|  |  |
| --- | --- |
| A red circle with a white letterDescription automatically generated | Supplementary material for  Foody, M.G.B., K. Dulias, P. Justeau, P.W. Ditchfield, L. Ladle, J. Gretzinger, S. Schiffels, D. Reich, R. Kenyon, D. Sayer, M.B. Richards, M. Pala & C.J. Edwards. 2025. **Ancient genomes reveal cosmopolitan ancestry and maternal kinship patterns at post-Roman Worth Matravers, Dorset.** *Antiquity* 99.  Author for correspondence ✉ c.j.edwards@hud.ac.uk |

**Index:**

**SM1.** Worth Matravers 2

**SM2.** Radiocarbon dating 7

**SM3.** Dietary stable isotopic analysis 14

**SM4.** Genetic methodology and results 17

**SM5.** Sex determination and uniparental marker systems 20

**SM6.** Pedigree diagrams for Families A, B, C and D 24

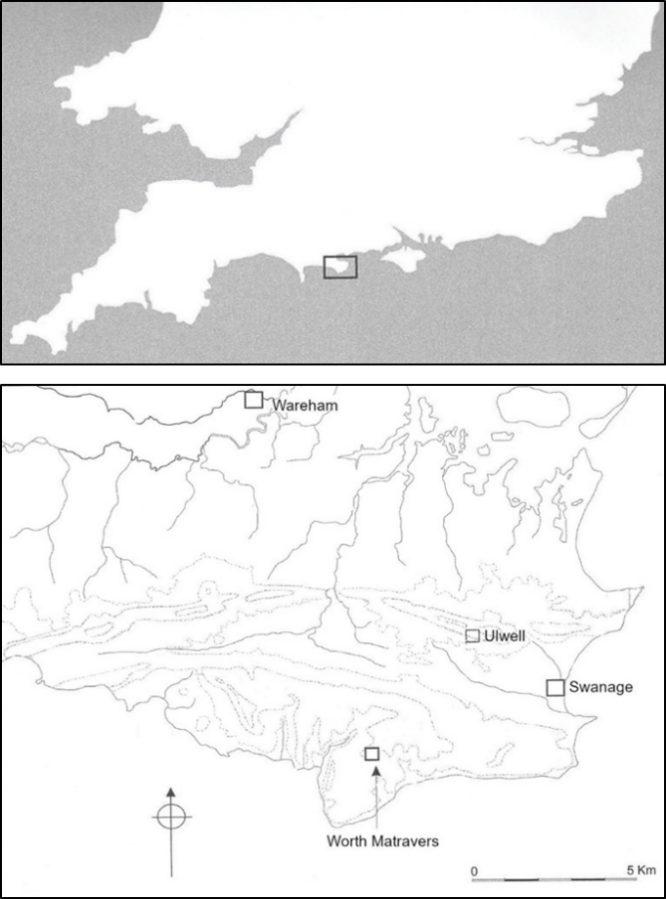
**SM7.** African ancestry of KD010 28

**SM8.** References 30

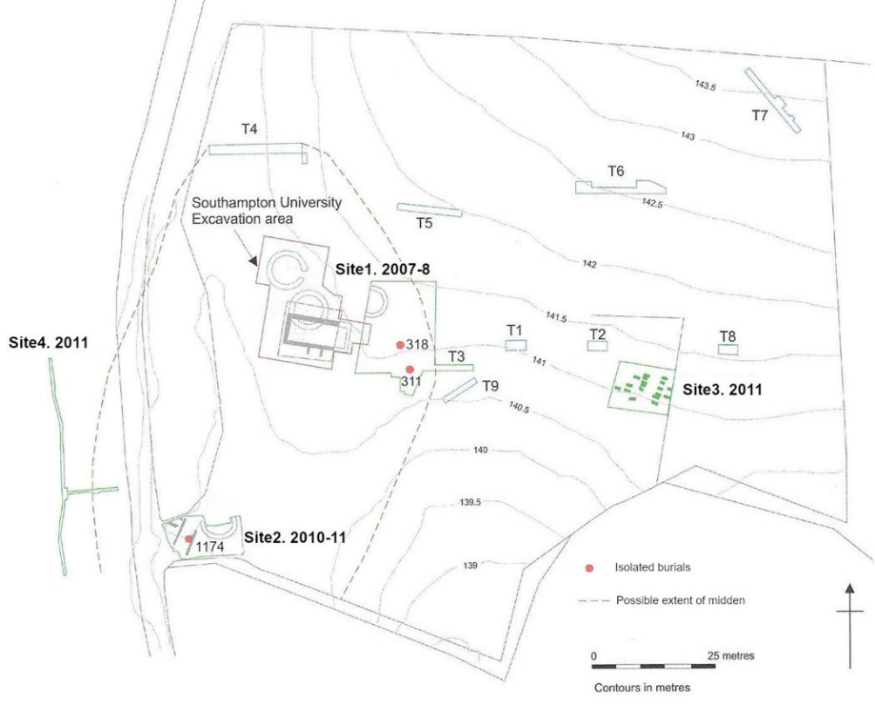
**SM1. Worth Matravers**

**SM1.1 The site of Worth Matravers**

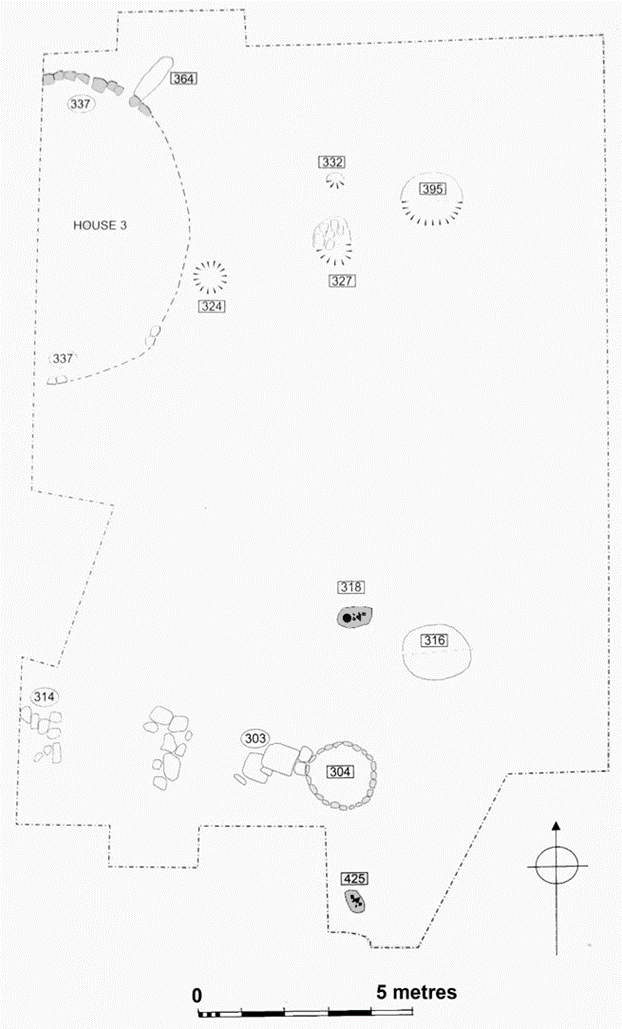
The site of Worth Matravers, on the Isle of Purbeck in Dorset (**Figure S1**), was excavated between 2007 and 2011 in four discrete interventions (Sites 1 to 4; **Figure S2**), with the results being published subsequently by Lilian Ladle in 2018. Located in south-east Dorset, ‘Football Field’ at Worth Matravers was occupied from the early fourth millennium BC to the sixth/seventh centuries AD. Earlier burials include disarticulated remains found in midden material deposited during the late Bronze Age/early Iron Age, and an adult female (#318, CE049), both from Site 1 (**Figure S3**). Nine infants (including #1174, CE050), and remains of at least 12 others, were located in a Roman barn at Site 2 (**Figure S4**), and the small post-Roman cemetery, consisting of 26 interments in 21 graves, was found at Site 3 (**Figure 1**).



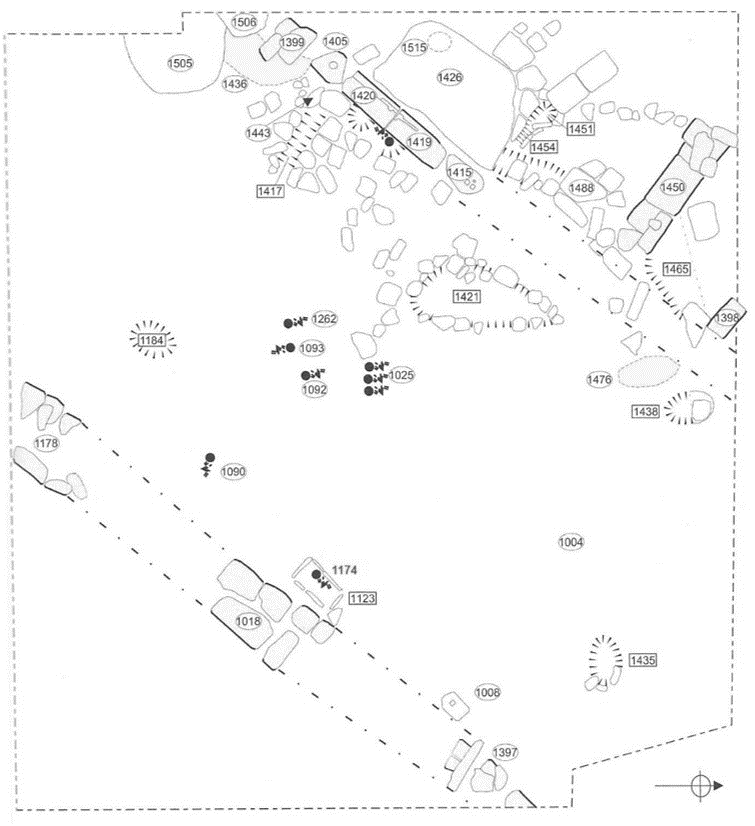
**Figure S1**. *Location of Worth Matravers in southern England and south-east Dorset. Contemporary sites at Ulwell (near Swanage) and Wareham are mentioned below (***SM1.2***). Modified from Ladle (2018).*



