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**Research Article**

# Ancient genomes reveal cosmopolitan ancestry and maternal kinship patterns at post-Roman Worth Matravers, Dorset

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Kinship can be difficult to discern in the archaeological record, but the study of ancient DNA offers a useful window into one form of kinship: biological relatedness. Here, the authors explore possible kin connections at the post-Roman site of Worth Matravers in south-west England. They find that, while clusters of genetically related individuals are apparent, the inclusion of unrelated individuals in double or triple burials demonstrates an element of social kinship in burial location. Some individuals also carried genetic signatures of continental ancestry, with one young male revealing recent West African ancestry, highlighting the diverse heritage of early medieval Britain.

Keywords: Britain & Ireland, post-Roman, Anglo-Saxon, ancient DNA, biological kinship, African ancestry

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## The role of kinship in archaeological investigations

Kinship was central to early-medieval societal organisation and, after the fall of Rome in AD 476, became a cornerstone of the legal, political and social landscape of Europe. Who you were related to defined your social position, relative freedoms and even the possibilities for marriage and procreation (Goody 1983; Herlihy 1985). The challenges and opportunities presented by kinship are described in many legal and cultural documents, including the early English Laws and Irish Hagiographies, which place emphasis on the paternal line (Murray 1983; Herlihy 1985). Yet kin associations were not exclusively limited to patrilineal relationships in the early medieval period: in Ireland, although descent groups had male founders, they were subsequently bilateral. For example, King Echach told St Patrick that he hoped "to extend my lineage from the body of my daughter, by the procreation of grandchildren" and expected his future son-in-law to join his household (Herlihy 1985: 33). The relationships encompassed by the term 'kin' varied across cultures, and the same documents suggest that the lived experience of residence and kinship were as adaptable in the first millennium AD as in earlier periods of prehistory (Fowler *et al.* 2022; Pearson *et al.* 2023), taking various forms depending on the circumstances, with social relationships often prioritised over biological relatedness, particularly where communities needed to adapt in the face of change.

Archaeological studies have tended to focus more on social identity and personhood, rather than kinship. Where family groups are proposed within mortuary contexts, indicators such as cemetery patterns, grave goods and the identification of inherited skeletal traits are seen as evidence for biological relatedness (Sayer 2009, 2020; Johnson & Paul 2016). Yet, the layout of cemeteries can also reveal information about the importance of kin groups, whether social or biological (Sayer 2020). Despite the risk of placing undue stress on genetic descent (Brück 2021; Brück & Frieman 2021; Ensor 2021), ancient DNA (aDNA) studies can help highlight and unravel the complexities of relationships in the archaeological record (Fowler 2022; Greaney 2022). Individuals in multiple burials, for example, may be biologically related (e.g. Pajnič *et al.* 2023), but often are not (e.g. Dulias *et al.* 2022), underscoring the potential for the existence of social kinship alongside genetic relationships (e.g. in Neolithic Anatolia, from *c.* 5000 BC; Pearson *et al.* 2023). Inter-site comparisons generate more controversy, such as the suggestion that genetic relatedness between individuals interred in several megalithic tombs in Neolithic Ireland (*c.* 4000–2500 BC) reveals a wide-reaching 'dynastic elite' (Cassidy *et al.* 2020; discussed by Greaney 2022; Smyth *et al.* 2025).

Studies based on cranial modification, dental metrics and stable isotopes largely propose that female exogamy and patrilocality were practised in early medieval Europe (476–1000 AD; e.g. Hakenbeck 2009; Stewart 2021; Hamerow *et al.* 2024). Genetic studies also highlight these practices in Late Neolithic/Bronze Age Europe (*c.* 5300–1500 BC; Haak *et al.* 2008; Knipper *et al.* 2017; Mittnik *et al.* 2019; Dulias *et al.* 2022) and early medieval Bavaria (late fifth–early sixth century AD; Veeramah *et al.* 2018). However, a recent study of the Durotrigian site of Winterbourne Kingston, Dorset (*c.* 1000 BC–AD 500), found a community characterised by female-line descent, as well as widespread matrilocality seen across Iron Age England (*c.* 800 BC–AD 43; Cassidy *et al.* 2025). In addition, Fowler (2022) notes that, rather than a purely patrilineal descent, the sharing of male genetic lineages at a site may indicate bilateral kinship, where relations are traced through either the father or the mother. This is particularly the case when the males present do not belong to the same Y-chromosome lineage and are thus not representatives of a stable paternal line.

## Early medieval England and the site of Worth Matravers

Early medieval England witnessed profound changes in language, politics and social organisation (Hines 1994). Historical sources and archaeological studies indicate waves of migrants arriving from the Continental North Sea region during this period, but the size and scale of this immigration is controversial (Hills 2009). Building on this, recent aDNA work demonstrates the large-scale arrival of new groups from the European continent in the fifth and sixth centuries AD onwards, altogether accounting for about two-thirds of the ancestry of people inhabiting England today (Gretzinger *et al.* 2022).

