and surface waters form the basis for interpretation of measurements made on archaeological remains. River water averages the inputs from its catchment and may not reflect local precipitation; however, drinking water in the past is more likely to have come from local streams, ponds, and wells than from a major river. Figure 2.2 presents an interpolated map of $\delta^{18}O$ derived from precipitation. Such time-averaged maps need to be used cautiously as they can conceal sub-decadal variations which may occur while an individual tooth is growing.

The relationship between $\delta^{18}O$ in enamel and location is complicated by several other factors. The major factor is that water in the human body is fractionated from ingested water, and then phosphate- and carbonate-oxygen in tooth-enamel is further fractionated from body-water. It is essential that the combined effects of these fractionations are accounted for using a calibration equation,[24] but this introduces significant uncertainty.[25] In addition to

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[22] W. A. Brand and T. B. Coplen, 'Stable Isotope Deltas: Tiny, yet Robust Signatures in Nature', *Isotopes in Environmental and Health Studies*, 48 (2012), 393–409.

[23] Kohn, 'Predicting Animal $D^{18}o$'.

[24] A. R. Millard and H. Schroeder, '"True British Sailors": A Comment on the Origin of the Men of the Mary Rose', *Journal of Archaeological Science*, 37 (2010), 680–2.

geographic variation, water ingested by humans can have higher $\delta^{18}O$ than local surface water due to evaporation processes. There may be a minor effect for use of standing water, e.g., ponds, that have suffered evaporation, but there is also the possibility that $\delta^{18}O$ is raised by brewing and boiling.[26] This latter effect is partially accounted for, as the calibration equations were developed using data from modern individuals who likely consumed boiled beverages,[27] but it needs to be borne in mind when interpreting results.

As the dataset of measurements on archaeological material has grown it has become possible to compare to previous measurements on enamel, and thus to avoid some of the uncertainty introduced by calibration. Ranges typical of higher rainfall western areas and lower rainfall eastern areas have been proposed using a compilation of data for Britain.[28] A more recent attempt to map variation across the same geographical area lacked data from

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[25] A. M. Pollard, M. Pellegrini, and J. A. Lee-Thorp, 'Technical Note: Some Observations on the Conversion of Dental Enamel $\Delta^{18}o_p$ Values to $\Delta^{18}o_w$ to Determine Human Mobility', *American Journal of Physical Anthropology*, 145 (2011), 499–504.

[26] R. Brettell, J. Montgomery, and J. Evans, 'Brewing and Stewing: The Effect of Culturally Mediated Behaviour on the Oxygen Isotope Composition of Ingested Fluids and the Implications for Human Provenance Studies', *Journal of Analytical Atomic Spectrometry*, 27 (2012), 778–85; V. Daux *et al.*, 'Oxygen Isotope Fractionation between Human Phosphate and Water Revisited', *Journal of Human Evolution*, 55 (2008), 1138–47.

[27] Daux *et al.*, 'Oxygen Isotope Fractionation'.

[28] J. A. Evans, C. A. Chenery, and J. Montgomery, 'A Summary of Strontium and Oxygen Isotope Variation in Archaeological Human Tooth Enamel Excavated from Britain', *Journal of Analytical Atomic Spectrometry*, 27 (2012), 754–64.

regions of poor skeletal preservation,[29] thus limiting its interpretative utility. A further problem with interpreting oxygen isotope results is that some early publications used a sample preparation method based on laser fluorination that produced values differing from previous and later methods. Many of these samples have been re-measured and the new data reported,[30] but without a revised archaeological interpretation.

Just as with strontium isotopes, oxygen isotopes can identify individuals who are non-local to their burial place, but identifying a place of origin is more difficult. Once the uncertainties of calibration are accounted for, the compatible regions on a map of $\delta^{18}$O of precipitation are broad bands. Nevertheless, because oxygen isotopes vary systematically across Europe, a migrant's broad direction of movement can often be inferred, even if a specific place of origin cannot be identified.

## Review of isotopic studies

Isotopic studies of medieval migration in England are here broadly divided into three periods on the basis of the cultural changes addressed. As the focus is specifically England, several studies on sites in Scotland, Wales, and the Isle of Man as well as continental Europe are omitted. Figures 2.1, 2.2 and 2.5 show the sites reviewed. Apart from Bamburgh, none of the sample sizes can be described as large, and mostly they are insufficient for intra-site statistical analysis (for example, comparing males and females). With only 446 analyses spread over more than 1100 years, including some individuals analysed more than once, the

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[29] M. Pellegrini *et al.*, 'Tooth Enamel Oxygen "Isoscapes" Show a High Degree of Human Mobility in Prehistoric Britain', *Scientific Reports*, 6 (2016), 34986.

[30] J. A. Evans, C. A. Chenery, and J. Montgomery, 'A Summary of Strontium'.

density and scale of data contrasts with some other chapters in this volume.[31] It is also the case that work has focused on individuals and sites where migration was expected (especially the earlier studies) which is a bias inherent in the dataset. The results have usually been divided into 'locals' and 'non-locals', but the area represented by 'local' isotopic signatures varies with the location. As this area of research has developed, more nuanced categorisations have been devised based on distance and detailed mapping of strontium isotope ratio baselines,[32] which ought to raise aspirations for the sophistication of our interpretation of medieval datasets.

### *Early Anglo-Saxon (c. 450–700)*

The earliest centuries discussed here (*c.* 450–700) fall within a phase of European history traditionally referred to as the "Migration Period", an obvious target for research on migrants. A large proportion of isotopic studies on medieval skeletal material from England has focused on this period. The isotopic data from these sites are plotted in Figures 2.3 and 2.4.

A strontium and oxygen isotope study of seven individuals from mid- to late fifth-century Ringlemere, Kent (Site 1), also made comparisons with analyses of individuals from sixth- to eighth-century cemeteries on similar geological formations, one near Hanover,

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[31] See in this volume Dyer, chapter 9, pp. XXX–XXX; McClure, chapter 5, pp. XXX–XXX; Lambert and Ormrod, chapter 11, pp. XXX–XXX.

[32] For example, C. Cavazzuti *et al.*, 'Flows of People in Villages and Large Centres in Bronze Age Italy through Strontium and Oxygen Isotopes', *PLoS ONE*, 14 (2019), e0209693.

Germany, and two near Caen, France.[33] This study illustrates the ambiguities of trying to provenance people using isotopes. The Hanover site was distinguished in both strontium and oxygen isotope ratios from Ringlemere, but the French sites overlapped in strontium isotope ratios; with only a little overlap in $\delta^{18}O_P$, even though the rainfall values in both places ought to be very similar. The $\delta^{18}O_P$ values from Ringlemere are anomalously higher than expected. Brettell and colleagues speculated that this, and similar observations at other sites, could be due to cultural factors specific to Early Anglo-Saxon England.

Twenty individuals from a cemetery at Wasperton, Warwickshire (Site 2) were analysed for strontium and oxygen isotopes, but five individuals were found to be diagenetically altered.[34] Seven individuals were undated and dates for the others ranged from the fourth to early sixth centuries. A tight group of seven samples, with a range of 1.1 ‰ in $\delta^{18}O_P$ and 0.0011 in $^{87}Sr/^{86}Sr$, was interpreted as being of local origin. Three individuals with higher $^{87}Sr/^{86}Sr$ but $\delta^{18}O$ within the local range were inferred likely to originate from regions dominated by Palaeozoic rocks in parts of the Midlands, the southwest of England, or in Wales. One deciduous tooth was assigned to the local group as its $\delta^{18}O$ value may have been elevated by breastfeeding, and at 0.6 ‰ above the next highest $\delta^{18}O_P$ in the local group this is

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[33] R. Brettell *et al.*, '"Impious Easterners": Can Oxygen and Strontium Isotopes Serve as Indicators of Provenance in Early Medieval European Cemetery Populations?', *European Journal of Archaeology*, 15 (2012), 117–45.

[34] J. Montgomery *et al.*, 'Stable Isotope Analysis of Bone', in M. O. H. Carver, C. Hills, and J. Scheschkewitz (eds), *Wasperton: A Roman, British and Anglo-Saxon Community in Central England* (Woodbridge, Boydell, 2009), pp. 48–9.

within the reported range of up to 1.2 ‰.[35] A further four individuals had elevated $\delta^{18}$O values and were interpreted as migrants from a warmer climate than northern Europe. One individual with lower strontium isotope ratio, but within the local range for oxygen isotope ratios, could have come from elsewhere in modern Warwickshire.

An individual from Great Chesterford, Essex (Site 3), radiocarbon dated to AD 415–545 (at 95% probability), was investigated as an early case of leprosy in Britain.[36] It was concluded that this person had been a continental immigrant, despite comparing the $\delta^{18}O_P$ of 16.6 ‰ with the data of Evans, Cheney, and Montgomery,[37] who had concluded that the range for lower rainfall areas of Britain (including Essex) was 15.9 to 18.5 ‰, and computing a *p*-value for the hypothesis of an origin in Britain of between 6 and 28 %. As the strontium isotope ratio of the individual is found on geological formations within 10 km of the burial and the $\delta^{18}$O is compatible with local values, there is no evidence that this man had migrated any significant distance.

The late fifth- to early seventh-century settlement and cemetery at West Heslerton, North Yorkshire (Site 4), was the focus of some of the earliest detailed studies of migration

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[35] K. Britton *et al.*, ‘Oxygen Isotope Analysis of Human Bone Phosphate Evidences Weaning Age in Archaeological Populations’, *American Journal of Physical Anthropology*, 157 (2015), 226–41.

[36] S. A. Inskip *et al.*, ‘Osteological, Biomolecular and Geochemical Examination of an Early Anglo-Saxon Case of Lepromatous Leprosy’, *PLoS ONE*, 10 (2015), e0124282.

[37] Evans, Chenery, and Montgomery, ‘A Summary of Strontium’.

using isotopes in the UK.[38] These studies were framed within the debate between migration and acculturation for the transition from Late Roman to Early Anglo-Saxon England, and thus primarily focused on detecting possible ‘Anglo-Saxon’ migrants. Montgomery *et al.*[39] considered 32 strontium isotope analyses, which they interpreted as showing two groups: the first was compatible with the local environment including eight juveniles, whilst the second, with higher $^{87}$Sr/$^{86}$Sr and comprising juveniles and adults of both sexes, was non-local. The diverse results were considered incompatible with a male, military-elite invasion model for the transition from Roman to Anglo-Saxon culture, but the isotope values were ambiguous as to place of origin. Budd *et al.*[40] utilised the same human strontium isotope data, but with a different set of environmental data, and combined with 24 oxygen isotope analysis. They inferred a single group of strontium isotope ratios which were all to be found within 15 km of

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[38] P. Budd *et al.*, ‘Anglo-Saxon Residential Mobility at West Heslerton, North Yorkshire, UK from Combined O- and Sr-Isotope Analysis’, in S. Tanner and J. G. Holland (eds), *Plasma Source Mass Spectrometry: Applications and Emerging Technologies* (Cambridge, Royal Society of Chemistry, 2003), pp. 195–208; P. Budd *et al.*, ‘Investigating Population Movement by Stable Isotopes: A Report from Britain’, *Antiquity*, 78 (2004), 127–40; J. Montgomery, ‘Lead and Strontium Isotope Compositions of Human Dental Tissues as an Indicator of Ancient Exposure and Population Dynamics’, Ph.D. thesis (Bradford, 2002); J. Montgomery *et al.*, ‘Continuity or Colonization in Anglo-Saxon England? Isotope Evidence for Mobility, Subsistence Practice, and Status at West Heslerton’, *American Journal of Physical Anthropology*, 126 (2005), 123–38.

[39] Montgomery *et al.*, ‘Continuity or Colonization’.

[40] Budd *et al.*, ‘Investigating Population Movement’.

the site. Their oxygen isotope results require reinterpretation in the light of re-measurement of these and four additional samples from the site by Evans, Chenery, and Montgomery.[41] The $\delta^{18}$O values range from the 2nd to 98th percentile of their large dataset and may be re-interpreted as suggesting 11 individuals compatible with local origins, 16 more westerly and one at the very limit of westerly values from Great Britain.

At the early fifth- to early seventh-century cemetery at Berinsfield, Oxfordshire (Site 5), 19 individuals were analysed for strontium and oxygen isotopes, together with the local strontium isotope variation of soils with about 8 km of the cemetery and Roman faunal remains from the site.[42] The study aimed to investigate whether there were continental migrants within the earliest phases of the cemetery's use. A relatively wide variation in local environmental $^{87}$Sr/$^{86}$Sr was found, with the human values mostly clustered between those of soils on the agriculturally productive first and second gravel terraces of the Thames that lie within 2 km of the site. Oxygen isotope results were also tightly clustered. Of four outliers identified, two with lower and one with higher $^{87}$Sr/$^{86}$Sr, were interpreted as migrants to the area who could have come from Britain, and one with low $\delta^{18}$O was suggested as a migrant from the continent. However, comparison of the data with the ranges derived from the study by Evans, Chenery, and Montgomery (2012)[43] suggests that all individuals, including the four possible migrants, fall within the range for Britain.

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[41] Evans, Chenery, and Montgomery, 'A Summary of Strontium'.

[42] S. S. Hughes *et al.*, 'Anglo-Saxon Migration Investigated by Isotopic Analysis of Burials from Berinsfield, Oxfordshire, UK', *Journal of Archaeological Science*, 42 (2014), 81–92.

[43] Evans, Chenery, and Montgomery, 'A Summary of Strontium'.

Empingham II in Rutland (Site 6) is another late fifth- to early seventh-century cemetery, where strontium isotope analysis of 11 adult humans was interpreted using analyses of fauna from the site and the nearby tenth- to twelfth-century site at Ketton.[44] The results from human remains showed very little variation and were interpreted as indicating a population subsisting on resources from specific local geological formations. No information on sex or grave furnishings was considered.

Nineteen individuals from the early medieval cemetery at Eastbourne, Sussex (Site 7), dating between AD 375 and 600, were analysed for strontium and oxygen isotopes.[45] A group of ten individuals formed a tight cluster compatible with local values, and were interpreted as having been raised in a local settlement. The other individuals had more scattered values but only one fell outside the observed range of UK values and most had values compatible with south-eastern England, though immigration from western Germany, Denmark, or northern France could not be ruled out. The 'local' group was mostly buried in the central and western part of the cemetery and had a greater number of grave furnishings than the 'non-locals'. The one non-UK individual was a possible female, buried in an isolated position in the south-east of the cemetery and lacked grave goods.