**Figure S2**. *Archaeological interventions undertaken at Worth Matravers between 2007 and 2011. The locations of the burials of the two Roman individuals analysed for this study are shown in red: CE049 (#318 at Site 1) and CE050 (#1174 at Site 2). The remaining isolated burial (#311 at Site 1) was radiocarbon dated by Krus (2018) and is discussed below (***SM2.1***). The post-Roman cemetery can be seen at Site 3. Modified from Ladle (2018).*



**Figure S3**. *Site 1 plan, showing late Iron Age features and the locations of the Roman adult #318 (CE049) analysed as part of this study, and Grave 425 (Sk.311; at the bottom of the plan), which was radiocarbon dated by Krus (2018) and discussed in* **SM2.1***. Modified from Ladle (2018).*



**Figure S4**. *Site 2 plan, showing the late Roman barn and the location of the nine infants, including the cist burial infant #1174 (CE050). Modified from Ladle (2018).*

The post-Roman cemetery at Worth Matravers was in use during the early medieval period, with calibrated radiocarbon dates varying from the early fifth to late eighth century AD (Krus 2018). This dedicated burial ground was, in all likelihood, associated with a small rural community located to the south of the site, probably in the vicinity of the present-day parish church. A number of graves incorporated limestone roofing tiles, recovered from nearby abandoned late Roman barns. Christian burial rites were apparent in the arrangement of east-west aligned graves and the paucity of grave goods, with only two grave goods found: a small copper alloy buckle buried with male KD012 in Grave 1667, and a rare find of a limestone anchor (Object SF 517), which had been used as a headrest for KD007, the adult male in double burial 1633. In contrast to the furnished graves that are often linked to Anglo-Saxon inhumations (Hills 2009), this lack of grave goods is consistent with other post-Roman/early medieval cemeteries from the west of Britain (Ladle 2018).

The excavated graves were arranged into six rows (**Table S1**) and the bodies were mainly oriented in an east-west direction, with individuals placed with their heads in a westward direction (**Figure 1**). The inhumations were adults, apart from a single child and three adolescents. An unusual feature of this cemetery was the high frequency of multiple interments in the same grave (four of the 21 graves excavated were multiple burials, with Graves 1633, 1678 and 1722 being double burials, and Grave 1685 holding three individuals). Worth Matravers is a well organised site, suggesting that these multiple graves were not the result of accidental placement.

Seven grave types were observed in the cemetery from simple earth-cut to complex cist-type burials (Ladle 2018; **Table S1**). Non-metric traits, such as the identification of septal apertures in the olecranon fossa of the humeri of KD016 and KD018 (Randall 2018), may be indicative of kinship within the site. Although the underlying cause of septal apertures is unknown (Myszka 2015), KD016 and KD018 were found to be first-degree related genetically (Family B; see main text and **SM6.2**).

**SM1.2 Regional and national contexts**

In Dorset, similar dated cemeteries are located at Ulwell near Swanage (Cox 1988; **Figure S1**), and at Tolpuddle Ball, east of Dorchester (Hearne & Birbeck 1999). These sites fit a growing list of similar cemeteries in Dorset, Somerset, Gloucestershire and Cornwall, which are characterised by rows of east-west burials, and a lack of coffins and grave goods. At the large early fourth to early eighth centuries AD cemeteries of Cannington in Somerset (Rahtz *et al*. 2000), and Poundbury in Dorchester (Farwell & Molleson 1993), the customs of the late Roman period were continued, although there is also evidence of increasingly non-Christian practices. The ‘West Country’ influence is also noticeable at Wareham in Dorset (Hinton 1992; **Figure S1**), where a monastic community was established in the post-Roman period. Five memorial stones survive commemorating individuals with British Celtic, Old Welsh, Hebrew and Latin names, suggestive of an indigenous and heterogeneous population. The nearest cemetery to Worth Matravers with any known Germanic influence is Christchurch in east Dorset (Jarvis 1983), where sixth and seventh century AD cremations and burials were accompanied by weapons.

The presence at Worth Matravers of an extensive unstratified midden site (Site 1; **SM1.1**) containing bronze work manufactured in Brittany, and glass from central Europe, supports a link to mainland Europe. This midden would have accumulated over several centuries during the late Bronze Age to early Iron Age transition, and these types of site were often used as 'gathering and meeting places' where exchange of local and exotic items and other commodities took place at regular intervals. There is also evidence from the extensive pottery assemblages at Worth Matravers of Continental influence from eastern France and western Germany (Ladle 2018).

**Table S1.** *Further details about the twenty Worth Matravers samples including, for the post-Roman cemetery (Site 3), the grave type, alignment and location (Row #) as discussed in Ladle (2018) and shown in* **Figure 1***. Additional information from Ladle (2018) is also included, with details of pathology taken from Randall (2018), including the finding of septal apertures in the humeri of the first-degree related individuals KD016 and KD018 (Family B;* **Table 3***).*



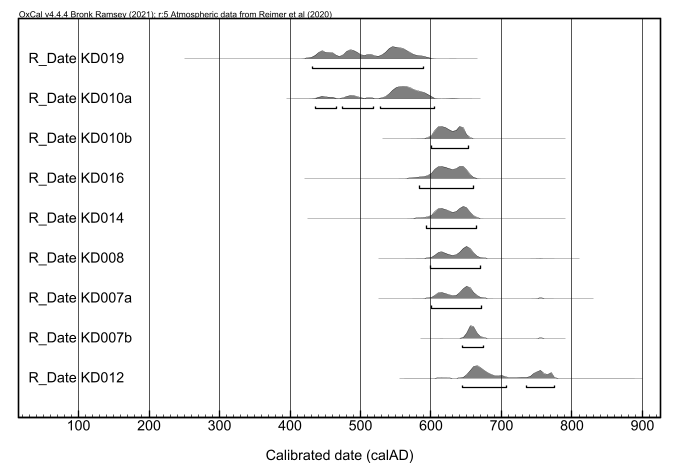
**SM2. Radiocarbon dating**

**SM2.1 Calibration of individuals from the post-Roman cemetery**

Previous radiocarbon dates were available for six of the post-Roman individuals from the cemetery (Site 3) – KD007, KD008, KD012, KD014, KD016 and KD019 (Krus 2018; **Figure S5**, **Table S2**). In addition, three further dates had been generated previously from Worth Matravers. Krus (2018) dated an adult female from Site 1 (Sk.311, Grave 425; **Figures S1**, **S3**). Although her date (1385 ± 31; SUERC-61172) was coeval with the age of the post-Roman cemetery, we did not include this individual in any analyses as her isolated burial was situated 30 metres west of the cemetery site. Also, CE049, a crouched female adult buried near a Late Iron Age pit (#318, Site 1; **Figures S1**, **S3**), previously described as buried in a typical Durotrigan position (Randall 2018), was dated as part of the ERC-funded *COMMIOS* project at the University of York. Although not of Iron Age date (1883 ± 24; SUERC-104571), she was from the Roman period, so again was discounted from the cemetery calculations. We also dated two molar teeth from individual KD010; one at 14Chrono (the radiocarbon dating lab at Queen’s University Belfast), and the other at the Oxford Radiocarbon Accelerator Unit (ORAU), and re-dated a left femur from KD007 at ORAU.

We calibrated all dates in cal. AD using OxCal version 4.4.4 (Bronk Ramsey 2009) and the most recent calibration curve, IntCal20 (Reimer *et al*. 2020) (**Figure S5**, **Table S2**). As mentioned in the main text, the previous calibration of samples from Worth Matravers included a small marine reservoir correction (Krus 2018). The rationale for this was based on comparison of the human skeletal carbon isotopic values to a rather restricted approximate range for fully terrestrial C3-based human diets, with 13C values of –23 to –20‰ (Mays 1988: 186). This range does not cover the full extent of variation seen in terrestrial C3 based ecosystems, nor does it allow for the effects of trophic level enrichment in 13C values, such as might be encountered in longer food webs, or in human diets where consumption of protein from omnivores, such as pigs that may be partly fed on human waste, has to be accounted for.

Similarly, the amount of marine reservoir correction applied by Krus (2018) was determined using a mixing model, where the end members were defined by 13C values of –12.5‰ for fully marine and –21.0‰ for fully terrestrial diets. The use of a value of –21.0‰ for a fully terrestrial end member results in calculated percentages of marine input into the diet that range from 12 to 20% (Krus 2018: tab. 43), which may represent a significant over-estimate of the amount of marine input into the human diet. In the absence of a local faunal stable isotopic base line that could be used to accurately assess what the true value of a local fully terrestrial signal would be, it is impossible to say, if any, what the true proportion of marine input into the diet was. Therefore, in the absence of this crucial evidence, we feel that it is safer not to apply any marine reservoir correction to these dates.

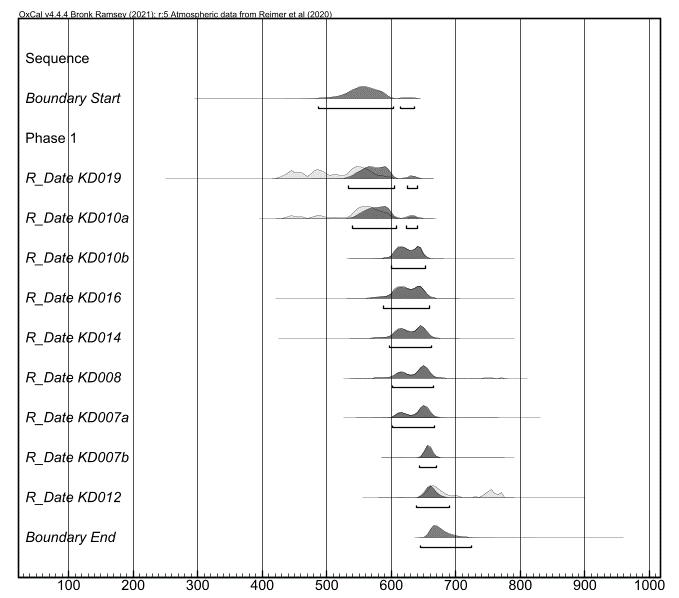


**Figure S5**. *Calibrated radiocarbon dates from the post-Roman cemetery at Worth Matravers, with repeat dates for KD007 and KD010 shown (see* **Table S2** *for details).*

**Table S2**. *Radiocarbon dates from seven post-Roman individuals from the post-Roman cemetery at Site 3 (Krus 2018, with KD007 re-dated and KD010 dated twice as part of this study), an adult female from Site 1 (Sk.311; Krus 2018) and one of the two Roman samples (also from Site 1; undertaken as part of the ERC-funded* COMMIOS *project at the University of York), with details of element sampled and associated radiocarbon lab codes. Calibration was undertaken using OxCal version 4.4.4 (Bronk Ramsey 2009) and the most recent calibration curve, IntCal20 (Reimer* et al*. 2020).*



By using the nine post-Roman dates from the cemetery site (**Table S2**) and the Span function in OxCal, we found that the cemetery was in use for between 40 and 215 years (95%), or between 75 and 120 years (68%). This is a similar range to that calculated by Krus (2018; 1–220 years span at 95% probability and 1–100 years at 68% probability). However, due to not including a marine correction, we found that the cemetery started to be used around 490–630 cal. AD and fell into disuse sometime between 650 and 725 cal. AD (both at 95%; **Figure S6**).