Dorset, in south-west England, lies at the western limits of early continental-influenced Anglo-Saxon cemeteries. The burials in this region instead show a continuation of late Roman practices, which involved extramural locations and the incorporation of Christian traditions, comprising simple east-west inhumations, typically without grave goods. The archaeological evidence suggests a marked cultural divide between Dorset (and areas to the west) and the Anglo-Saxon influenced areas to the east. To investigate kinship in early medieval Dorset, we analysed 20 individuals from the site of Worth Matravers on the Isle of Purbeck, where a high degree of Western British and Irish ancestry has previously been reported (77.4% ± 8.4%; Gretzinger *et al.* 2022). Worth Matravers sits west of the distribution of early Anglo-Saxon furnished burials found in southern and eastern England (Sayer 2020), and did not become part of Anglo-Saxon Wessex until the mid-seventh century AD (Yorke 2002). Here, we present the combined archaeological and genetic analysis of early medieval kinship and relational identity within the western British cultural area, where few analyses of Romano-British populations have been undertaken.

We sampled 18 of 26 individuals excavated from the post-Roman cemetery of Worth Matravers (Site 3; Figure 1), including all individuals from one triple and three double burials (Table 1). We also analysed two individuals (CE049 and CE050) from Roman contexts at Sites 1 and 2 (see online supplementary material (OSM) section 1.1; Figures S3 & S4), one of whom had previously been analysed by Patterson *et al.* (2022). Apart from a small copper alloy buckle buried in grave 1667, and the unusual find of a limestone anchor used as a headrest in grave 1633 (Ladle 2018), no other grave goods were discovered at the site. Although very little is known about communities in sub-Roman or early post-Roman Britain (fifth and sixth centuries AD; Thornton 2009), this lack of artefactual evidence is consistent with a persisting or emerging British cultural zone, and contrasts with the furnished Anglo-Saxon cemeteries of eastern England.

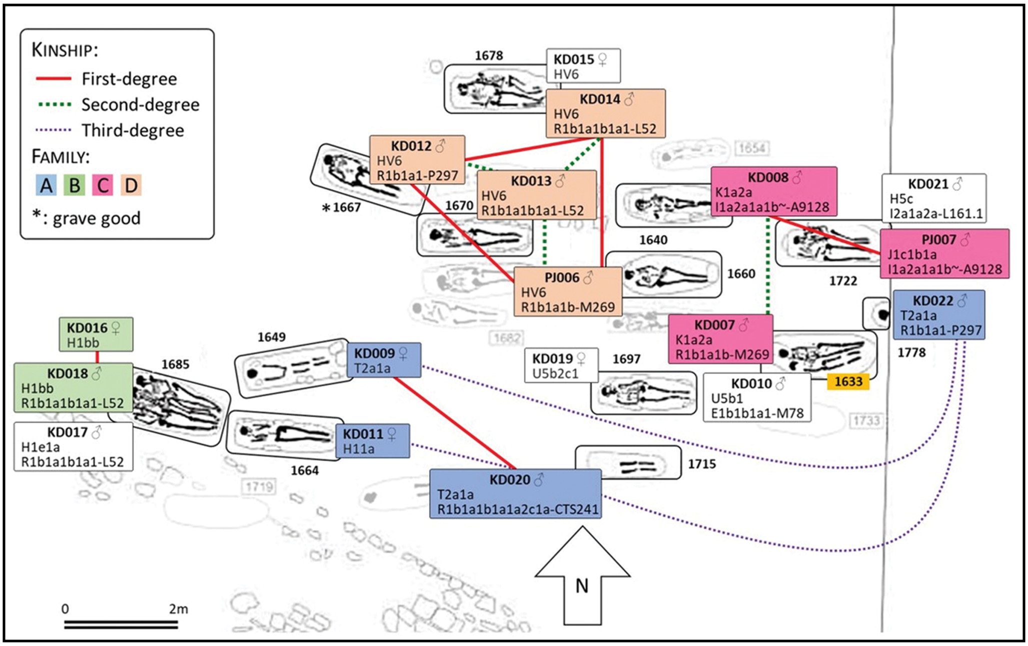

*Figure 1. Biological kinship within the post-Roman cemetery (Site 3). Burials sampled for aDNA are outlined in black (see Table 1). Coloured boxes indicate the DNA sample code, genetic sex, mitochondrial haplogroup, Y-chromosome haplogroup (where relevant) and genetic kinship for each individual (see Table 3). See Figure S2 for Roman individuals from Sites 1 and 2, and for detailed genealogies see OSM, section 6 (figure by authors, modifying cemetery plan from Ladle 2018, fig. 94).*

We undertook genomic and dietary-isotopic analyses to identify potential links between diet, burial location within the cemetery, and biological versus social kinship at the site and, through comparison with published data, investigated to what extent the community was isolated from, or connected to, others in the region and more widely. As poor preservation at the site hindered osteoarchaeological analysis (Randall 2018), we also determined the genetic sex of each individual to help understand the use of the multiple burials. More details about the site of Worth Matravers, the cemetery and the regional and national contexts can be found in the OSM (section 1).