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[44] J. A. Evans *et al.*, 'Anglo-Saxon Animal Husbandry Techniques Revealed Though Isotope and Chemical Variations in Cattle Teeth', *Applied Geochemistry*, 22 (2007), 1994–2005.

[45] S. S. Hughes *et al.*, 'Isotopic Analysis of Burials from the Early Anglo-Saxon Cemetery at Eastbourne, Sussex, U.K', *Journal of Archaeological Science: Reports*, 19 (2018), 513–25.

One fifth- or sixth-century individual (CAR-25) from the sequence at Carlisle Cathedral (Site 8) showed no evidence for migration using strontium and oxygen isotopes.[46]

A small, high-status seventh-century cemetery at Westfield Farm, Ely, Cambridgeshire (Site 9) yielded 15 graves of which 13 were analysed for oxygen isotopes in enamel carbonate.[47] Interpreting these data 'cautiously' by allowing a 2 ‰ local range, only three individuals fell into it, two just above it, six just below and two were very high. Lucy *et al.*[48] note that this can be interpreted as showing a majority of non-locals with at least four from outside Britain and two from a warmer area such as north Africa. Alternatively, they posit that such scattered data might be flawed due to diagenesis, and therefore no conclusions should be made.

A late seventh- to late eighth-century cemetery at Adwick-le-Street, South Yorkshire (Site 10), was unexceptional in its demographic profile, but strontium and oxygen isotope analysis identified probable migrants among the population.[49] Seven of the 37 skeletons were selected for isotopic analysis to cover the spatial extent of the two grave-rows. Despite the small sample, two had high strontium isotope ratios indicative of an origin outside England, possibly north-eastern Scotland or the Norwegian coast, a further two were inferred to have moved at least within England; three others showed no evidence for migration.

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[46] M. McCarthy *et al.*, 'A Post-Roman Sequence at Carlisle Cathedral', *Archaeological Journal*, 171 (2014), 185–257.

[47] Lucy *et al.*, 'The Burial of a Princess?'.

[48] Lucy *et al.*, 'The Burial of a Princess?'.

[49] J. I. McKinley *et al.*, 'A Conversion-Period Cemetery at Woodlands, Adwick-Le-Street, South Yorkshire', *Yorkshire Archaeological Journal*, 88 (2016), 77–120.

Of 18 burials excavated from a seventh-century cemetery at Bradford Peverell, Dorset (Site 11), strontium isotope analysis was undertaken on six individuals.[50] Three were very similar to the local soil, but three had moved from elsewhere, including a child aged 6–12, although the distance moved need not be great as all the ratios are predicted to be found within Dorset.

Two male skeletons from a partially excavated mass grave at Heronbridge, Chester, Cheshire (Site 12), were dated by radiocarbon to AD 530 to 660 and had fatal weapon injuries. Based on this evidence they were identified as casualties from the Battle of Chester (AD 616) between the Welsh and Northumbrian kings.[51] Strontium and oxygen isotope analysis was undertaken to establish which army they might have come from, and identified both as incompatible with a local or Welsh origin. It was argued that they had been Northumbrian soldiers, but with the suggestion that they were recruited from the margins of the kingdom or even from neighbouring kingdoms subject to Northumbrian overlordship.[52]

In summary, for the Early Anglo-Saxon period, the series of studies on migration period cemeteries (Ringlemere, Wasperton, West Heslerton, Berinsfield, Empingham, and

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[50] A.M. Doornbos, ‘Investigating Anglo-Saxon Population Movement Using Strontium Stable Isotope Analysis: Sampling Tooth Enamel from Individuals Found at Frome View, Bradford Peverell’, M.Sc. thesis (Bournemouth, 2010).

[51] M. Holst, *Osteological Analysis Heronbridge, Chester, Cheshire* (York, York Osteoarchaeology, 2004); D. Mason, ‘Ad 616: The Battle of Chester’, *Current Archaeology*, 202 (2006), 517–24.

[52] A. R. Millard, *Isotopic Investigation of the Origin of Battle Victims from Heronbridge* (Durham, Durham University Department of Archaeology, 2006).

Eastbourne), show wide variation in the proportion of migrants inferred from among those sampled. There is no consistent evidence from these data for a large proportion of migrants, even when only the earliest graves are considered. This should be unsurprising. Many of the expected source areas for migration across the North Sea are isotopically similar to places in England[53] and thus, however many immigrants there might have been, only a small proportion are likely to be detectable through analysis of isotopes. Collectively these studies tend towards analysis of skeletons with dateable graves, usually those with grave goods rather than those without, and therefore a bias towards higher-status individuals. There is some evidence for gender differences with females showing more frequent evidence of mobility, and this may well be a reflection of a patrilocal marriage system. The data from these cemeteries (Figures 2.3 and 2.4) show a low level of isotopic variation compared with later periods (Figures 2.4, 2.6, 2.7, 2.8), paradoxically suggesting the so-called Migration Period had lower levels of mobility and migration, or movement from different places, than other periods of England's past.

### *Middle-Saxon to Norman (c. 700–1100)*

This period saw two documented invasions of England—Viking and Norman. Many studies of Middle to Late Anglo-Saxon and Norman burials have been small, and focused on site-specific questions, with no studies specifically looking for Norman invaders (Figure 2.6). In contrast there have been several studies targeted on 'viking' burials,[54] which exemplify the

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[53] Brettell *et al.*, '"Impious Easterners"'.

[54] Cf. in this volume Hadley, chapter 7.

general tendency to apply isotope analysis where migrants are expected, and numerous migrants have been identified (Figure 2.7).

A major study examined 78 burials from the seventh- to ninth-century cemetery associated with the royal residence at Bamburgh, Northumberland (Site 13).[55] Strontium and oxygen isotope analyses were interpreted as showing over 50% of the population to be non-local. The high-status of the site created a prior expectation of immigrants, and the known practice of fostering noble children with the rulers of other polities also suggested the potential for non-local childhoods. The range of origins inferred was much wider than expected, including men, women, and children who had previously lived in Scandinavia and the Mediterranean. The overseas migrants showed some evidence of greater stature and fewer diseases when compared to those with local or UK isotope values, but no differences in burial practice.

Five individuals from a cemetery in use in the seventh and eighth centuries at Bicester, Oxfordshire (Site 14) were subject to oxygen and carbon isotope analysis.[56] Four were compatible with origins in southern England, while one had $\delta^{18}O$ too low for Britain with a different $\delta^{13}C$ value, and was inferred to be a continental immigrant.

Part of a cemetery in use between the ninth and thirteenth centuries was excavated at St Mary's Church, Kempsey, Worcestershire (Site 19), the site of a minster church and a later

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[55] S. E. Groves *et al.*, 'Mobility Histories of 7th–9th Century AD People Buried at Early Medieval Bamburgh, Northumberland, England', *American Journal of Physical Anthropology*, 151 (2013), 462–76.

[56] J. Lewis *et al.*, 'A Middle Anglo-Saxon Cemetery and Medieval Occupation at the Church of the Immaculate Conception, Bicester', *Oxoniensia*, 79 (2014), 147–72.

bishop's palace.[57] Oxygen isotope analysis was done on 23 teeth from 12 individuals, second premolars and third molars, to investigate mobility within lifetime as well as origins. At least six individuals had moved into the area between the formation times of the two teeth, and three, possibly five, had spent their childhoods in a warmer or more westerly location.

A church cemetery at Castle Cement Quarry, Ketton, Rutland (Site 20) was dated to the ninth to eleventh centuries by radiocarbon analysis, and Stamford-ware pottery dated an associated settlement to the tenth, eleventh, and twelfth centuries.[58] Of the 72 burials excavated, 25 were analysed for strontium isotopes. Sheep/goat, cattle, and pig teeth were also analysed, and a subsequent analysis along the growth axis of a cow tooth demonstrated that it probably lived locally all its life.[59] The seven juveniles analysed had a narrow range of strontium isotope ratios close to the mean value from the animals, suggesting that they originated from the settlement. The adults had a wider range of ratios but, apart from one male, were still tightly clustered on values expected for the local Jurassic lithology, with a similar range to the animals. Oxygen isotope measurements on the same samples have been

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[57] T. Vaughan *et al.*, *Archaeological Investigations on the Kempsey Flood Alleviation Scheme*, Worcestershire Archaeology Research Report, 7 (Worcester, Worcestershire Archaeology, 2017).

[58] J. A. Evans and S. Tatham, 'Defining "Local Signature" in Terms of Sr Isotope Composition Using a Tenth- to Twelfth-Century Anglo-Saxon Population Living on a Jurassic Clay-Carbonate Terrain, Rutland, UK', *Geological Society, London, Special Publications*, 232 (2004), 237–48.

[59] Evans *et al.*, 'Anglo-Saxon Animal Husbandry'.

reported without interpretation.[60] All but one of the values fall within the range identified for eastern areas of Britain, thus identifying another migrant.

Excavation of a cemetery typical of the eighth, ninth, and tenth centuries at Masham, North Yorkshire (Site 21), uncovered 58 graves from which 23 individuals were analysed for $\delta^{18}O$ and eight for strontium isotopes.[61] The $\delta^{18}O$ values had a range of 1.8 ‰ which is compatible with a single, local population. Strontium isotope analysis targeted eight individuals representing the extreme $\delta^{18}O$ values in order to test this idea. Three of those tested had high $^{86}Sr/^{87}Sr$, suggesting an origin outside England and, given their $\delta^{18}O$ values, most likely in southwest Norway. Another was not local but could have originated in any area with marine carbonate rocks.

In summary, seventh- to twelfth-century cemeteries (Figures 2.4 and 2.6) presumed to be associated with rural communities (Adwick-le-Street, Bradford Peverell, Bicester, Masham, Riccall, and Ketton) all show evidence for a few probable migrants, and some of those had come from beyond England. In contrast, higher-status cemeteries (Ely, Bamburgh, Kempsey) and military graves (Heronbridge) have produced larger numbers of migrants, including people with possible Mediterranean origins. If these findings came from half a millennium later, they would be unsurprising given the historical record of rural movement and aliens resident in England.[62] Perhaps Dyer's view of later medieval England that the

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[60] Evans, Chenery, and Montgomery, 'A Summary of Strontium'.

[61] J. Buckberry *et al.*, 'Finding Vikings in the Danelaw', *Oxford Journal of Archaeology*, 33 (2014), 413–34.

[62] See in this volume Dyer, chapter 9, pp. XXX–XXX; McClure, chapter 5, pp. XXX–XXX; Lambert and Ormrod, chapter 11, pp. XXX–XXX.

‘conventional view of the isolated and self-sufficient village [has been] shown to be a myth’ can be projected further back to early medieval England.[63]

### *Viking sites*

At Repton, Derbyshire (Site 15), an initial study using strontium and oxygen isotopes examined eight individuals thought to be from a seventh-century monastic cemetery and the Great Army of 873–4.[64] Recent reconsideration and redating of the charnel deposit has shown that it is likely these individuals also died in 873–4.[65] A further four individuals from the early tenth-century Cemetery 3M, considered to be possibly of Scandinavian origin based on grave styles and grave goods, have been analysed for strontium isotopes,[66] and more extensive study is in progress. The initial study argued that all three Viking-style burials, including a double burial, were clearly of non-local origin, two males from a charnel deposit were consistent with local origins, two females were non-local, and a child was also non-local.[67] However, reconsideration of the results in the light of re-measurement of the oxygen isotopes,[68] and improved understanding of isotopic variation, means that the re-evaluation of

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[63] See in this volume McClure, chapter 5, pp. XXX–XXX.

[64] Budd *et al*., ‘Investigating Population Movement’.

[65] C. L. Jarman *et al*., ‘The Viking Great Army in England: New Dates from the Repton Charnel’, *Antiquity*, 92 (2018), 183–99.

[66] C. L. Jarman, ‘Identities at Home and Abroad: An Isotopic Study of Viking Age Norway and the British Isles., M.A. thesis (Oslo, 2012).

[67] Budd *et al*., ‘Investigating Population Movement’.

[68] Evans, Chenery, and Montgomery, ‘A Summary of Strontium’.

the double burial by Montgomery *et al*. can be applied to all the individuals: ‘neither their strontium nor oxygen isotopes can place them securely beyond the shores of north-eastern England’,[69] including the Pennines and Peak District.

Skeletons found at Riccall Landing, North Yorkshire (Site 16),[70] had been interpreted as members of Harald Hardrada’s army killed in 1066, but subsequent skeletal analysis and radiocarbon dating showed a group of men, women, and children whose deaths spanned the eighth to twelfth centuries. Two groups of skeletons investigated using different methods for oxygen isotope analysis provided distinct results, but re-measurement of the first batch[71] yielded revised values consistent with the second batch. Consequently all 12 individuals should be considered to have strontium and oxygen isotope ratios consistent with local origins in the Vale of York.

Although there was evidence for Viking Age activity at Carlisle Cathedral (Site 8), only one of the dated and analysed skeletons proved to be from the late eighth to early ninth century, but strontium and oxygen isotopes showed no evidence that this individual had moved from a distance.[72]

Thirty-one individuals were sampled from a mass burial of at least 51 decapitated individuals from Ridgway Hill, Weymouth, Dorset (Site 17), dated to the late tenth or early

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[69] J. Montgomery *et al*., ‘Finding Vikings with Isotope Analysis – the View from Wet and Windy Islands’, *Journal of the North Atlantic*, Special Volume 7 (2014), 54–70.

[70] R. Hall *et al*., ‘The Medieval Cemetery at Riccall Landing: A Reappraisal’, *Yorkshire Archaeological Journal*, 80 (2008), 55–92.

[71] Evans, Chenery, and Montgomery, ‘A Summary of Strontium’.