**Figure S6**. *Span of dates at the post-Roman cemetery at Worth Matravers. The* x*-axis shows the calibrated AD date.*

It is worth pointing out that the phase model, and thus the putative duration of the cemetery, will have been affected by the need to accommodate the unusually high relative ages of KD010a and KD019 (435–605 and 430–590 cal. AD respectively; **Table S2**), which catch the calibration curve plateau that occurs at around 420–530 cal. AD (Krol *et al*. 2020).

**SM2.2 Analysis of radiocarbon dates of KD007 and KD010 from Grave 1633**

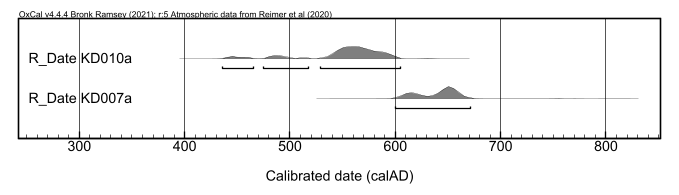
According to the site report (Ladle 2018), Grave 1633 was the first to be discovered at the site, at the east side of the cemetery, being identified initially by the presence of the skull of KD007 (skeleton 1632) uncovered during the topsoil strip. The positioning of the bones suggested that two bodies had been placed in the grave together, with KD010 (skeleton 1652) being placed first. KD010 was very close to KD007, and the lower part of his left arm rested in the pelvic area of KD007 (**Figure S7**).

Diagram

Description automatically generated

**Figure S7**. *Photograph and schematic plan of the two skeletons in Grave 1633 (taken from Ladle 2018). Skeleton 1632 (KD007) was an adult male and Skeleton 1652 (KD010) was an adolescent male.*

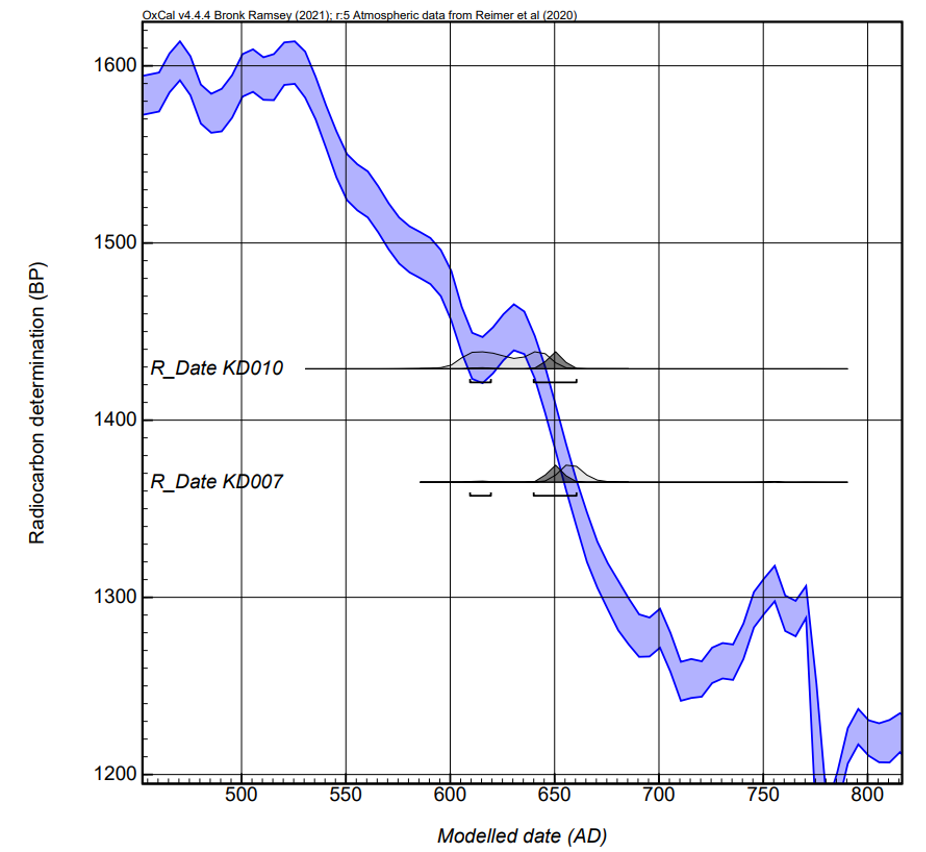
We originally had only one radiocarbon date from Grave 1633, from KD007, which had been undertaken by SUERC (Krus 2018). In order to investigate the connection between KD007 and its grave companion, KD010, who carried African genetic ancestry, we sent an upper molar tooth to 14Chrono, the radiocarbon dating lab at Queen’s University Belfast. While the 17–25 years-old male (KD010) was dated to 435–605 cal. AD (UBA-43717), the adult male (KD007), who was buried with his head resting on a stone anchor, was dated to 600–670 cal. AD (SUERC-61178) (**Figure S8**, **Table S2**).

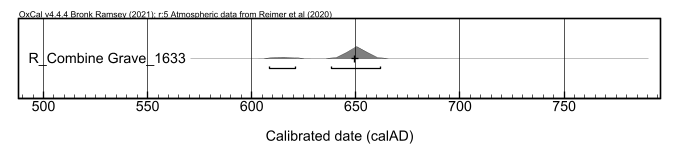


**Figure S8**. *Calibration of the original two radiocarbon dates for the individuals buried in Grave 1633, using OxCal v4.4.4 (Bronk Ramsey 2009) and IntCal20 (Reimer* et al*. 2020).*

As there was very little overlap in the two calibrated dates, and despite the KD010a date covering part of the calibration plateau, we wanted to double-check the statistical likelihood that these two individuals were buried at the same time, and so performed a chi-squared test using the R combine function in OxCal (Bronk Ramsay 2009). The two dates were not statistically the same (*T* = 10.3, greater than the required <3.8 required at the 5% level), suggesting that the young male KD010 was interred first, and then the grave was reopened for the burial of adult male KD007. While this was possible (as the grave was a plain earth-cut burial, which would be easier to enlarge and reuse at a later date, leaving little archaeological trace), this seems implausible given the orientation of the individuals within the grave (**Figure S7**). As the two dates were undertaken in different radiocarbon labs (SUERC and UBA), using slightly different methods, we dated both individuals again at ORAU (a portion of femur from KD007 and a lower molar tooth from KD010), in the same batch, and with the same preparation methods.

The new dates from ORAU are shown in **Table S2** as KD007b and KD010b. For each individual, we first tried to combine the two dates using the R combine function in OxCal. The results from KD007 (SUERC-61178 and OxA-43400) gave a date range of 645–670 cal. AD. However, although the two dates from KD010 (UBA-43717 and OxA-43401) combined to give a range of 580–645 cal. AD, they only combined at a 60% confidence limit and were not statistically the same (*T* = 8.5, greater than the required <3.8 required at the 5% level). Again, as mentioned earlier, this was most likely due to the plateau seen in the calibration curve around 420–530 cal. AD (Krol *et al*. 2020), which caused KD010a to have a large overall calibrated date (**Figure S9a**). As it is not possible to discount KD010a as an outlier (as the date is similar to that of KD019), when we compared the two individuals in the double burial to determine whether they were buried contemporaneously, we chose to only include the two dates generated by ORAU (OxA-43400 and OxA-43401) as they were generated at the same time, in the same lab and using the same techniques. The calculated date range for Grave 1633 was between 610–620 (10%) and 640–660 (86%) cal. AD, with a median age of 650 cal. AD (**Figure S9b**).

**(**a**)

**(**b**)

**Figure S9**. (**a**) *Plot showing the position of KD007 (OxA-43400) and KD010 (OxA-43401) on the calibration curve. The wiggle in the curve under KD010 is clearly visible.* (**b**) *The combined date for the two individuals buried in Grave 1633, showing a tight correlation pointing towards a contemporaneous burial at around 650 cal. AD. Both plots were generated using OxCal v4.4.4 (Bronk Ramsey 2009) and IntCal20 (Reimer* et al*. 2020), and we chose to only use the dates generated at ORAU, for the reasons described in the text above.*

**SM3. Dietary stable isotopic analysis**

We undertook dietary stable isotope analysis following the protocol outlined in Cole *et al*. (2020). The 13C ranged from –20.26 to –19.07 and 15N ranged from 8.49 to 11.07 (**Figure S10**, **Table S3**). The lack of any faunal dietary isotopic base line for this site makes the human dietary interpretation somewhat problematic, and the quantification of any potential minor marine protein component to the human diet impossible. However, at a broad scale, all individuals showed evidence for a C3-based, terrestrial-dependent diet, lacking any indication of significant marine protein in their diet. This is slightly unexpected given the proximity to the coast, and the remains of marine fauna, fish and shellfish that have previously been reported (Ladle 2018). While it is possible that there may have been a very minor marine component in the diet, in the absence of any faunal base line for comparison, any such possibility remains untestable. This has important implications for the radiocarbon dating that has been carried out both here and in previous studies of this assemblage (Krus 2018; **SM2**).