## Age range of the post-Roman cemetery

Radiocarbon dates are available from six of the burials at the post-Roman cemetery at Worth Matravers (Krus 2018). We obtained two further radiocarbon dates: one from KD010, an adolescent male, and a second from KD007, an adult male, buried together in grave 1633 (Table S2). An unpublished date is also available from one of the Roman individuals (Site 1; CE049, adult female). Previously reported dates employed a varying marine correction, typically applied to counteract the artificially increased age of marine resources and their consumers (Krus 2018), but our stable isotopic data (Figure S10, Table S3) suggests that such a correction is not necessary. The $\delta^{15}N$ values of individuals from Worth Matravers were not sufficiently elevated to suggest a substantial marine component in their diet, and the $\delta^{13}C$

**Table 1. Sample information for the 20 individuals sampled from the three sites at Worth Matravers. Grave and skeleton numbers from Ladle (2018), and age estimates from Randall (2018). More information in Table S1.**

| Grave # | Skeleton # | DNA code | Sample number | Site # | Site type | Era | Age |
|---|---|---|---|---|---|---|---|
| 318 | 320 | CE049 | FFWM08 320 | 1 | single burial | Romano-British | adult |
| 1123 | 1174 | CE050 | FFWM10 1174 | 2 | cist | Romano-British | 5–7 months |
| 1633 | 1632 | KD007 | FFWM11 1632 | 3 | cemetery | post-Roman | adult |
| 1633 | 1652 | KD010 | FFWM11 1652 | 3 | cemetery | post-Roman | 17–25 years |
| 1640 | 1642 | KD008 | FFWM11 1642 | 3 | cemetery | post-Roman | 17–25 years |
| 1649 | 1651 | KD009 | FFWM11 1651 | 3 | cemetery | post-Roman | 25–35 years |
| 1660 | 1662 | PJ006 | FFWM11 1662 | 3 | cemetery | post-Roman | 25–35 years |
| 1664 | 1666 | KD011 | FFWM11 1666 | 3 | cemetery | post-Roman | 35–45 years |
| 1667 | 1669 | KD012 | FFWM11 1669 | 3 | cemetery | post-Roman | 25–35 years |
| 1670 | 1672 | KD013 | FFWM11 1672 | 3 | cemetery | post-Roman | 17–25 years |
| 1678 | 1680 | KD014 | FFWM11 1680 | 3 | cemetery | post-Roman | 40–45 years |
| 1678 | 1681 | KD015 | FFWM11 1681 | 3 | cemetery | post-Roman | 15–16 years |
| 1685 | 1687 | KD016 | FFWM11 1687 | 3 | cemetery | post-Roman | 25–35 years |
| 1685 | 1688 | KD017 | FFWM11 1688 | 3 | cemetery | post-Roman | 45–49 years |
| 1685 | 1693 | KD018 | FFWM11 1693 | 3 | cemetery | post-Roman | 15–16 years |
| 1697 | 1699 | KD019 | FFWM11 1699 | 3 | cemetery | post-Roman | 25–35 years |
| 1715 | 1717 | KD020 | FFWM11 1717 | 3 | cemetery | post-Roman | adult |
| 1722 | 1724 | PJ007 | FFWM11 1724 | 3 | cemetery | post-Roman | 35–45 years |
| 1722 | 1725 | KD021 | FFWM11 1725 | 3 | cemetery | post-Roman | 17–25 years |
| 1778 | 1779 | KD022 | FFWM11 1779 | 3 | cemetery | post-Roman | 16–17 years |

values were not enriched beyond the normal terrestrial range (see OSM sections 2 and 3; see also supplementary materials of Sayer *et al.* 2025). Our calculations show that the cemetery was most likely in use for around 100 years, concentrated around cal AD 605–650 (OSM section 2), a finding similar to that determined by Krus (2018) using marine-calibrated dates.