[72] McCarthy *et al*., ‘A Post-Roman Sequence’.

eleventh century.[73] A further six individuals had dental modifications typical of southern Scandinavia at this time, but were not sampled. The group had diverse origins but a core group of 20 men had very similar strontium, oxygen, and lead isotope ratios and therefore possibly a common origin. The combined isotope data[74] showed that this group could not have originated in Scandinavia but more likely from somewhere in the area from modern-day Poland to Bulgaria. A further three men could have originated in many areas of north-west Europe including Britain, Ireland, or Denmark. Three men came from more northerly or easterly areas such as Arctic Scandinavia or eastern Russia, one of them possibly from Iceland. The remaining five men had origins which are hard to identify but exclude Denmark and areas of the Baltic Shield. Despite the historical association of Viking raiders with Denmark and Norway, it seems that this group mostly originated elsewhere in the Viking diaspora.

A mass burial found at St John's College, Oxford (Site 18)[75] may be a tenth-century military group, based on radiocarbon dating and skeletal analysis. Oxygen isotopes from 13 individuals and strontium isotopes from six of them, in combination with carbon and nitrogen

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[73] C. A. Chenery *et al*., 'A Boat Load of Vikings?', *Journal of the North Atlantic*, 7 (2014), 43–53; J. A. Evans *et al*., 'Lead Isotope Analysis of Tooth Enamel from a Viking Age Mass Grave in Southern Britain and the Constraints It Places on the Origin of the Individuals', *Archaeometry*, 60 (2018), 859–69.

[74] Evans *et al*., 'Lead Isotope Analysis'.

[75] A. M. Pollard *et al*., '"Sprouting Like Cockle Amongst the Wheat": The St Brice's Day Massacre and the Isotopic Analysis of Human Bones from St John's College, Oxford', *Oxford Journal of Archaeology*, 31 (2012), 83–102.

isotopes, suggest that these were not local men, although some could have originated in Britain. This, along with comparison with the data from Weymouth, led to a preferred identification as an executed Viking raiding party.

A lone burial of a woman with typically Scandinavian artefacts of the end of the ninth century was discovered at Adwick-le-Street, South Yorkshire (Site 10).[76] Strontium and oxygen isotope measurements led to a suggestion of Norwegian origins. However, the oxygen isotopes were measured with laser fluorination and have not been re-measured. Comparing the strontium isotopes to more recent compilations of data a more local origin cannot be excluded.[77]

Two isolated burials of the ninth century and one of the late ninth to early eleventh centuries were excavated at Coppergate, York (Site 22), and analysed for oxygen and strontium isotopes.[78] All were found not to have originated in York but two could have come from elsewhere in Yorkshire. The third had high $^{86}Sr/^{87}Sr$, and, given their $\delta^{18}O$ values, might have come from southwest Norway.

In summary, isotopic analysis of Viking burials (Repton, Ridgway Hill, St John's College, and Adwick-le-Street), identifiable by artefacts, or date and military demographic profile, do not yield much information about the settled communities of medieval England, but rather the origins of these warbands and armies. The isotopic evidence (Figure 2.7) seems

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[76] G. Speed and P. Walton Rogers, 'A Burial of a Viking Woman at Adwick-Le-Street, South Yorkshire', *Medieval Archaeology*, 48 (2004), 51–90.

[77] Evans *et al.*, 'Spatial Variations in Biosphere'; Evans, Chenery, and Montgomery, 'A Summary of Strontium'.

[78] Buckberry *et al.*, 'Finding Vikings'.

to point to a wider range of origins than the areas of Denmark and Norway that are implied by the historical record.

*Later medieval (c. 1100–1540)*

Only a few later medieval cemeteries have been investigated, generally with small or very small sample sizes (Figure 2.8). Local parish cemeteries remained in use after the medieval millennium and are rarely excavated, but most monastic cemeteries closed at the dissolution of the monasteries and are more likely to have been disturbed by redevelopment.

A pilgrim buried at Winchester in the late eleventh or early twelfth century (Site 23), who had evidence of leprosy, was shown by strontium and oxygen isotope analyses not to be local but, most parsimoniously, as coming from southeastern or central England although not from areas of chalk geology.[79]

Seven teeth from a deposit of burnt, broken, and disarticulated human bones from a pit at Wharram Percy, North Yorkshire (Site 24), dated to anywhere between the eleventh and early thirteenth centuries were analysed for strontium isotopes[80] and compared to nine samples from the village churchyard. In the entire sample only one individual was found to lie outside the likely local range, but need not have migrated more than 30 km.

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[79] S. Roffey *et al.*, ‘Investigation of a Medieval Pilgrim Burial Excavated from the Leprosarium of St Mary Magdalen Winchester, UK’, *PLOS Neglected Tropical Diseases*, 11 (2017), e0005186.

[80] S. Mays *et al.*, ‘A Multidisciplinary Study of a Burnt and Mutilated Assemblage of Human Remains from a Deserted Mediaeval Village in England’, *Journal of Archaeological Science: Reports*, 16 (2017), 441–55.

Three individuals from the twelfth- to sixteenth-century cemetery at Blackfriars, Gloucester (Site 25), were inferred to all have different origins based on strontium and oxygen isotope analyses, with two coming from west of the city and one from the north or east.[81] Three further individuals have been analysed along with re-measurement of the $\delta^{18}O$.[82] The range of the four $\delta^{18}O$ measurements is quite narrow, but the strontium isotope ratios are varied, suggesting multiple origins.

The Black Death cemetery at the Royal Mint (East Smithfield), London (Site 26) was used 1348–1350 as an emergency burial ground for the City of London. Thirty individuals were analysed for strontium and oxygen isotopes.[83] Medieval cities, and London especially, sourced foods from large distances, so assessment of the 'local' $^{86}Sr/^{87}Sr$ range was complex.[84] Eight were considered to be outside the local range of values for London, including both males and females, and all under the age of 45. Some of these individuals had isotope ratios compatible with origins in southern England; the nearest possible origins of five other individuals were thought to be Wales, western England, or Yorkshire.

A further ten Black Death victims from Charterhouse Square, London (Site 27), were analysed for strontium and oxygen isotopes, and four were found to be migrants to the city.

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[81] Budd *et al.*, 'Investigating Population Movement'.

[82] Evans, Chenery, and Montgomery, 'A Summary of Strontium'.

[83] E. J. Kendall *et al.*, 'Mobility, Mortality, and the Middle Ages: Identification of Migrant Individuals in a 14th Century Black Death Cemetery Population', *American Journal of Physical Anthropology*, 150 (2013), 210–22.

[84] See in this volume Rees Jones, chapter 10, pp. XXX–XXX and Dyer, chapter 9, pp. XXX–XXX.

Conservatively assuming they came from Britain, there were three from southern or eastern England, and one from northern England or Scotland.[85]

The skeleton known as St Bees Lady, from St Bees, Cumbria (Site 28), was subject to a detailed analysis,[86] which concluded that this high-status fourteenth-century woman should be identified as Maud de Lucy (d. 1398), including evidence from strontium isotopes that her origins could have been local.

Twelve individuals from the fourteenth- to early sixteenth-century cemetery of the Augustinian Priory excavated at Hull Magistrates Court (Site 29) were analysed for strontium and oxygen isotopes[87] to compare the mobility of those with trepenomal disease (probably venereal syphilis) to those without. Four individuals were inferred to be migrants, probably from the Baltic area, with which Hull traded extensively. They were equally balanced between males and females and those with and without evidence for infection. The $\delta^{18}O$ values of most of the individuals from Hull are low compared to other sites in the region (West Heslerton, Riccall, and Coppergate), and comparable to the lower part of the range

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[85] S. Pfizenmaier, *Charterhouse Square: Black Death Cemetery and Carthusian Monastery, Meat Market and Suburb*, Crossrail Archaeology, 7 (London, Museum of London Archaeology, 2016); S. Pfizenmaier and D. Walker, 'A Black Death Cemetery at Charterhouse Square, London EC1', *Medieval Archaeology*, 58 (2014), 364–70.

[86] C. J. Knüsel *et al*., 'The Identity of the St Bees Lady, Cumbria: An Osteobiographical Approach', *Medieval Archaeology*, 54 (2010), 271–311.

[87] C. A. Roberts *et al*., 'Isotopic Tracing of the Impact of Mobility on Infectious Disease: The Origin of People with Treponematosis Buried in Hull, England, in the Late Medieval Period', *American Journal of Physical Anthropology*, 150 (2013), 273–85.

shown by Viking Age sites. Although Hull is known to have attracted immigrants from the Baltic, there seems to be a very high proportion of non-locals from among the remains sampled, and perhaps alternative explanations should be sought, such as a systematic measurement error.

The most famous individual studied using isotopes is probably King Richard III (r. 1483–5),[88] whose burial was excavated in Leicester (Site 30). The strontium and oxygen isotope compositions of his tooth enamel were concluded to be compatible with western parts of England, including Ludlow where he resided for part of his childhood. A series of oxygen isotope measurements on dentine and a femur reflected his known childhood movements from eastern to western England and back. A high $\delta^{18}$O value from a rib was speculatively interpreted as reflecting increased wine consumption after he became king.

Investigation of late thirteenth- to early fourteenth-century individuals from the large cemetery at St Mary Spital, London (Site 31), compared two who were outliers in $\delta^{13}$C and $\delta^{15}$N measurements with eight who had diets more typical for that site.[89] Two individuals were interpreted as having high, non-local strontium isotope ratios, including one young adult female who was an outlier in the dietary isotopes; another with typical dietary isotopes was considered possibly an outlier in $\delta^{18}$O.

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[88] A. L. Lamb *et al.*, ‘Multi-Isotope Analysis Demonstrates Significant Lifestyle Changes in King Richard III’, *Journal of Archaeological Science*, 50 (2014), 559–65.

[89] K. E. Lakin, ‘Diet in Medieval London: Stable Isotope Analysis of Human and Faunal Remains’, Ph.D. thesis (Reading, 2010).

Two individuals from Carlisle Cathedral (Site 8) were radiocarbon dated to 1450–1640. They showed no evidence for migration based on strontium and oxygen isotopes.[90]

In summary, most of the later medieval sites (Wharram Percy, East Smithfield, St Mary Spital, Charterhouse Square [not plotted], Blackfriars Gloucester, and several individuals) fall in the same region (Figure 2.8) as the earliest medieval sites (Figure 2.3), with the exception of two individuals from Blackfriars who had high $^{86}$Sr/$^{87}$Sr values. Although the overall range is limited, many individuals show evidence for migration within England, as well as a few from overseas.

### Conclusions of isotope analysis

This survey of isotopic research on medieval migration in England shows that, although strontium isotopes have been in use in archaeology for about three decades, and oxygen isotopes for two, substantial revision of previously published results is necessary in the light of improved knowledge about geographical variation of strontium isotopes and about sources of variation in oxygen isotopes in humans. Most studies have used an ad hoc interpretative approach which leads to inconsistencies between studies, and thus there is a need for the development of a more formalised, perhaps quantitative, analysis of origins.

The sites considered lie in regions with a restricted range of $\delta^{18}$O of precipitation (Figure 2.2), only -6 to -9 ‰. However, the estimated drinking water values for the bulk of samples in all periods are somewhat higher than would be predicted when locations (Figure 2.2) are compared to predictions (Figures 2.3, 2.4, 2.6, 2.7, 2.8), just as previously noted for

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[90] McCarthy *et al.*, ‘A Post-Roman Sequence’.

several Early Anglo-Saxon sites.[91] This may well be due to cultural practices like brewing and boiling or some systematic offset in the drinking water predictions.[92]

The Beaker People isotope project[93] shows what can be done with a systematic survey focused on a single period. It analysed 264 samples from a 1000-year period with a wide geographical spread across Britain. The results demonstrated movement within and between communities where it was not anticipated, and showed the value of looking at a wide cross-section of individuals from the population of a cemetery, rather than focusing on burials with unusual features that encourage speculation about distant origins. With a similar approach, we could learn much about the movement of medieval people buried in unexceptional graves. This could also move the scale of isotopic evidence towards being comparable to later medieval historical evidence based on surnames, and legal and taxation records.[94] The studies to date of Black Death cemeteries in London have come closest to this, and an ongoing project on the Kingdom of Northumbria AD 300–800[95] may achieve similar aims for that region and time period.

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[91] Brettell *et al.*, '"Impious Easterners"'.

[92] Brettell, Montgomery, and Evans, 'Brewing and Stewing'; Brettell *et al.*, '"Impious Easterners"'.

[93] M. Parker Pearson *et al.*, 'Beaker People in Britain: Migration, Mobility and Diet', *Antiquity*, 90 (2016), 620–37.

[94] See in this volume Dyer, chapter 9', pp. XXX–XXX; McClure, chapter 5, pp. XXX–XXX; Lambert and Ormrod, chapter 11, pp. XXX–XXX.

[95] S. Semple *et al.*, 'People and Place: The Making of the Kingdom of Northumbria Ad 300–800', *Medieval Archaeology Newsletter*, 54 (2015), 1–2.

## Genetic Evidence

Our complement of DNA, the human genome, is about 3,200 million base-pairs in size, and we each carry two distinct copies, one inherited from our mother, and one from our father. All copies of the genome are different in sequence but vary only by about 0.1% on average,[96] reflecting the relative youth of *Homo sapiens* as a species, and the short time that has been available for the accumulation of diversity through mutation. This small difference nonetheless implies that any one genome will carry a few million base-pairs that distinguish it from the reference sequence, a composite and publicly available genome sequence with which any other human genome can be compared.

Sequence differences between genomes are non-randomly distributed within and among human 'populations'—a term used by geneticists to mean sets of individuals defined by some shared property that may be social, cultural, or geographical. This non-random distribution is referred to as population structure. Because of this, DNA analysis can identify genomes that differ markedly from a local sample, signalling migrants whose ancestry traces elsewhere. The general finding in indigenous samples is that geographical proximity via plausible past migration routes correlates with genetic similarity.[97] This relationship between genetic and geographical distance also implies that migrants from further afield will generally

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[96] 1000 Genomes Project Consortium, 'An Integrated Map of Genetic Variation from 1,092 Human Genomes', *Nature*, 491 (2012), 56–65.

[97] S. Ramachandran *et al.*, 'Support from the Relationship of Genetic and Geographic Distance in Human Populations for a Serial Founder Effect Originating in Africa', *Proceedings of the National Academy of Sciences of the USA*, 102 (2005), 15942–7.

be easier to detect than those from close by. The genetic legacy of a group of migrants to southern England would stand out more clearly if they were from Africa rather than from the Low Countries, for example.