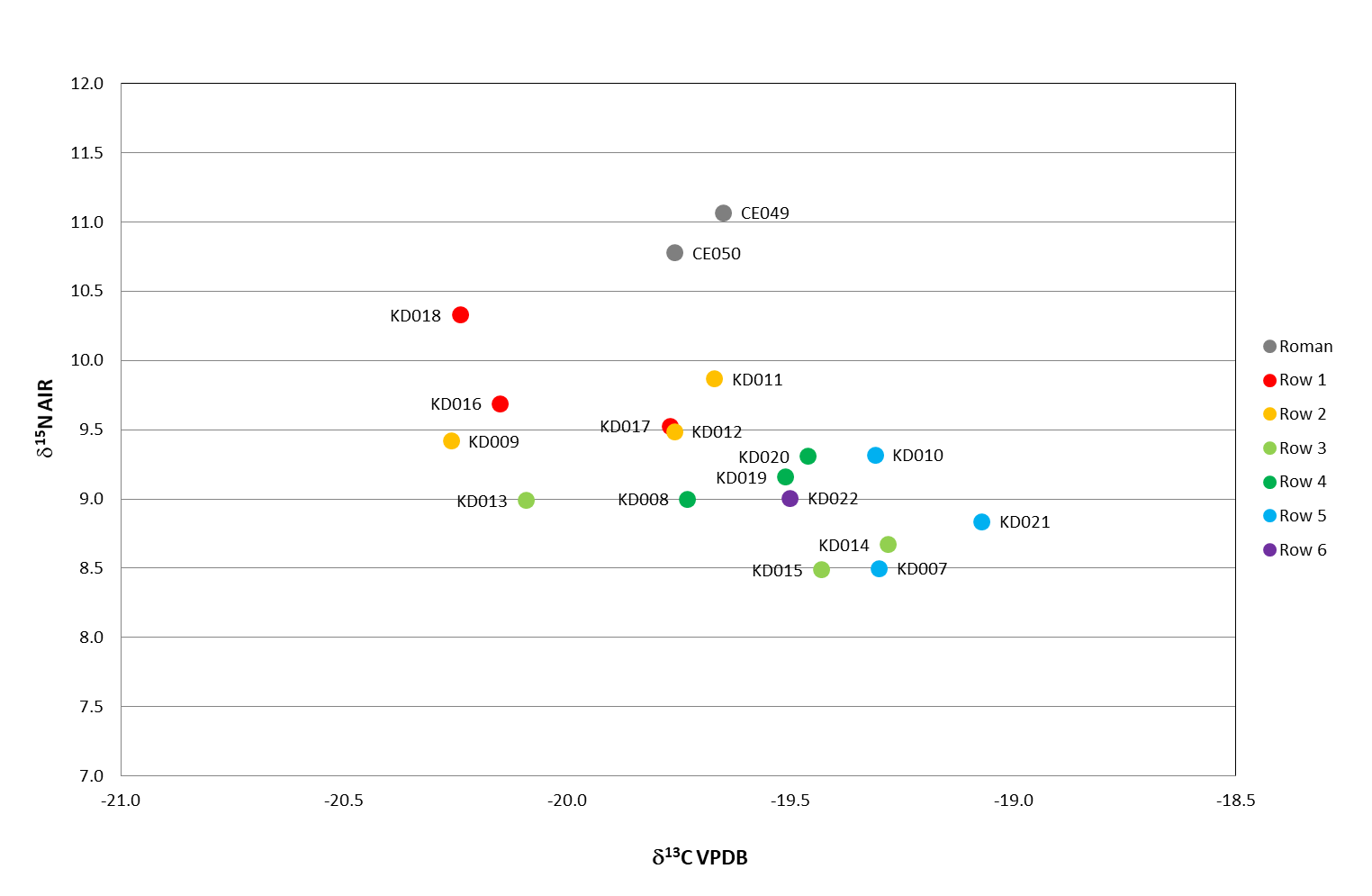
Although the two Roman individuals showed the highest nitrogen levels on the site, their carbon values fell within the range of the post-Roman samples. While this difference may potentially be a result of increased aquatic protein resource consumption, it could also be due to different agricultural practises between the Roman and post-Roman communities. However, it should be noted that one of these individuals (CE050) was an infant, aged 5 to 7 months, and her elevated 15N value was most likely due to a breast-feeding signal.

Amongst the post-Roman population, no dietary pattern could be attributed to sex or grave type (**Table S3**). However, there did appear to be a weak association dependent on burial position within the cemetery, with those buried closest to the west of the cemetery having slightly higher nitrogen and slightly lower carbon values. This suggested that these people were eating a more protein-rich diet, which might indicate a higher social standing.

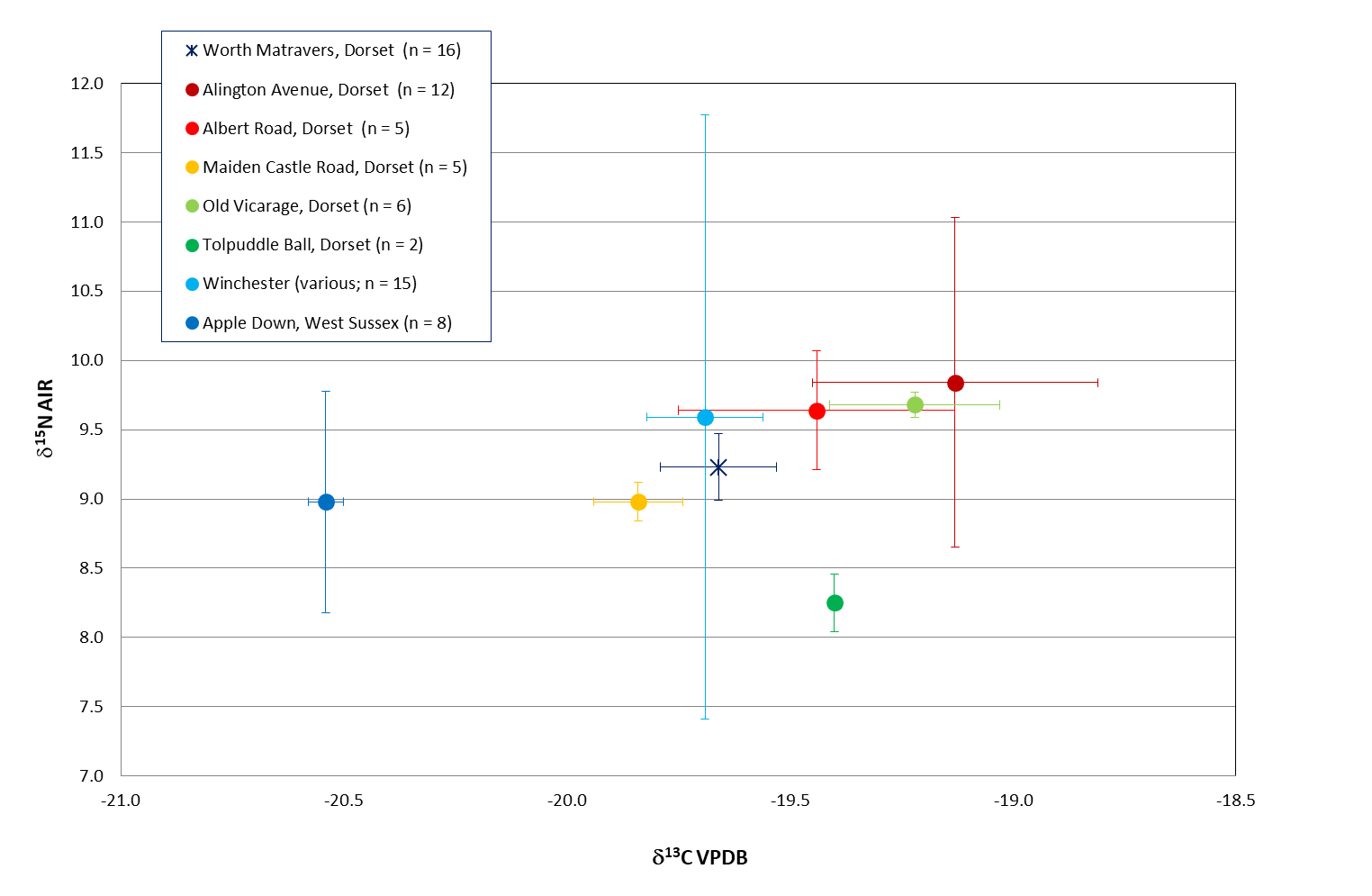
We compared the dietary stable isotopes of the individuals to five Romano-British sites dating to the third and fourth centuries AD from Dorset (Redfern *et al.* 2010), several late Roman sites dating to the late third to early fifth centuries AD from Winchester (Bonsall & Pickard 2015), and comparison data from the contemporaneous mid-fifth to late seventh century cemetery site of Apple Down, West Sussex (Beavan & Mays 2013; unpublished data). The post-Roman Worth Matravers individuals were very similar to populations from more inland locations, such as Albert Road, Maiden Castle Road, and Winchester, and thus probably had a comparable protein component in their diet. This contrasts strongly with the isotopic dietary evidence from Apple Down, where individuals exhibited a much lower 13C value (**Figure S11**).

**Table S3**. *Stable isotopic values generated as part of this study, apart from KD007 determined during radiocarbon dating at SUERC (Krus 2018). For ease of comparison, the age, sex and grave type information for each individual is included from* **Tables 1, 2 & S1***.*





**Figure S10**. *Dietary stable isotope analysis for the post-Roman individuals. The plot shows the differences in diet compared to the burial position in the cemetery (as noted in* **Table S1***). The two Roman individuals (CE049 from Site 1 and CE050 from Site 2) are noted.*



**Figure S11**. *The overall diet of the post-Roman population from Site 3 at Worth Matravers, compared to Roman individuals from other sites in Dorset (Redfern* et al*. 2010; Alington Avenue, Albert Road and Old Vicarage in Dorset are all located near Dorchester) and Winchester (Bonsall & Pickard 2015), alongside comparison data from the contemporaneous site at Apple Down, West Sussex (Beavan & Mays 2013; unpublished data).*

**SM4. Genetic methodology and results**

**SM4.1 DNA extraction, library preparation and sequencing**

We undertook sampling for DNA extraction at the Ancient DNA Facility at the University of Huddersfield, using dedicated clean-room conditions as described in Dulias *et al*. (2019). We prepared single-stranded uracil-DNA glycosylase (UDG) treated libraries for sequencing at the Harvard Medical School using the method described in Gansauge *et al*. (2020). We enriched the libraries simultaneously for autosomal sequences overlapping ~1240k SNPs (Fu *et al*. 2015) and the mitochondrial genome (Fu *et al*. 2013), and then sequenced the captured libraries on a HiSeqX10 instrument for 2×101 cycles using paired-end reads of 101bp in length.