## Stable isotope analysis of diet

We undertook dietary stable isotope analysis on 18 of the 20 individuals (Table S3), samples from the remaining two individuals being too small to undertake both aDNA and stable isotope analysis. Although the $\delta^{13}C$ range was diverse, values for all individuals are consistent with a $C_3$-based, terrestrial-dependent diet. Despite proximity to the coast, none of the post-Roman individuals have $\delta^{15}N$ values that suggest a substantial contribution from marine protein, indicating that there was no reliance on sea fish. The higher nitrogen values of the two Roman individuals suggests a possible change in diet or agricultural practices over time (see OSM section 3), but further datapoints are needed to elucidate this possibility.

**Table 2. Autosomal details for the 20 individuals from Worth Matravers. The number of single nucleotide polymorphisms (SNPs) covered from the 1240k targeted in the capture sequencing is shown, with associated Harvard lab codes. Low coverage individuals include KD015, KD020 and KD022, all with less than 30k SNPs and genome coverages of <0.03X. References: 1) Patterson *et al.* 2022; 2) this study; 3) Gretzinger *et al.* 2022.**

| Grave # | DNA code | DNA sample | Harvard code | Genome coverage | SNPs covered on 1240k | Reference |
|---|---|---|---|---|---|---|
| 318 | CE049 | lower left first molar | I20615 | 0.83X | 584 167 | 1, 2 |
| 1123 | CE050 | left petrous | I20616 | 0.70X | 833 511 | 2 |
| 1633 | KD007 | molar | I11567 | 0.08X | 89 918 | 3 |
| 1633 | KD010 | tooth | I11570 | 0.03X | 36 236 | 2, 3 |
| 1640 | KD008 | tooth | I11568 | 0.03X | 31 346 | 3 |
| 1649 | KD009 | tooth | I11569 | 0.27X | 271 187 | 3 |
| 1660 | PJ006 | tooth | I20636 | 0.03X | 35 318 | 3 |
| 1664 | KD011 | tooth | I11571 | 0.25X | 258 761 | 3 |
| 1667 | KD012 | tooth | I11572 | 0.05X | 53 089 | 2 |
| 1670 | KD013 | tooth | I11573 | 0.05X | 57 929 | 3 |
| 1678 | KD014 | tooth | I11574 | 0.06X | 71 621 | 3 |
| 1678 | KD015 | tooth | I11575 | 0.01X | 7592 | 3 |
| 1685 | KD016 | tooth | I11576 | 0.08X | 93 831 | 3 |
| 1685 | KD017 | tooth | I11577 | 0.07X | 84 382 | 3 |
| 1685 | KD018 | tooth | I11578 | 0.04X | 48 994 | 3 |
| 1697 | KD019 | tooth | I11579 | 0.30X | 301 393 | 3 |
| 1715 | KD020 | tooth | I11580 | 0.02X | 26 929 | 3 |
| 1722 | PJ007 | tooth | I20637 | 0.64X | 521 002 | 3 |
| 1722 | KD021 | tooth | I11581 | 0.19X | 204 022 | 3 |
| 1778 | KD022 | tooth | I11582 | 0.02X | 25 833 | 3 |

## Sex determination and uniparental markers

Detailed methods for DNA extraction, library preparation, sequencing, data processing and analysis are available in the OSM (section 4), and an overview of the autosomal data is shown in Table 2. We were able to determine the genetic sex of all 20 individuals. The two Roman individuals were both female, while the post-Roman cemetery included 13 males and five females (Table 3). Of the three double burials, both grave 1633 and grave 1722 contained two males, and grave 1678 contained one male and one female. The triple burial in grave 1685 contained two males and one female (Figure 1).

Uniparental markers are DNA components only inherited from one parent, without recombination, and include mitochondrial DNA and Y-chromosomal DNA. Although uniparental lineages categorised as local during the British Iron Age (*c.* 800 BC–AD 43) predominate at Worth Matravers, a diverse array of both mitochondrial and Y-chromosome haplogroups are observed at the cemetery, implying a cosmopolitan heritage (Table 3; OSM section 5). Thirteen Y-chromosome lineages are identified: nine belonging to subclade R1b–269, two to I1a2a1a1b~–A9128, one to I2a1a2a–L161.1 and one to E1b1b1a1–M78

**Table 3. Uniparental and kinship data from the Worth Matravers individuals, detailing genetic sex (XX female, XY male) alongside morphological sex determinations (Randall 2018), mitochondrial and Y-chromosome haplogroup assignment, likely sources of these uniparental lineages, and genetically identifiable family units with degrees of relatedness (Figure 1; OSM section 6).**