In principle, the analysis of population structure and its interpretation in terms of past migration or the admixture of populations can be applied both to people currently living, and to people long dead, provided DNA of a suitable quality for analysis can be isolated from their remains. In practice, genetic analysis of ancient samples has until recently been difficult or impossible due to technical limitations associated with old and damaged DNA,[98] and therefore many studies have focused on modern samples. The units of enquiry for such studies are groups, rather than individuals, partly because large samples are easy to obtain, and partly because the work can thus rest on the well-established theoretical framework of population genetics. This framework considers the frequencies of genetic types (alleles) within populations, and how these frequencies change through time under the influence of factors such as mutation, natural selection, non-random breeding, migration, and changes in population size.[99] In order to infer the features of events that happened many generations ago from the patterns of diversity in modern genomes, computer-modelling approaches are also needed that account for parameters such as historical population sizes, generation times, reproductive success, and past migration rates. An estimate of the time at which a past migration occurred typically comes with wide confidence interval limits, and this lack of precision can appear unimpressive to the archaeologist of the recent, historic past accustomed to the luxury of radiocarbon dating, or to the historian working with dateable texts.

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[98] M. Hofreiter *et al.*, ‘Ancient DNA’, *Nature Reviews Genetics*, 2 (2001), 353–9.

[99] Schraiber and Akey, ‘Methods and Models’.

Advances in DNA sequencing technologies (‘next-generation sequencing’, or NGS) over the past decade, and associated reduction in costs, now permit the unbiased analysis of genetic variation in modern samples.[100] However, the most profound influence of these new technologies has been in allowing more reliable and larger-scale analysis of genetic variation in ancient samples.[101] NGS methods are well suited to recovering information from short fragments of DNA that are found naturally in ancient specimens. They also allow damaged, and therefore ancient, DNA molecules to be distinguished from undamaged modern DNA molecules, and thus alleviate the problem of modern DNA contamination that has bedevilled the field since its inception. Sample sizes are likely to remain relatively small, and to derive from a biased set of contexts in which suitable skeletal material survives, but nonetheless the study of aDNA is likely to contribute the greatest insights into migration in the medieval period over the next few years.

In introducing the idea of genetic variation, one further point is worth considering: do the genetic variants make any material difference to the individuals who carry them? The vast majority of variants are ‘neutral’—they have no discernible effect on appearance, disease, or fitness—and most studies of past migration and population admixture focus on these. However, a few variants in the genotype do have consequences for the phenotype; these

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[100] 1000 Genomes Project Consortium *et al*., ‘A Global Reference for Human Genetic Variation’, *Nature*, 526 (2015), 68–74.

[101] L. Orlando, M. T. Gilbert, and E. Willerslev, ‘Reconstructing Ancient Genomes and Epigenomes’, *Nature Reviews Genetics*, 16 (2015), 395–408.

include features such as the pigmentation of eyes, hair, and skin, and aDNA studies of both prehistoric[102] and medieval[103] individuals have asked questions about these.

## The 'People of the British Isles' study: inferences from analysis of modern autosomal DNA

The most comprehensive study to use modern DNA diversity to make inferences about the medieval period is the 'People of the British Isles' (PoBI) project, whose aim was to provide a 'control' dataset of genetic variation to support medical genetic research, and also to illuminate the past.[104] The sampling strategy required each participant to have all four grandparents born within 60 km of each other in a rural area, in the hope of capturing past population structure efficiently. Despite the 'BI' in its moniker, the project's geographical

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[102] M. E. Allentoft *et al.*, 'Population Genomics of Bronze Age Eurasia', *Nature*, 522 (2015), 167–72; A. Keller *et al.*, 'New Insights into the Tyrolean Iceman's Origin and Phenotype as Inferred by Whole-Genome Sequencing', *Nature Communications*, 3 (2012), 698; I. Olalde *et al.*, 'Derived Immune and Ancestral Pigmentation Alleles in a 7,000-Year-Old Mesolithic European', *Nature*, 507 (2014), 225–8.

[103] T. E. King *et al.*, 'Identification of the Remains of King Richard III', *Nature Communications*, 5 (2014), 5631; R. Martiniano *et al.*, 'Genomic Signals of Migration and Continuity in Britain before the Anglo-Saxons', *Nature Communications*, 7 (2016), 10326.

[104] B. Winney *et al.*, 'People of the British Isles: Preliminary Analysis of Genotypes and Surnames in a UK-Control Population', *European Journal of Human Genetics*, 20 (2012), 203–10.

scope was the United Kingdom, with no samples collected for the Republic of Ireland (a similar, Ireland-centric project has since been undertaken).[105]

The genetic toolkit employed by the PoBI project was a set of about 500,000 common single-nucleotide polymorphisms (SNPs); the large number and genome-wide distribution of these SNPs means that they provide a relatively unbiased 'average' picture of variation descending from many independent ancestors. So far, data published from the PoBI analysis focus on the 'autosomal' genome—the 98% of our DNA that is inherited equally from both parents. Each of 2039 individuals was genotyped for this set of SNPs, and computational methods were applied to detect population structure. Conventional approaches based only on the frequencies of SNP alleles (such as the programs STRUCTURE[106] or ADMIXTURE[107]) are useful in clustering geographically coherent groups at the continental scale,[108] but at a more local scale such as that of Britain, these produce only limited information. In the PoBI dataset, use of ADMIXTURE differentiated clusters of individuals with Orcadian and Welsh

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[105] R. P. Byrne *et al.*, 'Insular Celtic Population Structure and Genomic Footprints of Migration', *PLoS Genetics*, 14 (2018), e1007152.

[106] J. K. Pritchard, M. Stephens, and P. Donnelly, 'Inference of Population Structure Using Multilocus Genotype Data', *Genetics*, 155 (2000), 945–59.

[107] D. H. Alexander, J. Novembre, and K. Lange, 'Fast Model-Based Estimation of Ancestry in Unrelated Individuals', *Genome Research*, 19 (2009), 1655–64.

[108] N. A. Rosenberg *et al.*, 'Genetic Structure of Human Populations', *Science*, 298 (2002), 2381–5.

ancestry from other samples and from each other, but revealed little further discernible differentiation.[109]

A more refined method, fineSTRUCTURE,[110] was therefore applied, that takes account not of only SNP allele frequencies, but also of how SNPs are associated with each other along chromosomes. The tendency of closely linked SNPs to be inherited together is referred to as linkage disequilibrium, and considering this property allows more subtle patterns of clustering among individual genomes to be teased out. These clusters reflect shared ancestry among groups of individuals. The method can define clusters hierarchically, as shown in the tree within Figure 2.9: the deepest branching points correspond to the separation of Orkney and Wales, as was observed in the less-discriminating ADMIXTURE analysis. Individual genomes were each assigned to one of seventeen genetic clusters without reference to geography, and the geographical distribution of the clusters was then investigated by placing each individual, as a cluster-specific symbol, at the centroid of the places of birth of their grandparents on a map (Figure 2.9). The fact that the symbols cluster together in a largely non-overlapping pattern dramatically illustrates the population structure that the method reveals. Striking examples of local differentiation include the separation of clusters corresponding to Cornwall and Devon, a clear distinction between north and south Wales, and separation of the north of England, Scotland, and Northern Ireland from the rest of England. These clusters were equated by the authors of the study with historical, medieval

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[109] S. Leslie *et al.*, ‘The Fine-Scale Genetic Structure of the British Population’, *Nature*, 519 (2015), 309–14.

[110] D. J. Lawson *et al.*, ‘Inference of Population Structure Using Dense Haplotype Data’, *PLoS Genetics*, 8 (2012), e1002453.

kingdoms including Gwynedd, Dyfed, Elmet, Rheged, and Dumnonia[111]—but this seems to be a case of unsupported back-projection. There is considerable heterogeneity among westerly regions sometimes grouped together as 'Celtic'. Just as striking as these finely differentiated local groups is the dominating presence of a widespread cluster, comprising 51% of the samples in the study, which covers all of central and southern England and extends up the east coast to north Yorkshire (red symbols in Figure 2.9). The homogeneity of this cluster implies considerable freedom of movement within it, and other authors[112] have noted that it corresponds to the traditional lowland zone of Britain (Fox 1943).[113]

The origins of the geographically differentiated clusters were investigated in terms of possible source populations from outside Britain and Ireland. To represent these continental sources, a set of 6209 individuals, collected for a medical genetics study at different European hospitals, was used—these samples lack the grandparentally based geographical precision of the PoBI samples. Analysis using fineSTRUCTURE defined 51 geographically differentiated European groups, whose contributions to the PoBI clusters could then be considered to provide an 'ancestry profile' for each. While some European groups feature as components of many or all of the PoBI clusters, interpreted as relatively ancient contributions, some are prominent in only a limited number of PoBI clusters. These were interpreted as relatively recent contributions, and are more relevant to the medieval millennium being

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[111] Leslie *et al.*, 'The Fine-Scale Genetic Structure'.

[112] J. Kershaw and E. C. Røyrvik, 'The "People of the British Isles" Project and Viking Settlement in England', *Antiquity*, 90 (2016), 1670–80.

[113] C. Fox, *The Personality of Britain: Its Influence on Inhabitant and Invader in Prehistoric and Early Historic Times* (Cardiff, 1943).

considered here. The fact that Norwegian groups comprise about 25% of the ancestry of the largest Orkney cluster was taken as validation of the approach, given Orkney's history as part of the Kingdom of Norway.

Analysis of the major central/southern English cluster in terms of European groups suggested a contribution of about 35% ancestry from a north-west German group that was interpreted as the result of early medieval, Saxon migrations—this same group did not contribute at all to the Welsh clusters. However, by considering the lengths of the genomic segments contributed, which decrease in size with each generation since the original admixture event occurred (and assuming a single pulse of admixture), this contribution was dated to 858 AD (with a 95% confidence interval of 802–914 AD). This is more than two centuries later than the major period of Saxon migration, but this apparent anomaly was explained on the basis that 'a migration event is likely to precede any subsequent population admixture, possibly substantially so, if the migrants mate largely within the migrant group for some time after their migration'.[114] At the same time, the study claimed relatively little input from Danish European groups, and therefore only a minor contribution from Danish Viking migrants. Although the PoBI study acknowledges that it is impossible to separate Saxon and Danish Viking contributions definitively, it nonetheless claims a very minor contribution of the latter, including 'no remnant of the Danelaw', which would presumably have been revealed as a genetic cluster that interrupted the homogeneous central/southern English cluster. This interpretation has been explicitly challenged by other authors,[115] who point out that the north-west German group might equally reflect Danish Viking contributions (the

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[114] Leslie *et al.*, 'The Fine-Scale Genetic Structure'.

[115] Kershaw and E. C. Røyrvik, 'The "People of the British Isles".

relatively late date of contribution fits much better), and also that the Danish European group, identified in modern residents of Copenhagen, might not adequately represent past Danish Viking migrants. The lack of a ‘Danelaw signal’ could be explained by free migration in lowland Britain over the last millennium.

In summary, the PoBI study,[116] although by far the most extensive and sophisticated attempt to use modern DNA diversity to understand the British past, has not settled debates about migrations associated with cultural transitions across the medieval millennium. The appropriateness of external datasets used to model European contributions remains in question, and the problem of distinguishing between geographically and temporally similar sources for ‘Anglo-Saxon’ and ‘Danish Viking’ contributions has not been overcome.

## Inferences from uniparentally inherited DNA in modern populations

As noted above, the PoBI analysis so far published[117] refers to the autosomes—the 98% of the genome inherited from both parents equally. Data from the same samples on uniparentally inherited parts of the genome (the maternally inherited mitochondrial DNA [mtDNA] and paternally inherited Y chromosome) were gathered but have not yet been published. Such analyses could throw light on potential sex-biased aspects of past contributions—this has been particularly revealing about the post-colonial history of the Americas, for example.[118] However, the disadvantage of these kinds of studies is that they

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[116] Leslie *et al.*, ‘The Fine-Scale Genetic Structure’.

[117] Leslie *et al.*, ‘The Fine-Scale Genetic Structure’.

[118] K. Adhikari *et al.*, ‘The Genetic Diversity of the Americas’, *Annual Review of Genomics and Human Genetics*, 18 (2017), 277–96.

focus only on a single (matrilineal or patrilineal) ancestor of any individual, rather than an average of their ancestors, and interpretations are vulnerable to the effects of 'genetic drift'—the chance loss or expansion of particular lineages.

Early work on Y-chromosomal and mtDNA variation in the British and Irish Isles[119] focused on Orkney, Wales, and Ireland, and provided evidence for male, but not female Scandinavian contributions to Orkney; similar conclusions were drawn from another independent study.[120] Subsequent work has focused on Y-specific analysis including that of England: one influential example[121] used samples from seven towns in a transect across England and Wales, from Norfolk to Anglesey (Figure 2.10), noting a sharp transition in Y-chromosome types between England and Wales. Together with a lack of significant differentiation between a Frisian sample (see Figure 2.10, used as a modern proxy for an early medieval 'Anglo-Saxon' source) and the English samples, this was taken as evidence for mass migration into England from the near continent in the post-Roman centuries. This study used population genetic modelling approaches to compare different possible explanations for the findings and to investigate the necessary demographic scales. This indicated that the putative immigration event had affected a remarkably high proportion (50–

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[119] J .F. Wilson *et al.*, 'Genetic Evidence for Different Male and Female Roles During Cultural Transitions in the British Isles', *Proceedings of the National Academy of Sciences of the USA*, 98 (2001), 5078–83.

[120] S. Goodacre *et al.*, 'Genetic Evidence for a Family-Based Scandinavian Settlement of Shetland and Orkney During the Viking Periods', *Heredity*, 95 (2005), 129–35.

[121] M. E. Weale *et al.*, 'Y Chromosome Evidence for Anglo-Saxon Mass Migration', *Molecular Biology and Evolution*, 19 (2002), 1008–21.

100%) of the Central English male gene pool. A subsequent study[122] analysed Y-chromosomal types in Britain and Ireland, and included possible source populations in Norway, Denmark, and northern Germany (the last two were indistinguishable). Although admixture approaches suggested more complex contributions of paternal lineages into England than previously found,[123] the overall level was estimated at 24–72%. Notably, Danish/northern German input was generally highest in regions with historical Danish influence, including York, Southwell, and Norfolk, and, therefore, in contrast to the autosomal PoBI study,[124] it was interpreted as a Viking signal.[125] This shows that historically different explanations can be arrived at from similar data.[126]

Following the earlier study suggesting Y-chromosome evidence for early medieval mass migration,[127] further work[128] attempted to explain the very high proportion of apparent Anglo-Saxon contribution, which, if considered as a single migration event, would involve implausibly large numbers of incomers (>500,000). This posited that indigenous inhabitants

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[122] C. Capelli *et al.*, ‘A Y Chromosome Census of the British Isles’, *Current Biology*, 13 (2003), 979–84.