**SM4.2 Genetic data processing and analysis**

After trimming barcodes and adapters (Haak *et al*. 2015), we processed the raw data bam files as detailed in Patterson *et al*. (2022), and undertook primary DNA read processing and sex determination as described in Dulias *et al*. (2022). We assigned mitochondrial and Y-chromosome haplogroups (**Table 3**), classifying them as either ‘British Local’ (sharing haplotypes with Bronze and Iron Age individuals from the British Isles), ‘Continental (North Sea)’ (sharing haplotypes with individuals from the Bronze Age, Iron Age, and early medieval North Sea region) or ‘France’ (sharing haplotypes with individuals from the Iron Age in this region).

lcMLkin (Lipatov *et al*. 2015) was used previously by Gretzinger *et al*. (2022), to look for relatedness among individuals, with identical results to the READ program (Kuhn *et al*. 2018). However, here we used READv2 analysis (*https://github.com/GuntherLab/READv2*) to look for relatedness among our individuals at Worth Matravers (**Table 3**). In addition, we tried to implement the KIN (Popli *et al*. 2023) and ancIBD (Ringbauer *et al*. 2024) programs to further investigate kinship. KIN has a cut-off at 0.05x coverage, so we were only able to analyse 11 of the 18 individuals. All possible combinations produced log-likelihood values of less than 1, which the program guidelines state are too low for reliable interpretation. ancIBD requires at least 0.25x average coverage depth for WGS data, plus 1.0x depth on dense target SNPs (corresponding broadly to at least 600k SNPs covered for 1240k captured aDNA data). Unfortunately, only four of our samples (KD009, KD011, KD019 and PJ007) had coverage ≥0.25x, and so it was not possible to run this program either.

We reassessed all samples analysed by Gretzinger *et al*. (2022), except KD015 as the autosomal coverage was too low (0.01X; **Table 2**). We combined these with other relevant ancient samples and either the Affymetrix Human Origins modern SNP genotyping dataset (Lazaridis *et al*. 2016), or super-populations taken from the 1000 Genomes Project (1000 Genomes Project Consortium 2015): GBR/EUR (European), AFR (African), EAS (East Asian), and SAS (South Asian). Following the methods detailed in Dulias *et al*. (2022), we constructed a Principal Component Analysis plot using smartpca of the EIGENSOFT package (Patterson *et al*. 2006; Price *et al*. 2006), including modern West Eurasian and North/West African populations (**Figure 2**). We also ran an unsupervised ADMIXTURE (Alexander *et al*. 2009) for *K* = 2 to *K* = 15, selecting *K* = 8 as it had the lowest CV error (**Figure 3**, **Table S4**).

**S4.3 Whole-genome results**

In general, as can be seen in **Figure 2**, most of the individuals from early medieval England were relatively similar, with no clear divide between groups at this level (although see Gretzinger *et al*. 2022 for a more fine-grained analysis). The exception was KD010, which was a clear outlier, as discussed below (**SM7**) and in the main text. The Worth Matravers Roman samples plotted similarly to those from the early medieval period, and there was an overlap between the post-Roman individuals and populations from across Europe. In all tests with the 1000 Genomes Project super-populations, the post-Roman Worth Matravers samples had more than 90% GBR/EUR ancestry, with the exception of KD010, which showed ~25% AFR ancestry. Our unsupervised ADMIXTURE highlighted the genetic homogeneity, comprising three main components maximised in western hunter-gatherers (WHG, blue), early European farmers (EEF, green) and Caucasus hunter-gatherers (CHG, red) (**Figure 3**, **Table S4**).

**Table S4**. *Unsupervised ADMIXTURE estimates for* K *= 8, with the percentage of the genome that can be designated as coming from WHG (western European hunter-gatherer), EEF (early European farmer), CHG (Caucasus hunter-gatherer) or AFR (West African) ancestry (as shown diagrammatically in* **Figure 3***). The ‘other’ four ancestry components have been added together as they were most likely artefacts due to the degraded nature of the ancient sample data. KD015 was excluded from the calculation due to low coverage (<10k SNPs;* **Table 2***).*



**SM5. Sex determination and uniparental marker systems**

**SM5.1 Genetic sexing of individuals from Worth Matravers**

We assigned genetic sex to all 20 individuals. The two Roman individuals (CE049 and CE050) were both female, while the post-Roman cemetery (Site 3) included 13 males and five females (**Table 3**). Significantly, and most likely due to the poor skeletal preservation at the site, five skeletons from the cemetery (KD008, KD012, KD013, KD021 and KD022) had been morphologically identified as female (Randall 2018) but were, in fact, genetically male. Of the three double burials, both Grave 1633 (KD007 and KD010) and Grave 1722 (KD021 and PJ007) contained two males. The triple burial 1685 contained two males (KD017 and KD018) and one female (KD016). Double burial 1678 contained one male (KD014) and one female (KD015).

**SM5.2 Male line of descent**

Using both Yleaf (Ralf *et al*. 2018) and pathPhynder (Martiniano *et al*. 2022) software packages, we identified 13 Y-chromosome lineages at Worth Matravers, all from the post-Roman cemetery (Site 3). Nine belonged to various R1b–M269 subclades, two to I1a2b–S296.1, one to I2a1a2a–L161.1, and one to E1b1b1a1–M78. A full list of all derived predictive markers can be found in the separate online file **Table S5**.

From previously published studies (Martiniano *et al*. 2016; Schiffels *et al*. 2016; Olalde *et al*. 2018; Patterson *et al*. 2022), British Middle/Late Bronze Age (MLBA), Iron Age, and Roman males carried overwhelmingly the major Y-chromosome haplogroup R1b–M269 (175/193 or 90.7%). The remainder comprised G2a2–CTS4367 (5/193 or 2.6%), I2a1–L460 (10/193 or 5.2%), or solitary I1–M253 and J2b–M12 lineages, likely the result of individual arrivals in the Iron Age and Roman period respectively (Martiniano *et al*. 2016; Patterson *et al*. 2022).

The two I1a2b–S296.1 lineages at Worth Matravers (seen in the related individuals, KD008 and PJ007 from Family C; **Table 3 & S5**) matched those seen at several cemeteries in England (Gretzinger *et al*. 2022), and the immediate ancestor, I1a2–S244/Z58, has been found in medieval cemeteries in both England and Germany. The sibling lineage, I1a2a–S246/Z59, and its descendants, have also been seen at many cemeteries in England, medieval Germany, an Iron Age site in Denmark, and in numerous early Viking burials in Scandinavia and the Baltic. This pointed to a clear North Sea/Germanic influence at Worth Matravers. The male line of descent at Worth Matravers indicated at least 15.3% (2/13) ancestry from the medieval North Sea region (**Table 3**); a higher fraction than the <6% CNE (central-northern European) fraction estimated for genome-wide ancestry by Gretzinger *et al*. (2022).

I2a1a2a–L161.1 (seen in KD021) was widespread in Neolithic Europe, but much rarer subsequently. Although there is no direct match to published data, this subclade was common in Britain and Ireland in the Neolithic, and the lineage at Worth Matravers, therefore, most likely derived ultimately from earlier populations in Britain.

The source of the lineages belonging to R1b–M269 was more difficult to determine, since this lineage was very widely distributed across western Europe in the Bronze Age. Its presence in the post-Roman males at Worth Matravers might be plausibly attributed to a local descent, although it is possible that it arrived from a source attributed to Iron Age France (as seen in autosomal analysis undertaken by Gretzinger *et al*. 2022). Four of the males could be classified only as R1b1a1b–M269 (individuals KD007 and PJ006) or its ancestor R1b1a1–P297 (in KD012 and KD022), and four as R1b1a1b1a1–L52 (in KD013, KD014, KD017 and KD018) (**Table 3**). Although the coverage was poor, with presence of the derived S521 marker (also known as CTS241 or DF13), KD020 could be classified as R1b1a1b1a1a2c1a-CTS241 (**Table S5**). CTS241 falls within the local British S461–L21 subclade of R1b–M269, which encompasses most of the British post-Beaker Complex males.

So, with the exception of KD007 (R1b1a1b–M269), all of the other R1b-M269 lineages at Worth Matravers could be assumed to be R1b1a1b1a1–L52 (or one of its descendants), even poorly resolved KD012 and PJ006, as these individuals were brothers of KD014, which had the L52 haplogroup. The R1b1a1b1a1–L52 lineage, therefore, represented at least 61.5% (8/13) of male lineages at the site, which could be the signal of a founder common paternal ancestor for the community.

The E1b1b1a1–M78 seen in KD010 is discussed in the context of genome-wide data below (**SM7**).

Overall, the male lineages seen at post-Roman Worth Matravers suggest that the male gene pool was extremely diverse and testifies not only to local ancestry, but also to multiple sources of ancestry that may have extended from France to Scandinavia, via the North Sea coast, and even West Africa – albeit quite possibly indirectly, since the appearance of the African ancestry on a European background goes back several generations. This corroborates the genome-wide picture, which suggested at least four distinct sources of ancestry: local British (WBI), Continental west European (CWE) and Continental North Sea European (CNE), as determined by Gretzinger *et al*. (2022), as well as West African.

**SM5.3 Female line of descent**

This pattern of high diversity was mirrored in the female line of descent, which was analysed by tracking the mitochondrial DNA (mtDNA). The 20 individuals from Worth Matravers carried 12 mitochondrial lineages (**Table 3**) and 14 unique haplotypes (**Table S6**). If we take into consideration the kinship data, and count each lineage shared by descent along the female line as one occurrence, then the 18 post-Roman individuals (from Site 3) carry 10 mitochondrial haplogroups and 12 unique haplotypes. Notably, all first- and second-degree relationships (ten relations, or six if we count relations involving multiple siblings as one occurrence) identified across the post-Roman cemetery involved the sharing of mitochondrial lineages, with only one exception – individuals KD008 and PJ007 from Family C, who are related along the paternal line of descent (**Figure 1**, **Table 3**). This suggested that close kin were almost exclusively associated with maternal connections.