| | | Sex | | mtDNA | | | Y chromosome | | |
|---|---|---|---|---|---|---|---|---|---|
| Grave # | DNA code | Morphological sex | Genetic sex | Coverage | Haplogroup | Likely haplotype source | Haplogroup (ISOGG v15.73) | Likely haplogroup source | Kinship |
| 318 | **CE049** | F? | XX | 203.6 | H1i | British Local | n/a | n/a | none |
| 1123 | **CE050** | U | XX | 212.4 | H6a2 | British Local | n/a | n/a | none |
| 1633 | **KD007** | U | XY | 157.1 | K1a2a | British Local or France | R1b1a1b-M269 | West/ Central Europe | **Family C** (second degree with KD008) |
| 1633 | **KD010** | U | XY | 181.6 | U5b1 | British Local or Continental (North Sea) | E1b1b1a1-M78 | West Africa | none |
| 1640 | **KD008** | F? | XY | 47.1 | K1a2a | British Local or France | I1a2a1a1b~-A9128 | Continental (North Sea) | **Family C** (first degree with PJ007, and second degree with KD007) |
| 1649 | **KD009** | U | XX | 420.3 | T2a1a | British Local | n/a | n/a | **Family A** (first degree with KD020, and third degree with KD022) |
| 1660 | **PJ006** | M? | XY | 104.9 | HV6 | Continental (North Sea) | R1b1a1b-M269 | West/ Central Europe | **Family D** (first degree with KD012 and KD014, and second degree with KD013) |

(*Continued*)

Table 3. (*Continued*)

| | | Sex | | mtDNA | | | Y chromosome | | |
|---|---|---|---|---|---|---|---|---|---|
| Grave # | DNA code | Morphological sex | Genetic sex | Coverage | Haplogroup | Likely haplotype source | Haplogroup (ISOGG v15.73) | Likely haplogroup source | Kinship |
| 1664 | **KD011** | F? | XX | 204.0 | H11a | British Local or Continental (North Sea) | n/a | n/a | **Family A** (third degree with KD020) |
| 1667 | **KD012** | F | XY | 85.8 | HV6 | Continental (North Sea) | R1b1a1-P297 | West/ Central Europe | **Family D** (first degree with KD014 and PJ006, and second degree with KD013) |
| 1670 | **KD013** | F | XY | 118.3 | HV6 | Continental (North Sea) | R1b1a1b1a1-L52 | British Local or France | **Family D** (second degree with KD012, KD014 and PJ006) |
| 1678 | **KD014** | M | XY | 228.4 | HV6 | Continental (North Sea) | R1b1a1b1a1-L52 | British Local or France | **Family D** (first degree with KD012 and PJ006, and second degree with KD013) |
| 1678 | **KD015** | U | XX | 31.0 | HV6 | Continental (North Sea) | n/a | n/a | none |
| 1685 | **KD016** | F | XX | 238.5 | H1bb | British Local | n/a | n/a | **Family B** (first degree with KD018) |
| 1685 | **KD017** | M | XY | 402.7 | H1e1a | British Local | R1b1a1b1a1-L52 | British Local or France | none |

(*Continued*)

Table 3. (*Continued*)

| | | Sex | | mtDNA | | | Y chromosome | | |
|---|---|---|---|---|---|---|---|---|---|
| Grave # | DNA code | Morphological sex | Genetic sex | Coverage | Haplogroup | Likely haplotype source | Haplogroup (ISOGG v15.73) | Likely haplogroup source | Kinship |
| 1685 | **KD018** | U | XY | 389.6 | H1bb | British Local | R1b1a1b1a1-L52 | British Local or France | **Family B** (first degree with KD016) |
| 1697 | **KD019** | F? | XX | 865.2 | U5b2c1 | British Local | n/a | n/a | none |
| 1715 | **KD020** | U | XY | 151.4 | T2a1a | British Local | R1b1a1b1a1a2c1a-CTS241 | British Local or France | **Family A** (first degree with KD009, and third degree with KD011 and KD022) |
| 1722 | **PJ007** | M? | XY | 192.6 | J1c1b1a | British Local | I1a2a1a1b~-A9128 | Continental (North Sea) | **Family C** (first degree with KD008) |
| 1722 | **KD021** | F? | XY | 600.5 | H5c | British Local | I2a1a2a-L161.1 | British Local | none |
| 1778 | **KD022** | F | XY | 626.9 | T2a1a | British Local | R1b1a1-P297 | West/ Central Europe | **Family A** (third degree with KD009 and KD020) |

(Table 3). The R1b lineage is characteristic of the British Y-chromosome landscape following the population migrations associated with the arrival of the Bell Beaker cultural traditions around 2450 BC (Olalde *et al.* 2018), while the I1a lineage, seen in related individuals KD008 and PJ007, most likely arrived from continental North Europe during the early medieval period (Gretzinger *et al.* 2022). Conversely, lineage I2a, seen in KD021, probably reflects a genetic component present in Britain since the Neolithic (Dulias *et al.* 2022).