[123] Weale *et al.*, ‘Y Chromosome Evidence’.

[124] Leslie *et al.*, ‘The Fine-Scale Genetic Structure’.

[125] Capelli *et al.*, ‘A Y Chromosome Census’.

[126] Capelli *et al.*, ‘A Y Chromosome Census’; Weale *et al.*, ‘Y Chromosome Evidence’.

[127] Weale *et al.*, ‘Y Chromosome Evidence’.

[128] M. G. Thomas, M. P. Stumpf, and H. Harke, ‘Evidence for an Apartheid-Like Social Structure in Early Anglo-Saxon England’, *Proceedings of the Royal Society Series B*, 273 (2006), 2651–7.

and their descendants were economically and legally disadvantaged compared to incomers and their descendants—a kind of social 'apartheid', that could have increased the 'Anglo-Saxon' proportion today via increased reproductive success.[129] Computer simulations were used to show that such a scenario could indeed lead to the high levels of 'Anglo-Saxon' patrilineages currently proposed, and the laws of Ine, the late seventh-century West Saxon king, were invoked to suggest that a social distinction was made between Saxons and 'Welsh' (native Britons), according them different legal status.[130] However, the observed frequency of any such Anglo-Saxon ancestry required the 'apartheid advantage' to act over 15 generations (about 400 years) following a plausibly small initial immigration.[131] This study was followed by challenges[132] over whether such a social organisation was necessary to explain the observed data, including the assertion, rejected by the 'apartheid' study's authors,[133] that

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[129] Thomas, Stumpf, and Harke, 'Evidence for an Apartheid-Like Social Structure'.

[130] See in this volume Findell and Shaw, chapter 3, pp. XXX–XXX.

[131] Thomas, Stumpf, and Harke, 'Evidence for an Apartheid-Like Social Structure'.

[132] J. E. Pattison, 'Integration Versus Apartheid in Post-Roman Britain: A Response to Thomas Et Al. (2008)', *Human Biology*, 83 (2011), 715–33; J. E. Pattison, 'Is It Necessary to Assume an Apartheid-Like Social Structure in Early Anglo-Saxon England?', *Proceedings of the Royal Society Series B*, 275 (2008), 2423–9; discussion 19–21.

[133] M. G. Thomas, M. P .H. Stumpf, and H. Härke, 'Integration Versus Apartheid in Post-Roman Britain: A Response to Pattison', *Proceedings of the Royal Society Series B*, 275 (2008), 2419–21.

contact over a much longer and earlier period could have contributed to the ancestry component within Britain ascribed to the Anglo-Saxons.[134]

Criteria for the recruitment of volunteers for DNA analysis can affect the results of studies by reducing the influence of recent incomers. As described above, the PoBI study specified that the birthplaces of all four grandparents of a DNA donor were clustered and rural.[135] Y-chromosome studies tend to focus on the place of birth of just one grandparent, the paternal grandfather, and in some cases[136] target small market towns, in the hope that this will reduce the effects of recent immigration. However, the Y-chromosome's male-specificity suggests an additional means by which potential DNA donors can be screened for recruitment—via their patrilineal surnames, which have been shown to have a general relationship with Y-chromosome types.[137] Restriction of male volunteers to surnames that are known to be 'local' to a place from census or other records might increase a signal that could otherwise have been diluted by recent (i.e. nineteenth- or twentieth-century) immigration. Sampling on the basis of surnames that appear in old lists from a specific area could provide a proxy for an 'older' pre-industrial population than might be gathered purely on the basis of

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[134] Thomas, Stumpf, and Harke, 'Evidence for an Apartheid-Like Social Structure'.

[135] Leslie *et al.*, 'The Fine-Scale Genetic Structure'.

[136] Capelli *et al.*, 'A Y Chromosome Census'; Weale *et al.*, 'Y Chromosome Evidence'.

[137] F. Calafell and M. H. D. Larmuseau, 'The Y Chromosome as the Most Popular Marker in Genetic Genealogy Benefits Interdisciplinary Research', *Human Genetics*, 136 (2017), 559–73; T. E. King and M. A. Jobling, 'What's in a Name? Y Chromosomes, Surnames and the Genetic Genealogy Revolution', *Trends in Genetics*, 25 (2009), 351–60.

grandparental place of birth.[138] In a study of West Lancashire and the Wirral peninsula, comparisons of surname-ascertained samples with samples based only on the grandparental criterion[139] showed significant differences in Y-chromosome composition, which were explained on the basis of a higher Scandinavian contribution to the surname-ascertained samples. In effect, such samples seem enriched in more ancient lineages, and depleted in lineages that arrived into the area more recently via migration from other parts of the islands of Britain and Ireland. West Lancashire and the Wirral were chosen for this study on the basis of their high densities of Norse Viking place-names which, together with written and archaeological evidence, suggested a strong Norse influence. Surnames have also been collected for the PoBI cohort, but their analysis has not been integrated fully into the genome-wide DNA analysis, despite some preliminary published observations.[140] One disincentive associated with the collection and use of surnames is the enhanced possibility of identifying participants, which could compromise the basis of ethical approval granted for the sampling.

Studies such as those discussed above use groups of samples, often labelled by geographical origin, and attempt to draw conclusions about them in terms of ancestral

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[138] F. Manni *et al.*, ‘New Method for Surname Studies of Ancient Patrilineal Population Structures, and Possible Application to Improvement of Y-Chromosome Sampling’, *American Journal of Physical Anthropology*, 126 (2005), 214–28.

[139] G. R. Bowden *et al.*, ‘Excavating Past Population Structures by Surname-Based Sampling: The Genetic Legacy of the Vikings in Northwest England’, *Molecular Biology and Evolution*, 25 (2008), 301–9.

[140] Winney *et al.*, ‘People of the British Isles’.

contributions from groups elsewhere. However, sometimes an individual modern genome is encountered that has unusual qualities that prompt reflection on the ancestry of its carrier. This is a more personalised approach that recalls the perspective taken by members of the public who undertake direct-to-consumer genetic testing,[141] and also resembles the approach taken to some ancient genome studies (discussed below), in which sample sizes are often very small.

Because Y-chromosome types display a high-degree of population differentiation,[142] when an 'exotic' example turns up in Britain that is typical of another continent, it attracts attention. However, like a metal detectorist's find of an exotic artefact in an English field, it usually lacks sufficient context to allow accurate interpretation. For example, a set of 1678 men carrying 40 different British surnames[143] contains two examples of unexpected African Y-chromosomal lineages, belonging to the haplogroups E1a (carried by 10% of sampled men with a specific surname), and A1a (39% of men with a second specific surname). Neither of these haplogroups was observed in any other surnames, nor in a control sample. The second example was further investigated by using genealogical research to connect the A1a-bearing

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[141] M. A. Jobling, R. Rasteiro, and J. H. Wetton, 'In the Blood: The Myth and Reality of Genetic Markers of Identity', *Ethnic and Racial Studies*, 39 (2016), 142–61.

[142] M. A. Jobling and C. Tyler-Smith, 'The Human Y Chromosome: An Evolutionary Marker Comes of Age', *Nature Reviews Genetics*, 4 (2003), 598–612.

[143] T. E. King and M. A. Jobling, 'Founders, Drift and Infidelity: The Relationship between Y Chromosome Diversity and Patrilineal Surnames', *Molecular Biology and Evolution*, 26 (2009), 1093–102.

men;[144] these men fell into two genealogies, tracing back to two ancestors born in the 1780s in the Leeds area, but these ancestors could not otherwise be linked. So, the African lineage was in Yorkshire in the eighteenth century, and associated with a surname itself founded perhaps in the fourteenth century, but there remains much uncertainty about when and how the African Y-chromosome type came to Britain. It could reflect Africans who arrived as a consequence of trade with Africa (including slaves) from the mid-sixteenth century onwards, or as members of the ethnically diverse Roman army many centuries earlier. It is important to remember that this Y-based study focuses on only a single ancestral lineage out of a multitude, and it is likely that the autosomal genomes of men carrying the exotic Y-chromosomes show no evidence at all of an African contribution, due to successive dilution with every generation. Likewise, they show no phenotypic evidence of African ancestry.

Notably, systematic studies of modern British populations using mtDNA have not yet been published; the focus on the Y chromosome reflects the generally greater degree of population differentiation shown by this male-specific part of the genome, thought to result from generally prevalent patrilocal marriage practices.[145]

## Examples of inference from ancient mitochondrial DNA (mtDNA)

Ancient DNA studies of British skeletal remains are not extensive; prior to the application of so-called next-generation sequencing to aDNA, the only published data available were from

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[144] T. E. King *et al.*, ‘Africans in Yorkshire? The Deepest-Rooting Clade of the Y Phylogeny within an English Genealogy’, *European Journal of Human Genetics*, 15 (2007), 288–93.

[145] M. T. Seielstad, E. Minch, and L. L. Cavalli-Sforza, ‘Genetic Evidence for a Higher Female Migration Rate in Humans’, *Nature Genetics*, 20 (1998), 278–80.

standard targeted sequencing approaches applied to mtDNA in ancient samples; mtDNA survives relatively well, since it is present in relatively large numbers of copies within cells. Analysis of a small (207-bp) mtDNA fragment was carried out in 48 samples from five different sites (Leicester, Norton [Cleveland], Dover, Salisbury, and Norwich), spanning the period 300–1000 AD, and these sequences were compared with a large modern database.[146] Interpretation was complicated by small per-site and per-period sample sizes, and also by the generally weak differentiation of mtDNA across western Europe.[147] The late Saxon Norwich sample differed from all earlier sites (including early Saxon and Romano-British samples), and was affiliated to modern southern European populations, while the pooled earlier samples had more northerly affiliations. This result is difficult to understand in terms of commonly held assumptions about migrations to Britain. The same dataset was later compared with modern English and other European samples,[148] demonstrating a reduction of genetic diversity through time. This was discussed in terms of possible natural selection for particular mtDNA lineages, perhaps following the Black Death; in this context it is interesting that

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[146] A. L. Töpf *et al.*, ‘Tracing the Phylogeography of Human Populations in Britain Based on 4th–11th Century mtDNA Genotypes’, *Molecular Biology and Evolution*, 23 (2006), 152–61.

[147] C. Batini *et al.*, ‘Population Resequencing of European Mitochondrial Genomes Highlights Sex-Bias in Bronze Age Demographic Expansions’, *Scientific Reports*, 7 (2017), 12086; M. Richards *et al.*, ‘Tracing European Founder Lineages in the near Eastern mtDNA Pool’, *American Journal of Human Genetics*, 67 (2000), 1251–76.

[148] A. L. Töpf *et al.*, ‘Ancient Human mtDNA Genotypes from England Reveal Lost Variation over the Last Millennium’, *Biological Letters*, 3 (2007), 550–3.

mtDNA haplogroup H, which is common today throughout Europe[149] but scarce among the early archaeological samples from Britain,[150] has been reported to provide some protection against sepsis[151]—though this finding has not been replicated. This led to the speculation that haplogroup H may have undergone positive selection,[152] but, as was acknowledged, it is difficult to exclude the alternative explanation of genetic drift. Showing that ‘exotica’ can be observed among mtDNA sequences, as well as among Y-haplotypes, one of the tenth-century Norwich skeletons carried a rare mtDNA type within haplogroup X[153] that had previously been reported as typical of Romani groups,[154] even though the arrival of the Romani in England was not recorded until the sixteenth century. The fact that the same small dataset gave rise to three different papers[155] is testament to the challenging nature of aDNA work prior to the introduction of NGS.

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[149] Richards *et al.*, ‘Tracing European Founder Lineages’.

[150] Töpf *et al.*, ‘Ancient Human mtDNA Genotypes’.

[151] S. V. Baudouin *et al.*, ‘Mitochondrial DNA and Survival after Sepsis: A Prospective Study’, *Lancet*, 366 (2005), 2118–21.

[152] Töpf *et al.*, ‘Ancient Human mtDNA Genotypes’.

[153] A. L. Töpf and A. R. Hoelzel, ‘A Romani Mitochondrial Haplotype in England 500 Years before Their Recorded Arrival in Britain’, *Biological Letters*, 1 (2005), 280–2.

[154] D. Gresham *et al.*, ‘Origins and Divergence of the Roma (Gypsies)’, *American Journal of Human Genetics*, 69 (2001), 1314–31.

[155] Töpf *et al.*, ‘Tracing the Phylogeography; Töpf *et al.*, ‘Ancient Human mtDNA Genotypes’; Töpf and Hoelzel, ‘A Romani Mitochondrial Haplotype’.

**Inference from genome-wide analysis of ancient DNA**

Two more recent studies have applied current techniques to obtain whole-genome sequence data from skeletal remains in English sites, dating from the Iron Age to the Late Anglo-Saxon period. The sites (Figure 2.11) lie in Cambridgeshire,[156] Yorkshire, and County Durham.[157]

The study by Schiffels and colleagues[158] generated genome sequences from the remains of ten individuals from three sites close to Cambridge (Hinxton, Oakington, and Linton). Hinxton is the rural home of the hi-tech Wellcome Genome Campus, workplace of the lead authors of this paper—one wonders if these bones would have yielded up their sequences at all, if one of the world's largest genome-sequencing centres had not, by chance, been built right next-door more than a millennium later. Radiocarbon dating showed that three individuals in the study were from the late Iron Age (Linton, plus two of the Hinxton individuals: ~100 BC), four from the Early Anglo-Saxon period (Oakington: fifth/sixth century), and three from the Middle Anglo-Saxon period (Hinxton: seventh/eighth century). Mitochondrial DNA and Y-chromosomal haplogroups among the ten individuals were all common within modern Western Europe, and therefore uninformative about ancestry.