As mentioned briefly in the main text, although the two individuals from Family B, KD016 and KD018, had the same mitochondrial haplogroup, H1bb (**Table 3**), and shared a first-degree relationship (either siblings or mother–son), we found a single unique mutation at the fast position 189 in KD018 (**Table S6**). Whereas KD016 had 39 calls of A at this position, KD018 had 11 calls of A and 44 calls of G. As in Dulias *et al*. (2022), we considered mutations with a read frequency of ≥0.7 as true variants, and positions as heteroplasmic only if the allele frequency was >0.3 or <0.7, and, therefore, the base call for KD018 was 189G. Although directly related individuals along the maternal line of descent are expected to share the exact same haplotype, it is possible, albeit rare, that they can differ by one nucleotide position, more commonly in the fast-evolving control region (Soares *et al*. 2009), particularly if the ancestral line was characterised by germline heteroplasmy (Stewart & Chinnery 2015).

To investigate the possible origin of the mitochondrial lineages seen at Worth Matravers, we followed the approach outlined in Supplementary Note 2 in Gretzinger *et al*. (2022), but also took into account Continental western Europe (France) as a potential source. We also analysed an additional genome, KD012, not included in that dataset. The two Romano-British individuals (both female) had local British maternal ancestry, but there was no evidence for continuity between these individuals’ maternal lineages and those of the post-Roman burials. The majority of the latter (66.7% of lineages; 12/18) were most likely local, but a smaller fraction (~30–40%) were likely from a Continental North Sea (CNE) source, and a possible 0–10% had ancestry that arrived with the French Iron Age (CWE) genome-wide ancestry component. So, despite the predominance of local ancestry, the maternal lineages, like the male lineages and genome-wide ancestry, appeared to have diverse origins, implying arrival from various Continental sources of both men and women.

**Table S6**. *Mitochondrial haplotypes for the 20 Worth Matravers individuals, with personal variants in bold, and reversions denoted with @ sign. Maternally-related individuals are highlighted with the same colour codes as used in* **Figure 1***, with more details in the main text and* **Table 3***.*



**SM6. Pedigree diagrams for Families A, B, C and D**

READv2 analysis showed the presence of four family units, A, B, C and D. These are discussed in the main text, but are shown here as graphical pedigrees. In each figure, an inset picture shows the location of the individuals in the cemetery, and mitochondrial haplotypes are shown in red text and Y-chromosome haplogroups in blue text.

**SM6.1 Family A**

We found that KD009 (a 25–35 years-old female, buried in Grave 1649) and KD020 (an adult male, buried in Grave 1715) were first-degree related. They shared a unique T2a1a mitochondrial haplotype with two personal variants 297G and 8470G (**Table S6**) and so were maternally related. Both were third-degree related to the other individual with haplogroup T2a1a, KD022 (a 16–17 years-old male, buried in Grave 1778). However, KD022 had a different haplotype (with mutations 152C, 310C and 15712G; **Table S6**), so there was no direct connection along the maternal line of descent. We also found a third-degree link between KD020 and KD011 (a 35–45 years-old female, Grave 1664), but no corresponding link between KD009 and KD011. These relationships can be explained if KD022 was a paternal first cousin to siblings KD009 and KD022, and KD011 was KD020’s great-granddaughter (**Figure S12**).

It should be noted that, for this pedigree to be correct, there would have to be at least 100 years between the burial of KD020 and his great-granddaughter, KD011, which is the most likely span of use for the cemetery. However, as detailed in **SM2**, the cemetery most likely started to be used around 490–630 cal. AD and fell into disuse sometime between 650 and 725 cal. AD, a span of >200 years, so this scenario may be plausible.

A group of bodies

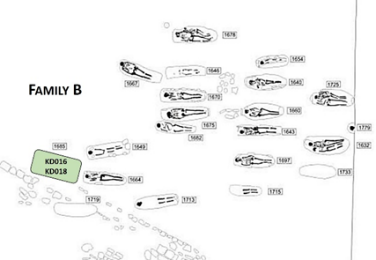
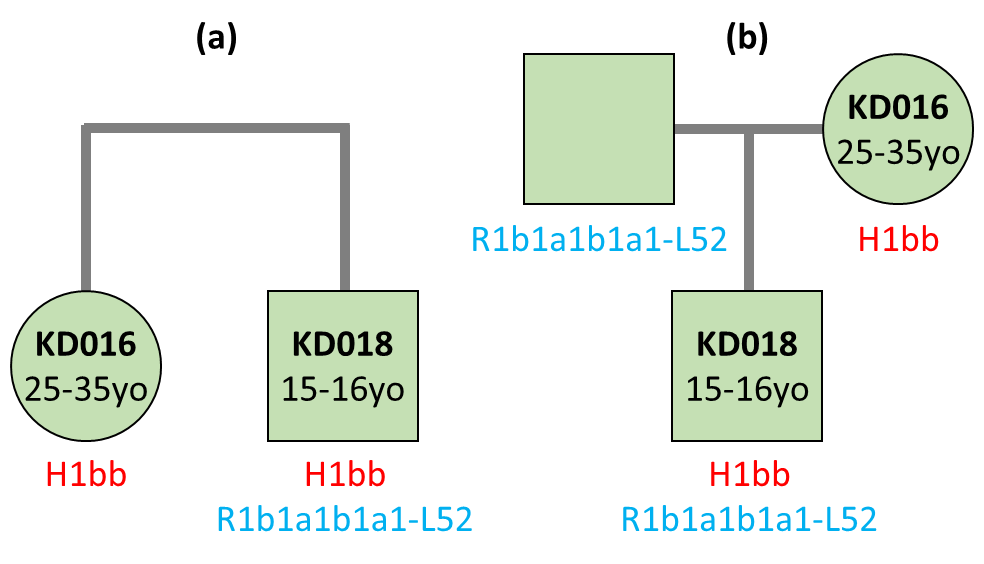
Description automatically generated with medium confidenceA diagram of a tree

Description automatically generated

**Figure S12.** *A putative pedigree diagram for Family A, showing the sister–brother relationship between KD009 and KD020. The T2a1a\* haplotype of KD022 varies from that carried by KD009 and KD020 by three mutations (main text,* **Table S6***), so he was most likely related a paternal first cousin to the siblings.*

**SM6.2 Family B**

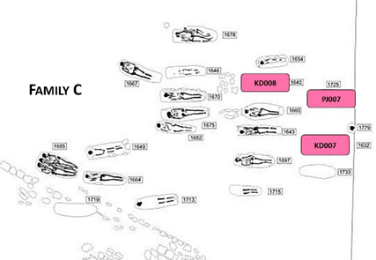
Within the triple burial 1685, we found a first-degree relationship between KD016 (a 25–35 years-old female) and KD018 (a 15–16 years-old male); a biological kinship that is supported by the septal apertures exhibited by both in the olecranon fossa of their humerus bones (Randall 2018). As these two individuals shared the mitochondrial haplogroup H1bb (**Table S6**), despite their haplotype differing at a single nucleotide position (the fast site np 189; **SM5.3**), the bodies were most likely interred at the same time, and so were either siblings (**Figure S13a**) or mother and son (**Figure S13b**). Further discussion of the H1bb haplotype of both individuals can be found above in **SM5.3**. The third skeleton in the triple burial, KD017 (45–49 years-old male), had the same high-frequency Y-chromosome haplogroup (R1b1a1b1a1–L52) as KD018 (and also the two related males from Family D, KD013 and KD014). Although this might suggest that the triple burial represents a family unit of father (KD017), mother (KD016) and son (KD018), KD017 was not closely related to KD018, nor, to the third-degree level, to anyone else tested at the cemetery.

**Figure S13.** *Pedigree diagram for Family B. The link between KD016 and KD018 was either* **(a)** *sister–brother, or* **(b)** *mother–son.*

**SM6.3 Family C**

This family unit comprised three male individuals, all from different graves, but ones which were positioned close together in the cemetery. PJ007 (35–45 years-old from Grave 1722) shared a first-degree relationship with KD008 (17–25 years-old from Grave 1640) and, as both had Y haplogroup I1a2a1a1b–A9128 but carried different mitochondrial genomes, they shared a father–son relationship (**Figure S14**). KD008 was also second-degree related to KD007 (an adult, double Grave 1633), who had a different Y haplogroup but a shared K1a2a mitochondrial haplotype (**Table S6**), which suggests a maternal relationship. As these two males were most likely interred around the same time (**Table S2**), they could have been half–brothers (**Figure S14a**) or nephew and uncle **(Figure S14b**).