Intriguingly, the E1b lineage exhibited by KD010 has a likely source in West Africa (OSM section 7). This matches the West African fraction seen in the genome-wide analysis of this individual (discussed below), together indicating that this Y-chromosome was inherited from a West African ancestor several generations back in the family tree. A similar African-derived genome-wide ancestry is identified in a young female from the contemporaneous cemetery at Updown (Eastry, Kent) in south-east England (EAS003; Sayer *et al.* 2025).

Slightly less diversity is seen in the female line of descent (Table 3). The two Roman individuals (both female) appear to have local Western British and Irish maternal ancestry and, although we see no continuity between the maternal lineages of these and the 18 post-Roman burials, genome-wide analysis points to a closer genetic relationship between the three Worth Matravers burial sites than between post-Roman Worth Matravers and contemporaneous burials from eastern England (Gretzinger *et al.* 2022). Most of the mitochondrial lineages identified at Worth Matravers may be considered local during the British Iron Age, with no indication of African ancestry along the maternal line. Several haplotypes, however, suggest that some individuals had continental northern European ancestry (HV6 and possibly H11a and U5b1), while others bore possible traces of descent from Iron Age France (K1a2a). Despite the predominance of local ancestry, therefore, both maternal and paternal lineages display diverse ancestry, implying that the community buried at Worth Matravers reflects both local genetic continuity and the inward migration of men and women from the European continent before, and possibly during, the early medieval period.

## Kin relationship estimation

We used READv2 analysis to identify four first-degree (parent–offspring or sibling), two second-degree (grandparent–grandchild, aunt/uncle–niece/nephew or half-sibling), and two third-degree (great-grandparent–great grandchild or first cousin) kin relationships (Figure 1, Table 3; OSM 6). To lessen any effect of false positive results (that are inherent when using READv2 with low coverage genomes; Marsh *et al.* 2023), we coupled the results with osteoarchaeological information (Table S1) and the non-recombining uniparental markers (Table 3), to determine and support familial links within the cemetery (see OSM sections 5 and 6). From these results we identify four potential family units in the cemetery.

**Family A** (Figure S12): KD009 (25–35-year-old female, grave 1649) and KD020 (adult male, grave 1715) share a unique T2a1a mitochondrial haplotype and a first-degree relationship, so they are possibly siblings. Both are related in the third degree to KD022 (16–17-year-old male, grave 1778), who may have been their paternal first cousin (see OSM section 6.1). KD020 is also third-degree related to KD011 (35–45-year-old female, grave 1664), who was most likely their great-granddaughter.

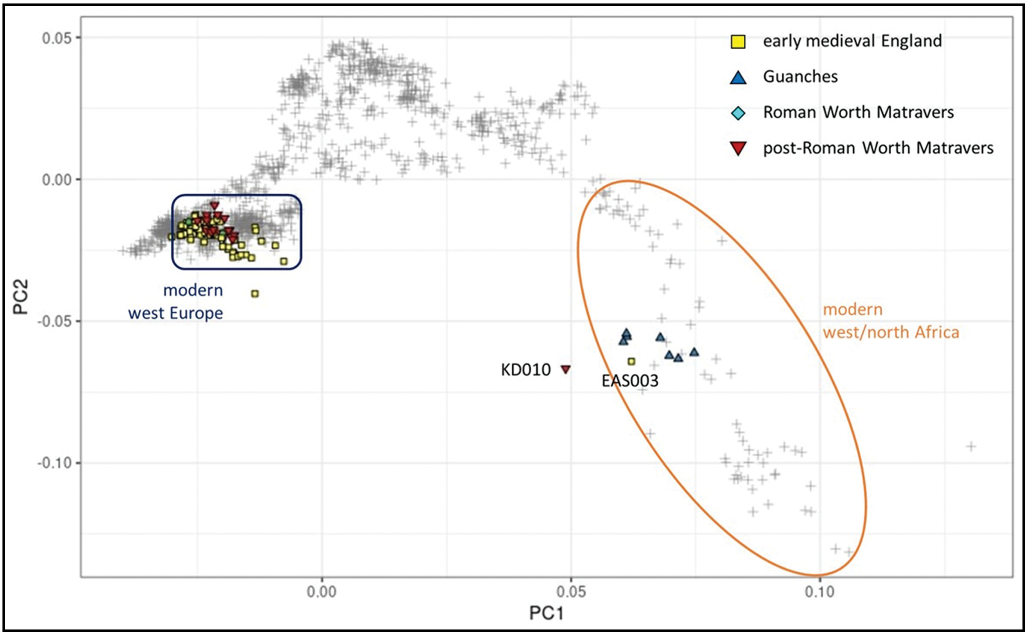

*Figure 2. Principal component analysis displaying the Worth Matravers individuals, alongside other early medieval aDNA samples from England (yellow squares; Gretzinger* et al. *2022) and contemporaneous North African individuals (blue triangles; seventh to eleventh centuries AD Guanches from the Canary Islands; Rodríguez-Varela* et al. *2017). Modern samples (grey crosses) from West Eurasia and West/North Africa are shown in the underlying plot (figure by authors).*

**Family B** (Figure S13): within the triple burial 1685, we found a first-degree relationship between KD016 (25–35-year-old female) and KD018 (15–16-year-old male). These two individuals share the mitochondrial haplogroup H1bb so were either siblings or mother and son. The third individual in the triple burial, KD017 (45–49-year-old male), does not show close familial links with any other individual in the cemetery but does have the same high-frequency Y-chromosome haplogroup as KD018 and two males from Family D (Table 3).