The ancient genomes were compared with modern genomes from western Europe using a summary method, principal components analysis (Figure 2.12): they fell within the range of modern variation, though the Iron Age samples were more similar to the English and French, while most of the early medieval samples were more similar to the Scottish and

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[156] S. Schiffels *et al.*, 'Iron Age and Anglo-Saxon Genomes from East England Reveal British Migration History', *Nature Communications*, 7 (2016), 10408.

[157] Martiniano *et al.*, 'Genomic Signals of Migration'.

[158] Schiffels *et al.*, 'Iron Age and Anglo-Saxon Genomes'.

Norwegian modern genomes. Now, the authors exploited a key property of whole-genome sequences—the presence of rare variants. SNP-based analyses such as that conducted in the PoBI project[159] analyse only common sequence variants that show variation in most human populations. Although the patterns of association of such variants can contain fine-grained information about coancestry, by definition the common SNPs themselves must have arisen many tens of thousands of years ago. Rare variants, by contrast, can be relatively recent in origin, and have the potential to demonstrate specific relationships between populations through patterns of sharing. Rare variants in the ancient samples were compared with those in a panel of European reference genome sequences. Middle Anglo-Saxon samples shared a higher proportion of rare variants with modern Dutch samples than did the Iron Age samples. The Oakington Early Anglo-Saxon individuals were diverse: two resembled Middle Anglo-Saxon samples and were interpreted as recent immigrants; one resembled the Iron Age samples, and therefore appears to have been indigenous; the fourth Oakington individual showed an intermediate pattern of rare variant sharing suggesting mixed ancestry. This genetically mixed picture was contrasted[160] with the segregated 'apartheid' model[161] suggested previously to explain the Y-chromosome data.[162] Measuring the frequencies of the rare variants in modern British samples, and modelling past admixture based on rare variant proportions, allowed an estimate of an average 'Anglo-Saxon' ancestry in modern East English samples of 38% (with a broad spread from 25–50%). A new method, Rarecoal, was

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[159] Leslie *et al*., 'The Fine-Scale Genetic Structure'.

[160] Schiffels *et al*., 'Iron Age and Anglo-Saxon Genomes'.

[161] Thomas, Stumpf, and Harke, 'Evidence for an Apartheid-Like Social Structure'.

[162] Weale *et al*., 'Y Chromosome Evidence'.

developed to fit a demographic model to the pattern of rare alleles in large sample sets: this confirmed that the early medieval individuals were most closely related to modern Danish and Dutch populations.

Overall, this study supports a genetic shift from the Iron Age to the early medieval period in lowland Britain, and thereafter admixture between indigenous and immigrant populations in the Early Anglo-Saxon period, shown by evidence from Oakington. Later samples from Hinxton show no such admixture, so may reflect continued immigration through the Middle Anglo-Saxon period.

The second study of ancient British genomes from the first millennium comes from Martiniano *et al.*,[163] who sequenced nine samples from northern England. One of these was an Iron Age female from Melton in Yorkshire, dated between 210 BC and 40 AD, seven were males from a second–fourth century Roman cemetery in York (Driffield Terrace), and one was a male from a Middle Anglo-Saxon cemetery at Norton on Tees.

The genome of one of the Driffield Terrace individuals was strikingly different from the rest, and most closely related to modern Palestinian, Jordanian, and Syrian genomes; also, his Y chromosome belonged to a lineage found most frequently in the Middle East. Here, the authors turned to stable isotopes—the study was pioneering in applying both genomic and isotopic analysis in a British context. Isotopic analysis of the Driffield Terrace skeletons supported the outlier status of the genetically differentiated individual, who showed a particularly low $^{87}Sr/^{86}Sr$ ratio and high $\delta^{18}O$ value compared to the others, and to a larger set of samples from Roman York. These findings strongly suggest that this man's ancestry and

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[163] Martiniano *et al.*, 'Genomic Signals of Migration'.

childhood were in the Middle East, but it was not possible to be more geographically specific than this.

Comparison of the genomes of the remaining six Driffield Terrace individuals with data on modern populations, including the the use of FineSTRUCTURE as in the PoBI study,[164] showed highest affinities with Welsh samples. All of them also carried a Y-chromosome type that today reaches its highest frequencies in Ireland and the west Britain, and forms the basis of the transition observed in the transect study of Weale *et al.*[165] between England and Wales. The Iron Age genome was similar to these Roman era genomes, but the early medieval genome was very different, pointing to a genetic shift in Yorkshire following the early centuries AD. Analysis of SNPs within genes that are involved in pigmentation variation indicated that the early medieval and one of the Roman era individuals had blue eyes and blond hair, while the remaining Roman era individuals were brown-eyed and dark-haired.

Overall, this study is consistent with that of Schiffels *et al.*[166] in providing evidence for a marked difference in genetic composition accompanying transition into the early medieval period: the early inhabitants of northern England were genetically very different from modern people from the same region. It also suggests continuity over a long period prior to this transition.

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[164] Leslie *et al.*, ‘The Fine-Scale Genetic Structure’.

[165] Weale *et al.*, ‘Y Chromosome Evidence’.

[166] Schiffels *et al.*, ‘Iron Age and Anglo-Saxon Genomes’.

As if to remind us of the rapid advance of ancient DNA studies, a study[167] appeared on the biology preprint server, BioArxiv (it has not yet undergone peer review), during the final preparation of this chapter, presenting a population genomic analysis of Viking Era remains based on the genome sequences of 442 individuals, including English burials. The study shows that Norwegian, Danish, and Swedish ancestries were distinct in the medieval period, and analyses the genomes of ten men from Ridgway Hill, Weymouth, Dorset, and 22 from St John's College, Oxford. Genomic data suggest that these 'execution' sites contained men from different places of origin, consistent with the stable isotope data (discussed above), including British, Danish-like, and Norwegian-like ancestries. This study did not include any data from Danelaw sites, reinforcing the need for additional investigations.

## Conclusions on genetic analysis

Genome-wide data on modern individuals will continue to accumulate, as the cost of whole-genome sequencing declines. Data that are accumulated for medical genomics projects such as UK Biobank (500,000 individuals[168]) are spectacular in scale, but lack the fine-grained geographical resolution that is needed to support studies of population history.[169] Ultimately, it may be that the best modern DNA data come from members of the public who have paid for their own DNA testing and shared their data, both genomic and genealogical.

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[167] A. Margaryan *et al*., 'Population Genomics of the Viking World', BIoArxiv 703405; doi: https://doi.org/10.1101/703405 (2019).

[168] C. Bycroft *et al*., 'The UK Biobank Resource with Deep Phenotyping and Genomic Data', *Nature*, 562 (2018), 203–9.

[169] Leslie *et al*., 'The Fine-Scale Genetic Structure'.

Currently, ancient DNA is providing the most exciting and tantalising results, and this seems set to continue. The two studies described above[170] show that aDNA from before the medieval period compared with early medieval aDNA and modern DNA can be informative about the impact of medieval migrations. Neither of the studies provide any information on the numbers of migrants needed to effect the changes that they infer. Both studies have very small sample size—a total of only nineteen genomes has been analysed so far—and together tell us about only two regions of England: clearly more genome sequences are needed over a broader time period and a wider geographical range to paint a more reliable and nuanced picture. Explicit methods for combining ancient and modern data in a coalescent framework that accounts for the passage of time are still needed, and integration of aDNA data with the PoBI data and FineSTRUCTURE analysis would be illuminating.

## General conclusions and perspectives

In the sections above, we have described previous work undertaken using isotopic and genetic approaches to understanding migration in medieval England. It has been natural to separate these two sources of evidence. This is partly because of the profound differences in underlying methodology, but also because isotopes can speak to us only about an ancient individual from their own remains through their own exposure to their own environment, whereas the passage of DNA through the generations means that the genome of an individual, whether modern or ancient, informs not only about themselves but also about their genetic relationships with others, and their ancestry and origins. In this, DNA and isotopes represent

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[170] Martiniano *et al.*, ‘Genomic Signals of Migration’; Schiffels *et al.*, ‘Iron Age and Anglo-Saxon Genomes’.

respectively nature (in the sense of inheritance) and nurture. There are also differences in geographical resolution—it is very unlikely that genetic analysis will discriminate short-distance migrants, particularly in Western Europe, but in particular circumstances isotopic analysis promises to do just that.

When we consider ancient samples, it is clear that combining isotopic and genetic approaches, and integrating these with other forms of evidence, has much to offer, and can provide us with a richer and better supported picture of past migration. At the time of writing, there is only one English site in which the two approaches have been applied to the same sites and samples in a published study,[171] providing insights into the diversity of Roman York. Here, the genetically outlying male is also an outlier in strontium and oxygen isotope data, consistent with migration from the Middle East. If the two forms of evidence were applied together more consistently, we might learn much from the cases where the two do not chime together so closely.

Current projects suggest that more data about migration in the medieval period will be forthcoming: for example, in the 'After the plague: health and history in medieval Cambridge' project (Wellcome Collaborative Grant 200368/Z/15/A www.aftertheplague.com),[172] based around a cemetery site at St John's College, Cambridge, the remains of over 90 individuals have been sampled and are being compared to a further 120 individuals from other medieval sites around Cambridge;[173] this may detect evidence for migrants, but will also provide a large dataset in which genetic and isotopic data can be compared. Large-scale UK

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[171] Martiniano *et al*., 'Genomic Signals of Migration'.

[172] Wellcome Collaborative Grant 200368/Z/15/A www.aftertheplague.com.

[173] Toomas Kivisild and John Robb, personal communication.

infrastructure projects such as the High Speed Two railway[174] are also likely to seed projects providing opportunities for integrated projects on medieval sites. All of these analyses will contain inherent biases: investigated sites are almost always in lowland areas due to construction activity driving archaeological excavation, and there are also preservation issues connected with the acidity of soils in upland and western areas, alluded to previously.

Genomic analysis of ancient human remains has more to offer than the sequences of the ancient individuals themselves, potentially providing insights that could help to understand past migration and social structure in medieval England, as well as the diets and diseases of its inhabitants. With genome sequence information in hand, the relationships of individuals within cemeteries could be deduced: for example, large kindreds have been identified in sixth-century Longobard sites.[175] Such analyses in appropriate English sites could inform about kinship during the early medieval period, and contribute to debates about the importance of kinship in social structure. Combined with isotope analyses, we could learn about the differing movements of members of nuclear and extended families, with, for example, the potential to compare movements of mothers and fathers. Bones and teeth can yield the sequences of pathogenic bacteria, including *Yersinia pestis*, the infectious agent of the plague,[176] and calculus (calcified dental plaque) can provide direct evidence of diet,[177]

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[174] https://www.hs2.org.uk/building-hs2/arcaheology/.

[175] C. E. G. Amorim *et al.*, ‘Understanding 6th-Century Barbarian Social Organization and Migration through Paleogenomics’, *Nature Communications*, 9 (2018), 3547.

[176] K. I. Bos *et al.*, ‘A Draft Genome of Yersinia Pestis from Victims of the Black Death’, *Nature*, 478 (2011), 506–10.

and of the microbes living in the mouths of ancient individuals;[178] all of these could in principle inform about migration, if suitable comparative data were available. Finally, modifications that occur to human DNA molecules during life, and associated with the expression of genes and their regulation, can also be detected via ancient genome sequencing.[179] These 'epigenetic' modifications can reflect responses to environmental stress during the lives of individuals,[180] and thus provide a DNA-based counterpart to the environmental signal represented in isotope ratios.

Isotopic studies are likely to benefit from improved mapping and understanding of strontium isotopes in the environment. Increasingly studies are using multiple teeth from one individual to examine lifetime movements, and there is the possibility that even intra-tooth isotope variation might be usable to yield even finer temporal resolution. However, we need to know more about when strontium and oxygen are incorporated in enamel to exploit this potential fully.

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[177] L. S. Weyrich *et al.*, 'Neanderthal Behaviour, Diet, and Disease Inferred from Ancient DNA in Dental Calculus', *Nature*, 544 (2017), 357–61.

[178] C. J. Adler *et al.*, 'Sequencing Ancient Calcified Dental Plaque Shows Changes in Oral Microbiota with Dietary Shifts of the Neolithic and Industrial Revolutions', *Nature Genetics*, 45 (2013), 450–5, 5e1.

[179] J. S. Pedersen *et al.*, 'Genome-Wide Nucleosome Map and Cytosine Methylation Levels of an Ancient Human Genome', *Genome Research*, 24 (2014), 454–66.

[180] D. Gokhman, A. Malul, and L. Carmel, 'Inferring Past Environments from Ancient Epigenomes', *Molecular Biology and Evolution*, 34 (2017), 2429–38.

Both isotope and genetic analyses depend on visual comparisons, such as within PCA (Figure 2.12) and to maps (Figures 2.1 and 2.2), which introduce subjectivity into interpretations and require a large manual effort in re-interpretations in the light of new comparative data. Quantifying these comparisons with statistical approaches which explicitly incorporate geographic structure will be necessary as datasets increase in size. Indeed, we foresee that future interpretations of combined genetic and isotopic analyses, including their correlations and contradictions, will require more powerful and objective model-based statistical approaches to both types of data, with common elements that allow better integration of the two sources of evidence.

So, there is wonderful scope for ‘personalised’ scientific analysis of human remains: genome sequencing to provide information on kinship and localised prediction of ancestry, analogous to modern direct-to-consumer genealogical testing; isotopic evidence informing about early life and migration. However, now, at least, the ‘ordinary’ people of the past, and the journeys of their lives, remain largely a closed book. We can but hope that falling costs of some analyses, increasing numbers of researchers with relevant training and imaginative projects and funders will allow the pages of this book to be opened.