... A diagram of a diagram

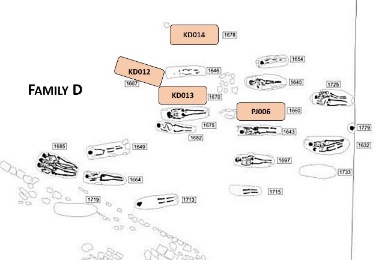
Description automatically generated

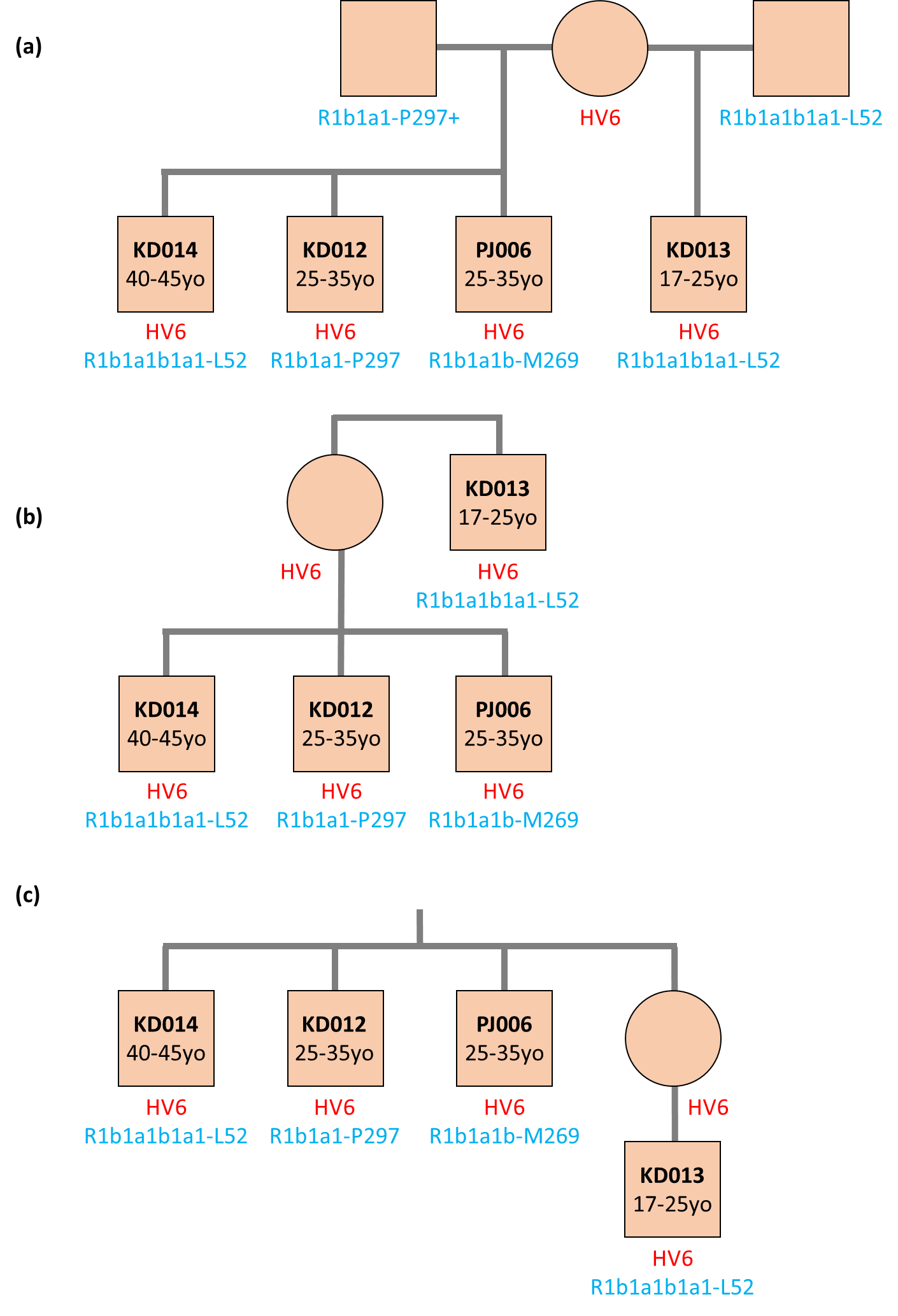
**Figure S14.** *Pedigree diagram for Family C, showing the father*–*son link between PJ007 and KD008. The two figures show how KD007 may be related to KD008, either* **(a)** *as a half*–*brother, or* **(b)** *as an uncle.*

**SM6.4 Family D**

This family comprised four male individuals buried in separate but nearby graves. KD014 (40–45 years-old, buried in double Grave 1678), KD012 (25–35 years-old, buried with a copper alloy buckle in Grave 1667), and PJ006 (25–35 years-old, from Grave 1660) were first-degree related. Although their Y-chromosome haplogroups were resolved to different levels (R1b1a1–P297, R1b1a1b1a1–L52 and R1b1a1b–M269 respectively; **Table 3**), these haplogroups are related and the missing marker information was most likely due to low coverage of the Y-chromosome (**Table S5**). Therefore, as all three carried the same HV6 mitochondrial haplotype, and most likely the same Y-chromosome (**SM5**), they were probably brothers (**Figure S15**). KD013 (17–25 years-old, Grave 1670) was second-degree related to them all, carried the same maternal HV6 haplotype, and also shared the ubiquitous Y haplogroup R1b1a1b1a1-L52 with KD014 (and possibly all his siblings), suggesting that he was either their half–sibling (**Figure S15a**), an uncle (**Figure S15b**), or a nephew (**Figure S15c**).

In the cemetery, the HV6 haplotype was carried by another individual: female KD015 (15–16 years-old), who shared Grave 1678 with male KD014. However, she was not related to any of the other members of Family D. As her mitochondrial haplotype was the same as KD012, KD014, PJ006, and KD013 (**Table S6**), the lack of relatedness may be due either to the extremely low coverage of KD015 (this sample was excluded from genomic analyses as it contains less than 8K SNPs; **Table 2**), or to an ancestral connection deeper than the third-degree. The significance of this maternal connection is supported by the observation that, although we can see several examples of shared Y-chromosome lineages without direct biological kinship (males carrying R1b1a1b1a1–L52, which it is possible may represent unresolved lineages), all instances of shared mitochondrial lineages appear to be associated with close biological kinship among the samples analysed. For this reason, we cannot exclude the possibility that KD015 could be related to members of Family D along the maternal line, and that this relatedness might have determined her position in the cemetery and placement in the double burial.





**Figure S15.** *Pedigree diagram for Family D, showing the brotherhood link between KD014, KD012, and PJ006. The three figures show how KD013 may be related to them as:* **(a)** *a half*–*brother,* **(b)** *an uncle, or* **(c)** *a nephew.*

**SM7. African ancestry of KD010**

Following on from our discussion about the male lineages (above), the E1b1b1a1–M78 seen in KD010 presented a puzzle. KD010 had an associated autosomal ADMIXTURE fraction amounting to ~25%, with a likely ultimate source in West Africa (**Figure 3**, **Table S4**).

The E1b1b1a–L539 ancestor has been proposed to have originated in the region of present-day Gambia, with E1b1b1a1–M78 seen in a male individual from Upper Palaeolithic Morocco at Taforalt, dating to around the time of its formation (14–15 ka; YFull: *https://www.yfull.com/tree/E/*). He had ~25% genome-wide West African, 25% East African and 50% Natufian ancestry (van de Loosdrecht *et al*. 2018). By contrast, although modern Mozabite Berbers in Algeria also exhibit this genome-wide West African component, they lack East African ancestry and, instead, include some WHG (western European hunter-gather) and a proportion of EEF (early European farmer) ancestry, implying a European input. The only modern Mozabite individual with a recorded Y-chromosome haplogroup carries E1b1b1b1a1–M183, which split from the E1b1b1a1–M78 lineage ~24 ka (YFull: *https://www.yfull.com/tree/E/*), and is seen in first-millennium AD medieval Guanches from the Canary Islands (Rodríguez-Varela *et al*. 2017), as well as predominating more generally in modern North Africans.

As any sub-Saharan African genome-wide components were rapidly lost when E1b1b1a1–M78 was transmitted to the Levantine Neolithic (*e.g.* PPNB Jordan ~9.6 ka; Lazaridis *et al*. 2016), where the genome-wide profile was ~100% Natufian, and its presence in other Neolithic individuals (*e.g.* Ukraine Trypillia; Mathieson *et al*. 2018) also occurred without any African ancestry, KD010 appears to have had recent ancestry directly from Africa. The only ancient sample from Africa with an identical male lineage was from Sudan (individual I19143, dating 650–1050 AD; Sirak *et al*. 2021: Supplementary Data 13). He had a genome-wide signature of ~50% ‘Nilotic’ African and 50% West Eurasian ancestry, similar to the Taforalt burial (van de Loosdrecht *et al*. 2018).

From the maternal perspective, KD010 exhibited the mtDNA haplotype U5b1, which has a well-established European origin. Although U5b1 was widely distributed across western and northern Europe during the early medieval period, it could equally well have been rooted in the local Bronze Age/Iron Age, or introduced from the Continent at a later date. However, the scenario of a European origin for KD010’s maternal lineage is strengthened by his personal coding-region variant m.3105A>G, which, within U5b1, is part of the diagnostic motif of sub-haplogroup U5b1i. Among ancient samples, U5b1i has been detected in France since the Middle to Late Neolithic (Seguin-Orlando *et al*. 2021), as well as in Chalcolithic samples from Spain and Portugal (Olalde *et al*. 2018, 2019).

If we examine the genome-wide ADMIXTURE profile of KD010 in more detail (**Figure 3**, **Table S4**), and exclude the African proportion, the European fractions were represented in similar proportions to those of the other post-Roman burials from Site 3 at Worth Matravers. This suggests that the West African component (yellow) contributed to the ancestry of KD010 without the additional EEF (green) admixture that is present in North Africans, which would have raised the proportion of EEF relative to WHG (blue) and CHG (red). This again suggests a recent ancestry for KD010 in West Africa.

This genomic pattern of KD010 was remarkably similar to that of a young female burial (EAS003) from the contemporaneous cemetery at Updown Eastry, Kent, which is discussed in the parallel paper by Sayer *et al*. (2025). She had around one-third West African ancestry but, again, had European fractions in fairly similar proportions to those found in other English burials (**Figure 3**). Curiously, there was a male at Updown (EAS006; Gretzinger *et al*. 2022) who had a genome-wide profile that was very similar to the Updown female but without the African component. He carried a Y-chromosome lineage of E1b1b1a1b1a–V13/L142.1, which is a more derived subclade that was part of the Mediterranean Neolithic expansion of haplogroup E1. As well as a match in early medieval Germany close to the Rhine, it has been seen sporadically in ancient Europeans and even Central Asians, as well as modern males from the Near East and Europe. However, it has not been located in sub-Saharan Africans, despite there being an extremely large database of modern individuals.

**SM8. References**

1000 Genomes Project Consortium. 2015. A global reference for human genetic variation. *Nature* 526: 68–74. https://doi.org/10.1038/nature15393

Alexander, D.H., J. Novembre & K. Lange. 2009. Fast model-based estimation of ancestry in unrelated individuals. *Genome Research* 19: 1655–64. https://doi.org/10.1101/gr.094052.109

Beavan, N. & S. Mays. 2013. The human skeletons, in J. Hines & A. Bayliss (ed.) *Anglo-Saxon graves and grave goods of the 6th and 7th centuries AD: a chronological framework* (Society for Medieval Archaeology Monograph 33): 101–31. London: Routledge.