**Family C** (Figure S14): this family unit comprises three males from different graves. PJ007 (35–45-year-old, grave 1722) shares a first-degree relationship with KD008 (17–25 years old, grave 1640); as both carry the Y haplogroup I1a2a1a1b–A9128 but different mitochondrial genomes, a father–son relationship is suggested. KD008 is also second-degree related to KD007 (adult, double grave 1633), who has a different Y haplogroup but shares the K1a2a mitochondrial haplotype, suggesting that these two individuals could have been half-brothers or nephew and uncle.

**Family D** (Figure S15): this family comprises four male individuals buried in separate but nearby graves. KD012 (25–35 years old, grave 1667), KD014 (40–45 years old, double grave 1678) and PJ006 (25–35 years old, grave 1660) all share a first-degree relationship and were probably brothers. KD013 (17–25 years old, grave 1670) is second-degree related to all three, and was either their half-sibling, an uncle or a nephew.

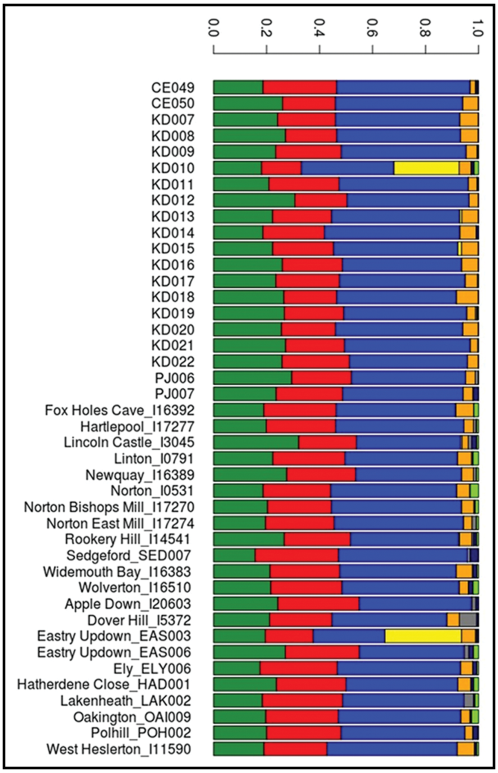

*Figure 3. Unsupervised ADMIXTURE analysis at K = 8 (the number of assumed ancestral groups thought to have contributed to the genetic makeup of the tested populations; Alexander* et al. *2009), following the percentages shown in Table S4. Code numbers for Worth Matravers are taken from Table 1, and other codes are as listed in Gretzinger* et al. *(2022). Most of the sample comprises three main components, characteristic of western European hunter-gatherers (blue), early European farmers (green), and Caucasus hunter-gatherers (red). KD010 (Worth Matravers) and EAS003 (Updown) stand out as the only individuals with a substantial yellow component, characteristic of West African populations. Smaller components are likely artefacts of DNA degradation (figure by authors).*

When all these results are taken into consideration, an unusual pattern emerges. Although almost 70 per cent (9/13) of the males sampled show biological kinship links to another individual, this kinship predominantly involves the maternal line of descent, with the single exception of the father–son duo KD008 and PJ007. No direct female-to-female relationships are identified, though this might be explained by the small female sample size, as it is also the case that only two (or possibly three, see OSM section 6.4) direct female-to-male links are seen, in Family A and B. The female and male in each of these two families share a mtDNA haplotype, suggesting again a maternal relationship (mother–son or sister–brother) rather than a paternal daughter–father link. This prevalence of maternal links in the cemetery is striking considering the male bias in the burials: only five of the 18 individuals analysed (28%) were female. The expectation, given this over-representation of males, would be an increased chance of capturing male lines of descent, but this does not seem to be the case at Worth Matravers. Admittedly, we must be cautious in interpreting the significance of this pattern as being due to matrilocality at Worth Matravers; both the sample size and the number of biological kinship connections are small and biased towards first-degree links, and there remain an additional eight individuals buried at the cemetery that were not analysed here. Nevertheless, Worth Matravers highlights the potential for in-depth analysis of uniparental markers, particularly when combined with autosomal biological kinship determination, to reveal the importance of both biological and social kinship in early mediaeval funerary practices.