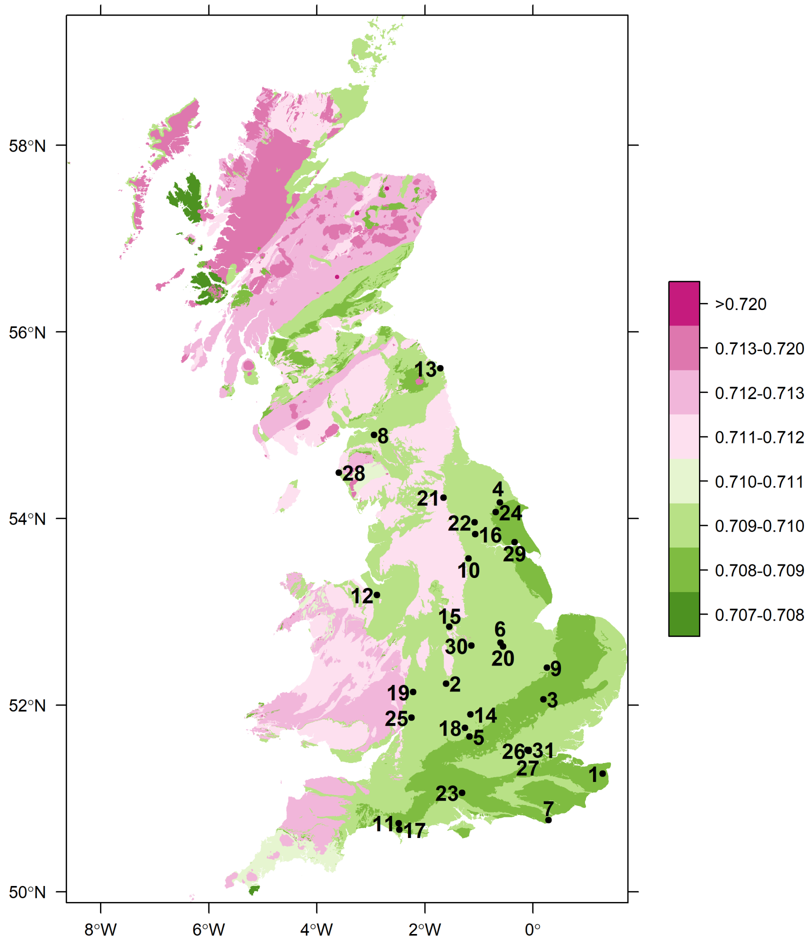

Fig. 2.1 Strontium isotope map of Britain with the locations of the sites discussed in the text (after Evans *et al*., ‘Spatial Variations’. For key see Figure 2.3).

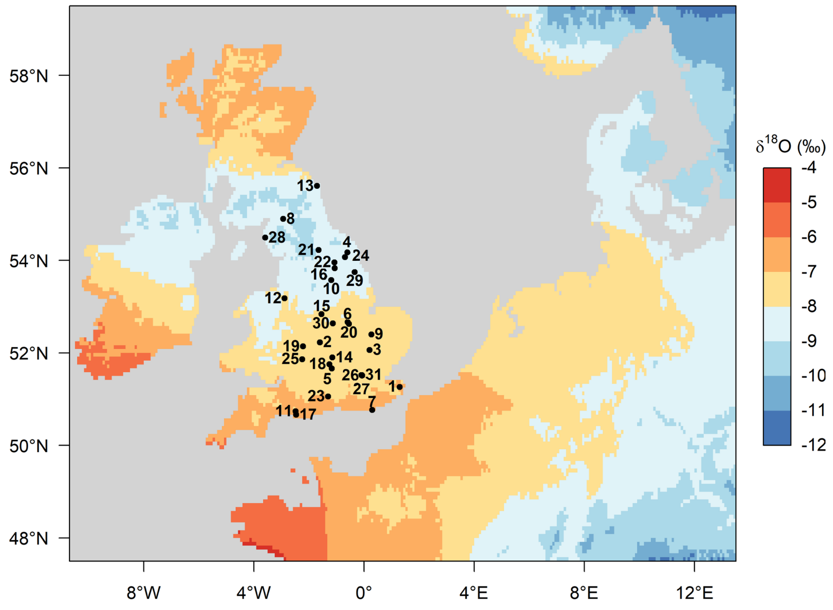

Fig. 2.2. Oxygen isotope variation in north-west Europe with the locations of the sites discussed in the text (after G. J. Bowen and J. Revenaugh, ‘Interpolating the Isotopic Composition of Modern Meteoric Precipitation’, *Water Resources Research*, 39 (2003), 1299, doi:10.129/2003WR002086. For key, see Figure 2.3).

| Key | Site | County | Number of isotope analyses | | |
|---|---|---|---|---|---|
| | | | Both O & Sr | O only | Sr only |
| 1 | Ringlemere | Kent | 7 | | |
| 2 | Wasperton | Warwickshire | 20 | | |
| 3 | Great Chesterford | Essex | 1 | | |
| 4 | West Heslerton | East Yorkshire | 28 | | 6 |
| 5 | Berinsfield | Oxfordshire | 19 | | |
| 6 | Empingham II | Rutland | | | 11 |
| 7 | Eastbourne | Sussex | 29 | | |
| 8 | Carlisle Cathedral | Cumbria | 4 | | |
| 9 | Westfield Farm Ely | Cambridgeshire | | 13 | |
| 10 | Adwick-le-Street | South Yorkshire | 7 | | 2 |
| 11 | Bradford Peverell | Dorset | | | 6 |
| 12 | Heronbridge, Chester | Cheshire | 2 | | |
| 13 | Bamburgh | Northumberland | 84 | | 2 |
| 14 | Bicester | Oxfordshire | | 5 | |
| 15 | Repton | Derbyshire | 8 | | 4 |
| 16 | Riccall Landing | North Yorkshire | 12 | | |
| 17 | Ridgway Hill, Weymouth | Dorset | 10 | | |
| 18 | St John’s College Oxford | Oxfordshire | 6 | 7 | |
| 19 | Kempsey | Worcestershire | | 23 | |
| 16 | Riccall Landing | North Yorkshire | 12 | | |
| 20 | Ketton | Rutland | | | 26 |
| 21 | Masham | North Yorkshire | 8 | 15 | |
| 22 | Coppergate | York | 3 | | |
| 23 | Winchester | Hampshire | 1 | | |
| 24 | Wharram Percy | North Yorkshire | | | 16 |
| 25 | Blackfriars Gloucester | Gloucestershire | 4 | | 2 |
| 26 | Royal Mint (East Smithfield) | London | 29 | 1 | |
| 27 | Charterhouse Square | London | 10 | | |
| 28 | St Bees | Cumbria | | | 1 |
| 29 | Hull Magistrates Court | East Yorkshire | 12 | | |
| 30 | Richard III, Leicester | Leicestershire | 2 | | |
| 31 | St Mary Spital | London | 10 | | |
| **Total** | | | **306** | **64** | **76** |

Fig. 2.3. Sites mentioned in the text, with numbers of isotope analyses from each. The key refers to the numbering of the sites in Figures 2.1 and 2.2.

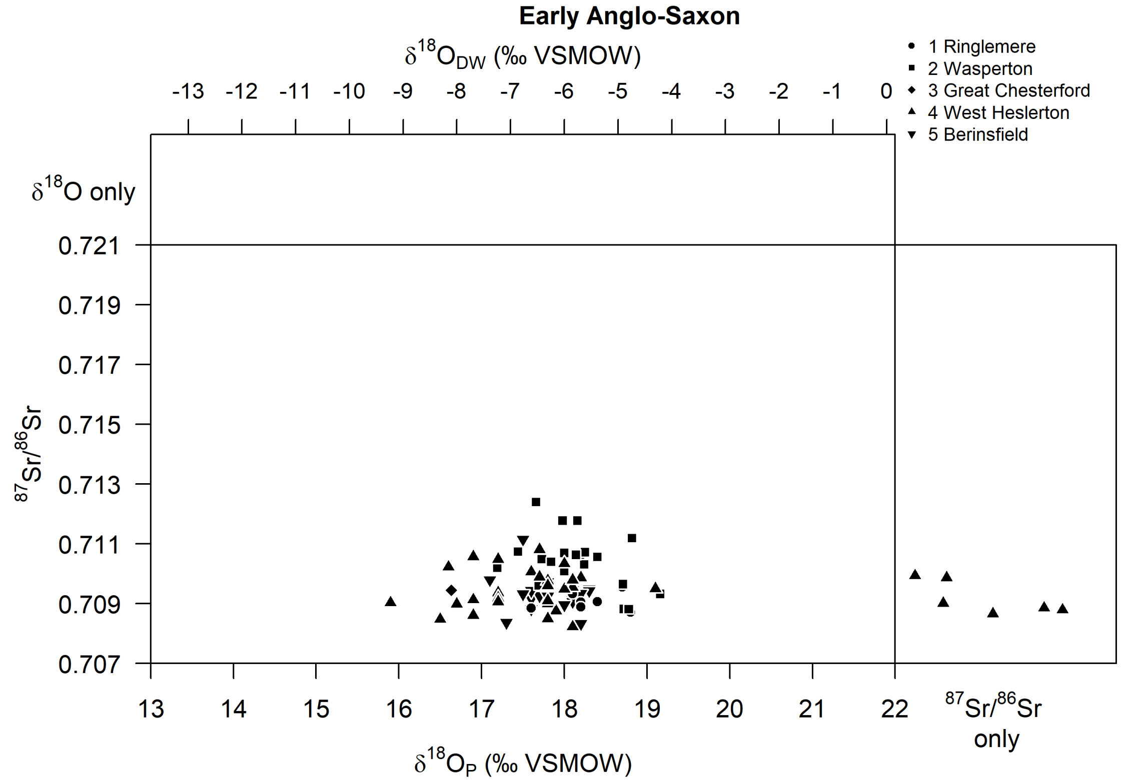

Fig. 2.4. Strontium and oxygen isotope data from Early Anglo-Saxon England (*c*. 450–700) (part 1). Where oxygen isotope measurements were made on carbonate, these have been converted to phosphate ($\delta^{18}O_P$) values using the equation from Chenery *et al*., ‘The Oxygen Isotope Relationship’. The lower scale shows $\delta^{18}O_P$ and the upper scale shows the calibration of those values to drinking water ($\delta^{18}O_{DW}$) values using equation 6 from Daux *et al*., ‘Oxygen Isotope Fractionation’.

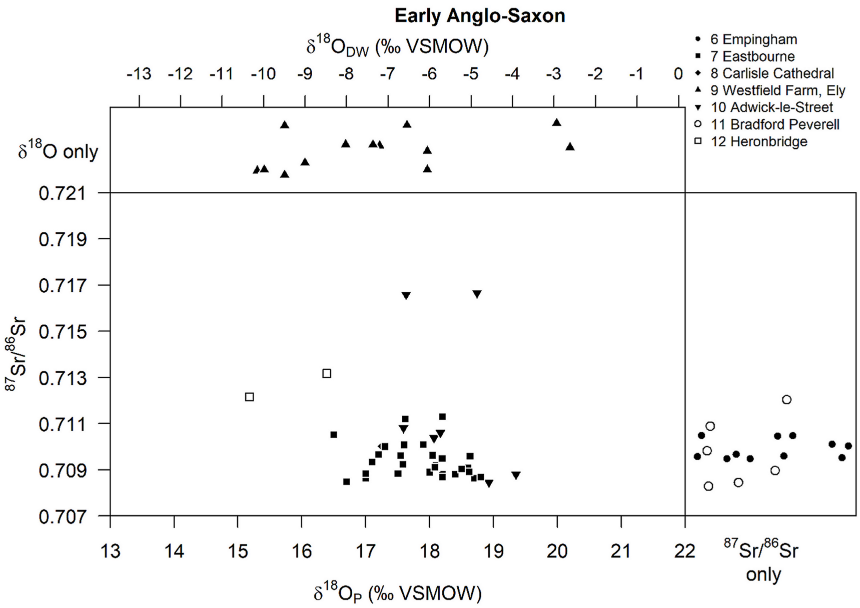

Fig. 2.5. Strontium and oxygen isotope data from Early Anglo-Saxon England (*c*. 450–700) (part 2). See caption to Figure 2.4 for details of conversions and comparisons.

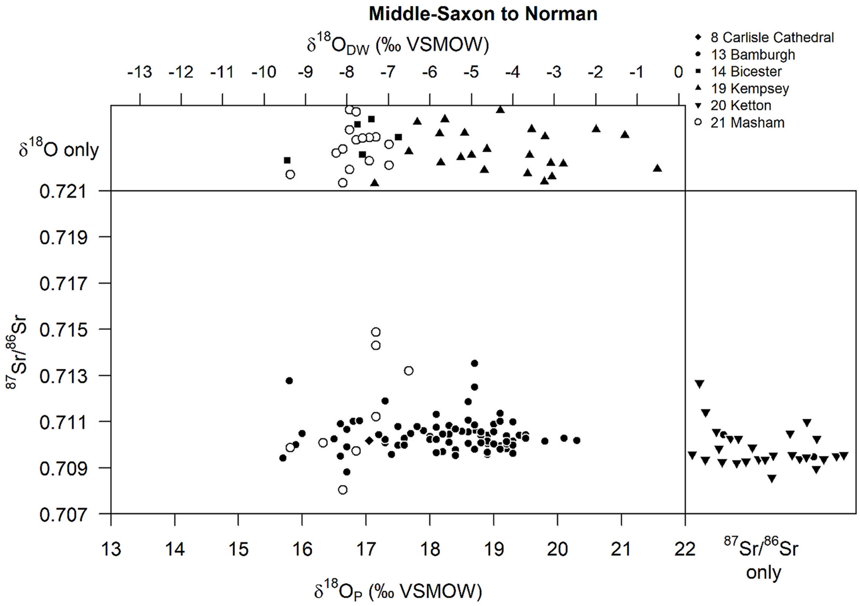

Fig. 2.6. Strontium and oxygen isotope data from non-‘Viking’ sites from Middle-Saxon to Norman England (*c*. 700–1100). See caption to Figure 2.4 for details of conversions and comparisons.