Bonsall, L.A. & C. Pickard. 2015. Stable isotope and dental pathology evidence for diet in late Roman Winchester, England. *Journal of Archaeological Science: Reports* 2: 128–40. https://doi.org/10.1016/j.jasrep.2015.01.009

Bronk Ramsey, C. 2009. Bayesian analysis of radiocarbon dates. *Radiocarbon* 51: 337–60. https://doi.org/10.1017/S0033822200033865

Cole, G., P.W. Ditchfield, K. Dulias, C.J. Edwards, A. Reynolds & T. Waldron. 2020. Summary justice or the King’s will? The first case of formal facial mutilation from Anglo-Saxon England. *Antiquity* 94: 1263–77. https://doi.org/10.15184/aqy.2020.176

Cox, P. 1988. A seventh century inhumation cemetery at Shepherd’s Farm, Ulwell near Swanage, Dorset. *Proceedings of the Dorset Natural History and Archaeological Society* 110: 37–47.

Dulias, K. *et al.* 2019. Maternal relationships within an Iron Age burial in the High Pasture Cave, Isle of Skye. *Journal of Archaeological Science* 110. https://doi.org/10.1016/j.jas.2019.104978

– 2022. Ancient DNA at the edge of the world: continental immigration and the persistence of Neolithic male lineages in Bronze Age Orkney. *Proceedings of the National Academy of Sciences USA* 119. https://doi.org/10.1073/pnas.2108001119

Farwell, D.E. & T.I. Molleson. 1993. *Excavations at Poundbury 1966–80. II: the cemeteries* (Dorset Natural History and Archaeological Society Monograph 7). Dorchester: Dorset Natural History and Archaeological Society.

Fu, Q., M. Meyer, X. Gao, U. Stenzel, H.A. Burbano, J. Kelso & S. Pääbo. 2013. DNA analysis of an early modern human from Tianyuan Cave, China. *Proceedings of the National Academy of Sciences USA* 110: 2223–27. https://doi.org/10.1073/pnas.1221359110

Fu, Q. *et al*. 2015. An early modern human from Romania with a recent Neanderthal ancestor. *Nature* 524: 216–19. https://doi.org/10.1038/nature14558

Gansauge, M.-T., A. Aximu-Petri, S. Nagel & M. Meyer. 2020. Manual and automated preparation of single-stranded DNA libraries for the sequencing of DNA from ancient biological remains and other sources of highly degraded DNA. *Nature Protocols* 15: 2279–2300. https://doi.org/10.1038/s41596-020-0338-0

Gretzinger, J. *et al.* 2022. The Anglo-Saxon migration and the formation of the early English gene pool. *Nature* 610: 112–19. https://doi.org/10.1038/s41586-022-05247-2

Haak, W. *et al*. 2015. Massive migration from the steppe was a source for Indo-European languages in Europe. *Nature* 522: 207–11. https://doi.org/10.1038/nature14317

Hearne, C.M. & V. Birbeck. 1999. *A35 Tolpuddle to Puddletown Bypass DBFO, Dorset, 1996–8* (Wessex Archaeology Report 15). Salisbury: Wessex Archaeology.

Hills, C. 2009. Anglo-Saxon DNA, in D. Sayer & H. Hayes (ed.) *Mortuary practices and social identities in the Middle Ages: essays in burial archaeology in honour of Heinrich Härke*: 123–40. Exeter: University of Exeter Press.

Hinton, D.A. 1992. The inscribed stones in Lady St Mary Church, Wareham. *Proceedings of the Dorset Natural History and Archaeological Society* 114: 260.

Jarvis, K.S. 1983. *Excavations in Christchurch 1969–1980* (Dorset Natural History and Archaeological Society Monograph 5). Dorchester: Dorset Natural History and Archaeological Society.

Krol, T.N., M. Dee & A. Nieuwhof. 2020. The chronology of Anglo‐Saxon style pottery in radiocarbon dates: improving the typo‐chronology. *Oxford Journal of Archaeology* 39: 410–41. https://doi.org/10.1111/ojoa.12202

Krus, A. 2018. Radiocarbon dating and Bayesian modelling of the post-Roman cemetery, in L. Ladle (ed.) *Multi-period occupation at Football Field, Worth Matravers, Dorset: Excavations 2006–2011* (British Archaeological Reports British Series 643): 216–220. Oxford: BAR.

Kuhn, J.M.M., M. Jakobsson & T. Günther. 2018. Estimating genetic kin relationships in prehistoric populations. *PLoS ONE* 13. http://dx.doi.org/10.1101/100297

Ladle, L. 2018. *Multi-period occupation at Football Field, Worth Matravers, Dorset: Excavations 2006–2011* (British Archaeological Reports British Series 643). Oxford: BAR.

Lazaridis, I. *et al*. 2016. Genomic insights into the origin of farming in the ancient Near East. *Nature* 536: 419–24. https://doi.org/10.1038/nature19310

Lipatov, M., K. Sanjeev, R. Patro & K.R. Veeramah. 2015. Maximum Likelihood estimation of biological relatedness from low coverage sequencing data. *bioRxiv*. Published online 29 July 2015. https://doi.org/10.1101/023374

Martiniano, R. *et al*. 2016. Genomic signals of migration and continuity in Britain before the Anglo-Saxons. *Nature Communications* 7. https://doi.org/10.1038/ncomms10326

Martiniano R., B. De Sanctis, P. Hallast & R. Durbin. 2022. Placing ancient DNA sequences into reference phylogenies. *Molecular Biology and Evolution* 39. https://doi.org/10.1093/molbev/msac017

Mathieson, I. *et al*. 2018. The genomic history of southeastern Europe. *Nature* 555: 197–203. https://doi.org/10.1038/nature25778

Mays, S. 1998. *The archaeology of human bones*. London: Routledge.

Myszka, A. 2015. Septal aperture aetiology: still more questions than answers. *Folia Morphologica* 74: 219–24. https://doi.org/10.5603/fm.2015.0034

Olalde, I. *et al*. 2018. The Beaker phenomenon and the genomic transformation of northwest Europe. *Nature* 555: 190–96. https://doi.org/10.1038/nature25738

– 2019. The genomic history of the Iberian Peninsula over the past 8000 years. *Science* 363: 1230–34. https://doi.org/10.1126/science.aav4040

Patterson, N., A.L. Price & D. Reich. 2006. Population structure and eigenanalysis. *PLoS Genetics* 2. https://doi.org/10.1371/journal.pgen.0020190

Patterson, N. *et al*. 2022. Large-scale migration into Britain during the Middle to Late Bronze Age. *Nature* 601: 588–94. https://doi.org/10.1038/s41586-021-04287-4

Popli, D., S. Peyrégne & B.M. Peter. 2023. KIN: a method to infer relatedness from low-coverage ancient DNA. *Genome Biology* 24. https://doi.org/10.1186/s13059-023-02847-7

Price A.L., N.J. Patterson, R.M. Plenge, M.E. Weinblatt, N.A. Shadick & D. Reich. 2006. Principal components analysis corrects for stratification in genome-wide association studies. *Nature Genetics* 38: 904–909. https://doi.org/10.1038/ng1847

Rahtz, P., S. Hirst & S.M. Wright. 2000. *Cannington cemetery* (Britannia Monograph Series 17). Malet Street: Society for the Promotion of Roman Studies.

Ralf, A., D. Montiel González, K. Zhong & M. Kayser. 2018. Yleaf: software for human Y-chromosomal haplogroup inference from next-generation sequencing data. *Molecular Biology and Evolution* 35: 1291–94. https://doi.org/10.1093/molbev/msy032

Randall, C. 2018. The human remains, in L. Ladle (ed.) *Multi-period occupation at Football Field, Worth Matravers, Dorset: Excavations 2006–2011* (British Archaeological Reports British Series 643): 221–33. Oxford: BAR.

Redfern, R.C., C. Hamlin & N. Beavan Athfield. 2010. Temporal changes in diet: a stable isotope analysis of late Iron Age and Roman Dorset, Britain. *Journal of Archaeological Science* 37: 1149–60. https://doi.org/10.1016/j.jas.2009.10.022

Reimer, P.J. *et al.* 2020. The IntCal20 Northern Hemisphere radiocarbon age calibration curve (0–55 cal kBP). *Radiocarbon* 62: 725–57. https://doi.org/10.1017/RDC.2020.41

Ringbauer, H., Y. Huang, A. Akbari, S. Mallick, I. Olalde, N. Patterson & D. Reich. 2024. Accurate detection of identity-by-descent segments in human ancient DNA. *Nature Genetics* 56: 143–51. https://doi.org/10.1038/s41588-023-01582-w

Rodríguez-Varela, R. *et al*. 2017. Genomic analyses of pre-European conquest human remains from the Canary Islands reveal close affinity to modern North Africans. *Current Biology* 27: 3396–402. https://doi.org/10.1016/j.cub.2017.09.059

Sayer, D. *et al*. 2025. West African ancestry in seventh-century England: two individuals from Kent and Dorset. *Antiquity* 99.

Schiffels, S. *et al*. 2016. Iron Age and Anglo-Saxon genomes from East England reveal British migration history. *Nature Communications* 7. https://doi.org/10.1038/ncomms10408

Seguin-Orlando A. *et al*. 2021. Heterogeneous hunter-gatherer and Steppe-related ancestries in Late Neolithic and Bell Beaker genomes from present-day France. *Current Biology* 31: 1072–83. https://doi.org/10.1016/j.cub.2020.12.015

Sirak, K.A. *et al*. 2021. Social stratification without genetic differentiation at the site of Kulubnarti in Christian Period Nubia. *Nature Communications* 12. https://doi.org/10.1038/s41467-021-27356-8

Soares P. *et al.* 2009. Correcting for purifying selection: an improved human mitochondrial molecular clock. *American Journal of Human Genetics* 84: 740–59. https://doi.org/10.1016/j.ajhg.2009.05.001

Stewart, J. & P. Chinnery. 2015. The dynamics of mitochondrial DNA heteroplasmy: implications for human health and disease. Nature Reviews Genetics 16: 530–42. https://doi.org/10.1038/nrg3966

van de Loosdrecht, M. *et al*. 2018. Pleistocene North African genomes link Near Eastern and sub-Saharan African human populations. *Science* 360: 548–52. https://doi.org/10.1126/science.aar8380