## Whole-genome analysis and African ancestry

Analysis of genome-wide ancestry patterns at Worth Matravers reveals one clear genetic outlier: KD010 from double burial 1633 (Figures 2, 3 & S7). KD010 plots with seventh- to eleventh-century AD Guanches from the Canary Islands in a principal components analysis

(Figure 2; Rodríguez-Varela *et al.* 2017) and exhibits a substantial West African ancestry in ADMIXTURE analysis (in yellow on Figure 3, Table S4). KD010 carries the pan-European maternal lineage U5b1 and a paternal haplotype belonging to the E1b1b1a1–M78 haplogroup, which is consistent with West African ancestry. This combination of maternal and paternal lineage and genome-wide ancestry patterns is most likely the product of admixture between a European woman and a West African man at around the grandparent level. As this admixture was relatively recent, it is unlikely to represent a relic from the Roman period, but instead suggests an ongoing cosmopolitanism in the post-Roman period that was not limited to the influx of northern continental ancestry (as shown by the presence of the I1a2 Y-chromosome haplogroup; Table 3).

Despite his genetic differences, KD010 evidently received similar treatment in death to other individuals at the site and consumed a comparable diet during his lifetime (Figure S10). Notably, though, this individual was buried in a double burial (grave 1633) alongside an older adult male with local genetic ancestry (KD007, member of Family C), whose head was resting on a Purbeck limestone anchor (Figure S7). This type of headrest, although recognised from Romano-British and early medieval periods, is extremely rare, particularly in securely dated contexts (Bellamy & Trevarthen 2018). As there was no close biological kin relationship between KD010 and KD007, their double burial might suggest a possible work (such as apprentice and master) or social kin relationship. The presence of the anchor further suggests an association with the sea, its size implying use on either a small vessel or as one of multiple anchors on a larger boat. Both seafaring connections and local coastal fishing are demonstrated in this area and time period (Ladle 2018). Further discussion of the ancestry of KD010 can be found in the OSM (section 7).

The African ancestry exhibited by KD010 documents the genetic influence of geographically distant populations, as is also seen in the African ancestry of EAS003 from early Anglo-Saxon Updown (Sayer *et al.* 2025) and in the Middle Eastern ancestry of an individual (3DRIF-26) from Roman York (Martiniano *et al.* 2016). It has been suggested that the arrival of such geographically distant ancestry in England relates to the movement of West African gold, via Carthage, which was traded into Britain by the Roman and Byzantine Empires (Sayer *et al.* 2025). Indeed, the cosmopolitan impact of the Roman Empire does seem to re-emerge in post-Roman Britain following the Byzantine conquest of North Africa in AD 533–534, and the genetic heritage of both KD010 and EAS003 provide very human links to intercontinental exchange.

## Concluding remarks

Both biological and social kin relationships were a fundamental part of life in early medieval England. In examining genomic data from 20 individuals buried at Worth Matravers in Dorset, we identify the importance of both male and female relatives in the local community during the relatively short duration of cemetery use, perhaps hinting at a form of adaptive bilateral descent, where relations were traced through both the father and the mother (Murray 1983; Herlihy 1985). Many of the burials at the post-Roman Worth Matravers cemetery contained closely related males (Families C and D) but maternal relationships are also evidenced through shared mitochondrial haplotypes.

Detailed analysis of uniparental markers and autosomal kinship data at Worth Matravers shows that biological relationships informed the placement of burials, with family groups identifiable in the organisation of graves. Given this emphasis on the proximity of genetic kin in the cemetery, the inclusion of unrelated individuals in multiple burials potentially also highlights the importance of social kinship, or cultural perceptions of kinship. The diverse genetic heritage of the Worth Matravers individuals emphasises the cosmopolitan nature of England in the early medieval period, pointing to an integrated population with far-flung ancestral connections.

The transition from the Roman to early medieval period in Britain was complex and regionally varied. Together, the genetic and cultural evidence from Worth Matravers points to pluralistic family histories and social bonds that created and sustained this community. Such familial flexibility allowed this small, rural, coastal community to negotiate concepts of kinship and create new relationships during a time of considerable change, while the genetic lineages identified in the cemetery reveal how it was connected to the wider political and cultural worlds.

## Data availability

Newly generated sequencing reads for samples KD012 (ERS18231868) and CE050 (ERS18231869) have been deposited in the European Nucleotide Archive (https://www.ebi.ac.uk/ena), accession number PRJEB67644.

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## Online supplementary material (OSM)

To view supplementary material for this article, please visit https://doi.org/10.15184/aqy.2025.10133 and select the supplementary materials tab.

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