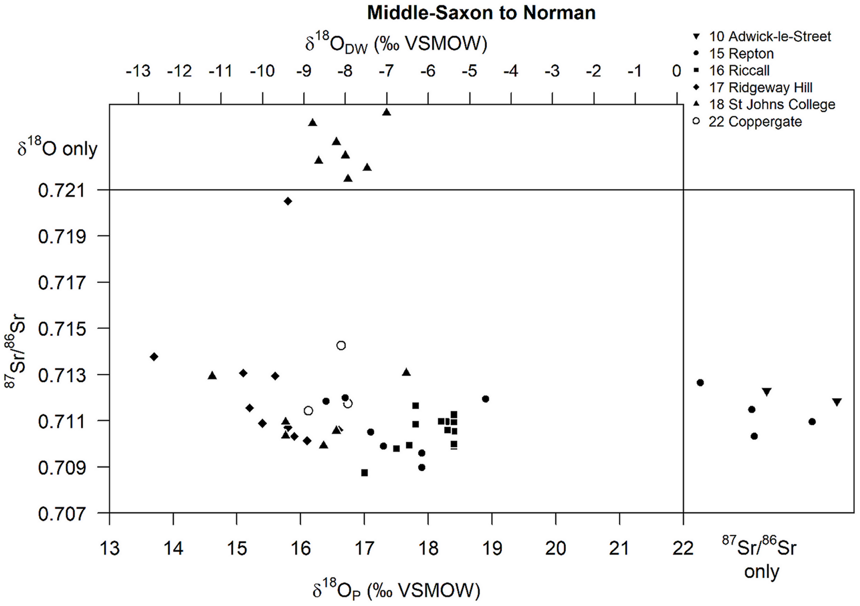

Fig. 2.7. Strontium and oxygen isotope data from presumed ‘Viking’ or Norse sites from Middle-Saxon to Norman England (*c*. 700–1100). See caption to Figure 2.4 for details of conversions and comparisons.

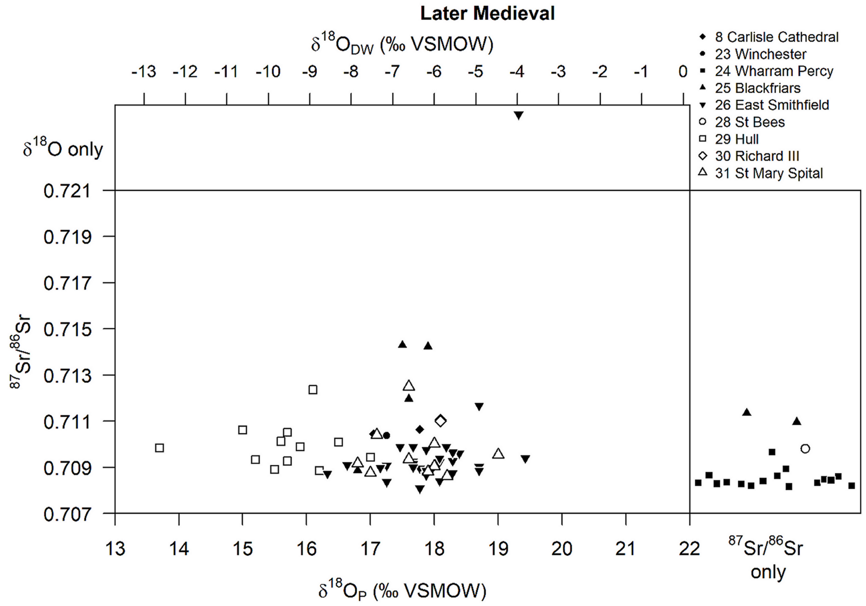

Fig. 2.8. Strontium and oxygen isotope data from Later Medieval England (*c*. 1100–1540). See caption to Figure 2.4 for details of conversions and comparisons.

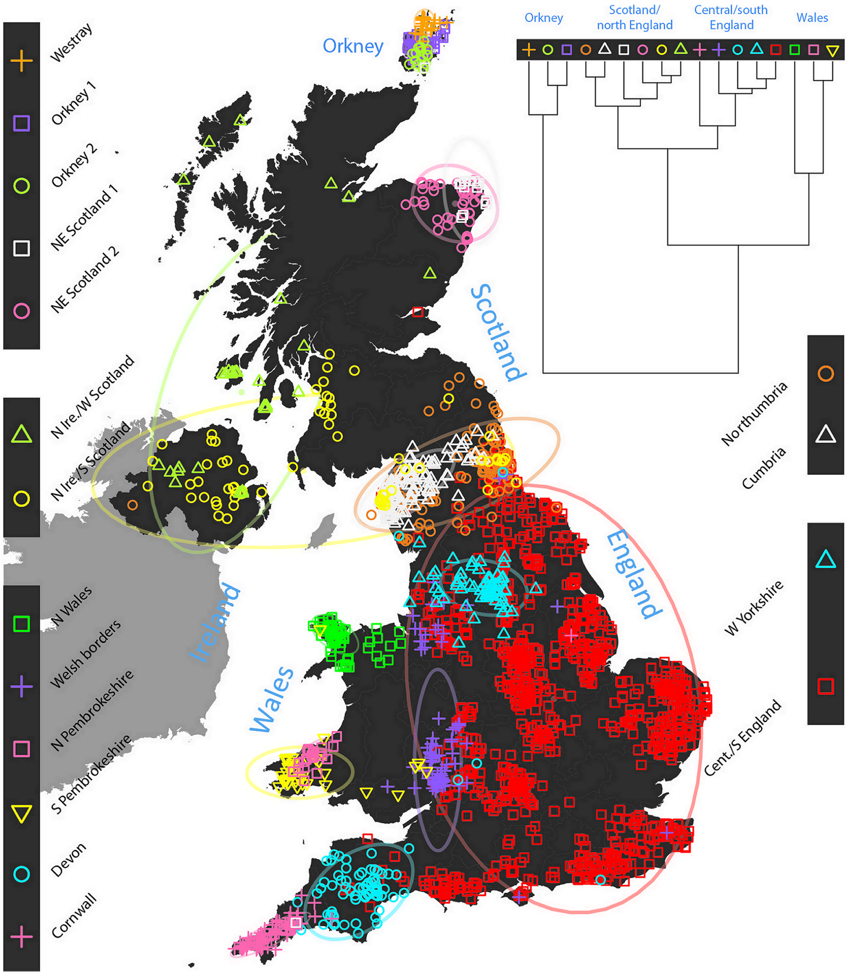

Fig. 2.9.. Clustering of 2039 individuals in the People of the British Isles study into 17 clusters based on autosomal SNP data. For each individual, the coloured symbol representing the genetic cluster to which they are assigned is plotted at the centroid of grandparental birthplaces. Cluster names and symbols are given to the left and right, and ellipses approximate the geographical range of each cluster. The tree (top right) shows the hierarchical relationships of clusters. From Leslie *et al.*, ‘Fine-scale genetic structure’; original contains OS data, Crown copyright and database rights (2012).

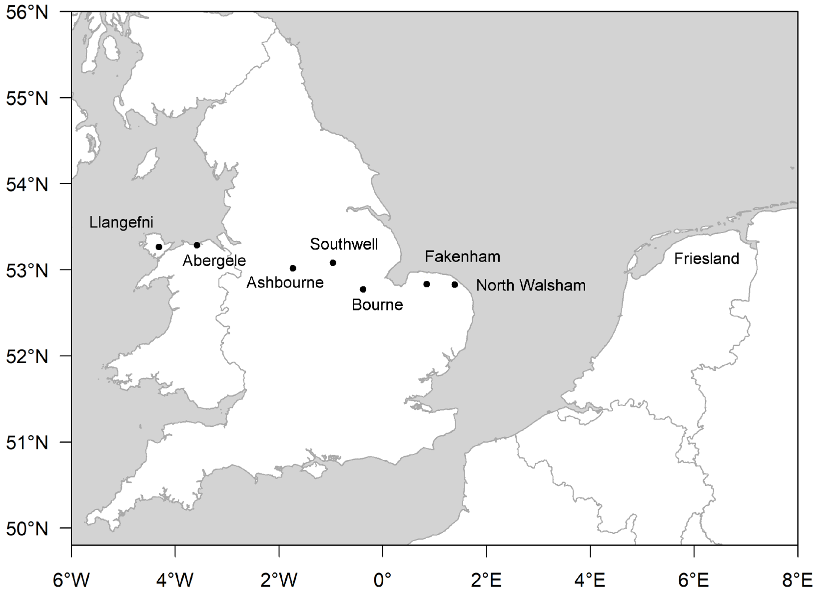

Fig. 2.10. Y-chromosomal sampling locations in the E–W transect of England. Sampling locations are from Weale *et al*., ‘Y Chromosome Evidence’; also shown is Friesland, which showed insignificant differentiation from the English sites.

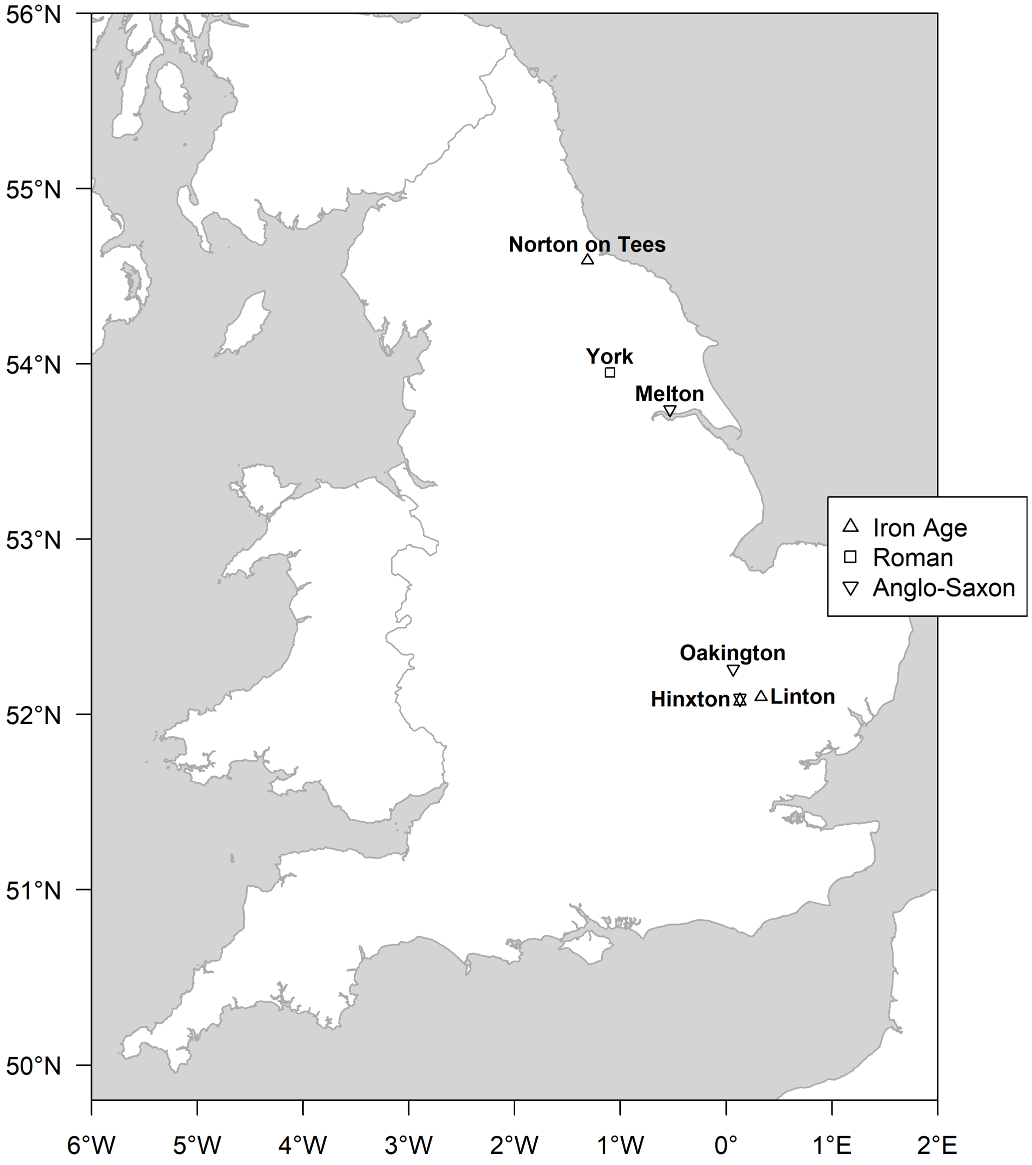

Fig. 2.11. Locations of sites yielding whole-genome sequence data from ancient samples, modified from Schiffels *et al*., 'Iron Age and Anglo-Saxon Genomes' (three eastern sites), and Martiniano *et al*., 'Genomic Signals of Migration' (three northern sites).

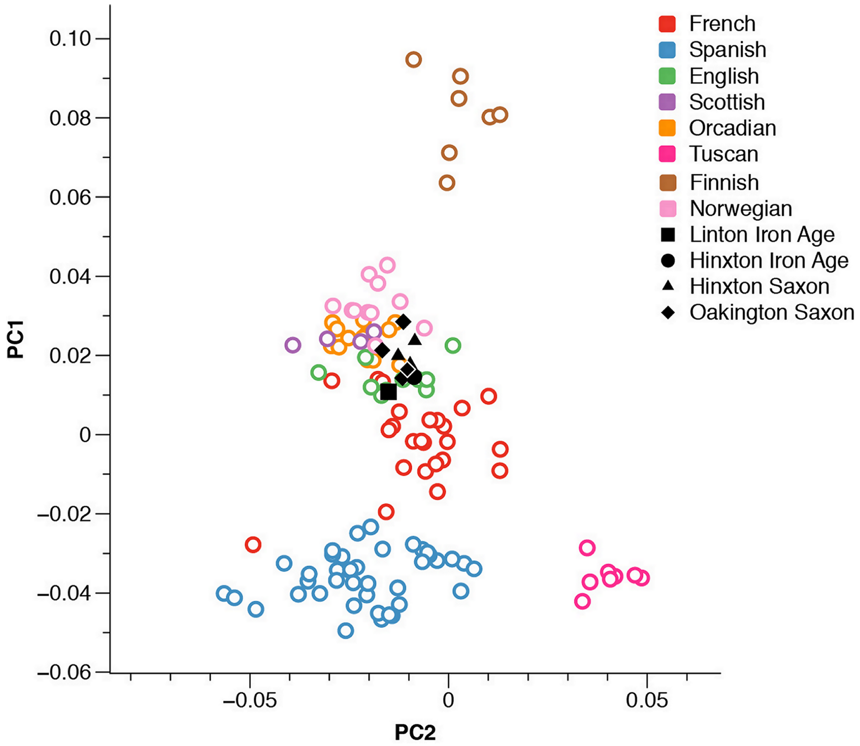

Fig. 2.12. Principal component analysis of ancient genomes from Cambridgeshire compared with modern European genomes.

The first two principal components (PC1 and PC2) are shown. Coloured symbols represent modern individuals, and filled black symbols represent ancient individuals as explained in the key (after Schiffels *et al*., ‘Iron Age and Anglo-Saxon Genomes’).