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# Beachy Head Woman: clarifying her origins using a multiproxy anthropological and biomolecular approach

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ABSTRACT

The skeletal remains of an individual colloquially referred to as Beachy Head Woman (BHW) were re-discovered in the Eastbourne Town Hall collection in 2012, and have remained the subject of significant public interest since. Radiocarbon dating yielded a calibrated date of between 129 and 311 calCE indicating that she lived during the period of the Roman occupation of Britain and, over more than a decade, there have been several attempts to unravel her geographical origins and ancestry. Here, we present results of all bioanthropological and biomolecular analyses performed to date. Initial osteological analyses indicated possible sub-Saharan origin, with BHW thus presented as one of the earliest Africans in Britain. However, her story was complicated by subsequent (unpublished) biomolecular analyses, which suggested she likely grew up on the south coast of Britain and had recent European ancestry. Here we present high quality ancient DNA data indicating that Beachy Head Woman has a strong genetic affinity to individuals from rural Britain during the Roman occupation and modern day Britons. We find no signals of admixture that would suggest recent sub-Saharan ancestry. Phenotypic predictions suggest she had blue eyes, intermediate (between pale and dark) skin pigmentation and light hair. Combined, our multiproxy approach indicates that Beachy Head Woman was of local British ancestry.

## 1. Introduction

In the early 2010s, the 'Eastbourne Ancestors Project' (EAP) sought to reveal the stories of over 200 skeletons in the collection of Eastbourne Council in the UK (Seaman and Forsyth, 2014). As part of this project, in 2012, a skeleton was discovered in a box in the basement of Eastbourne Town Hall. The only contextual information available for the remains was an English Heritage label detailed *'Beachy Head (1959)*'. Despite an extensive search of museum archives, no other contextual information or records of any associated excavation could be uncovered. As the skeleton had been morphologically assessed to be female, it was dubbed 'Beachy Head Woman' (BHW), with Beachy Head referring to the stretch of coastline just outside Eastbourne in the South of England (Fig. 1).

BHW's origins would soon garner public interest when results of early (2013) craniofacial analyses (see 1.3 Bioarchaeological Assessment and *S.1.2*) suggested she was of recent sub-Saharan ancestry. The discovery of the 'first black Briton known to us' (Olusoga, 2016, p. 33) gained traction across several media outlets (e.g. BBC News, 2014; Campbell, 2020; Steafel, 2021; The Times, 2014; Van der Pool, 2016), non-fiction books (e.g. Adi, 2022; Olusoga, 2016, pp. 31–33; Sethi, 2021, p. 285), educational resources (e.g. Hackney Learning Trust, n.d.; Khan and Torrington, 2023; School History, n.d.; The Royal Mint, n.d.) and academic publications (e.g. Goodwin, 2020; Osborne, 2020, p. 250; Swank, 2022, p. 533; Vrikki et al., 2020, p. 87). However, over the proceeding decade as further analyses of BHW's remains were conducted (but not previously published), this interpretation began to shift.

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Here, we present the entire suite of biomolecular and morphometric work that has been performed on the individual over that period, alongside the analysis of newly generated ancient DNA data. We detail how the interpretation of BHW ancestry has changed over the last decade as a result of recent advances in scientific methods and technology.

## Part 1 Early Analysis: 2012–2024

Authors of this paper involved in this phase of analyses include Caroline Wilkinson (craniofacial), Ian Barnes and Selina Brace (aDNA).

### 1.1. *Site and samples*

Beachy Head refers to a stretch of coastline two miles east of the town of Eastbourne on the south coast of the UK (Fig. 1). The surrounding area has an extensive archaeological history, notably a well-excavated rural settlement immediately north of Beachy Head at Bullock Down, which was occupied from the conquest to the end of the Roman period (Rudling, 1982). To the west are possible rural sites at Birling and East Dean attested by occupation scatters (East Sussex HER: MES7411, MES7408, MES7407 and MES3046). To the east of Beachy Head are the palatial villa at Eastbourne (Rudling, 1982, p. 343; Russell, 2006, pp. 143–144, 264; Sutton, 1952) and the Roman fort at Pevensey, constructed in the very late 3rd century (Fulford and Rippon, 2011).

The burial evidence for the immediate region is sparse (Rudling, 1979, p. 353 Fig. 1; 1982, Figure 68; 2008, p. 128) but includes seven apparently Romano-British inhumations found in the late 19th century (Seaman, 2018; Whitley, 1890, pp. 113–115; East Sussex HER: MES3045). While grave goods were donated to Eastbourne Museum (Sussex Archaeological Society, 1892; Whitley, 1890, p. 114) they are thought to have been destroyed during WWII; there is no mention of skeletons being deposited.

### 1.2. *Radiocarbon dating*

$C^{14}$ radiocarbon dating from a sample of BHW was performed at Oxford University's Radiocarbon Accelerator Unit (ORAU) which produced an uncalibrated date of 1831 ± 24 BP (OxA-*28343)*. Using the IntCal20 calibration curve (Reimer et al., 2020) generated a calibrated date of between 129 and 311 calCE (95 % CI; SI Fig. 1), a period that corresponds with evidence for increased Roman activity in the region.

### 1.3. *Bioarchaeological Assessment*

The osteological assessment of BHW was undertaken according to established guidelines from the Biological Association for British Anthropologists; Institute of Archaeologists; and English Heritage (Seaman and Forsyth, 2014). This included macroscopic analysis to determine the individual's biological sex, age, stature, and any pathology or trauma visually evident. Methods and results were detailed in a report for Eastbourne Borough Council, the relevant details (those pertaining to BHW) are included in the SI (*S.1*). BHW's biological sex was categorised as 'possible female'. Her age range was assigned as young adult, aged between 18 and 25 at death and she was estimated to be 1.52m tall. Cause of death could not be established from the skeleton, however, there was evidence of antemortem trauma including an ossified hematoma present on the midshaft of the right femur.

In 2013, macroscopic craniofacial analysis was carried out at the University of Dundee to reconstruct BHWs appearance, (for original report see *S.1.2)*. The cranium was almost complete, except for the loss of both maxillary and mandibular incisors, and canines. Whilst some traits such as a wide palate, mild brow ridges and a marked nuchal line were suggestive of a male, cranial features were overall indicative that the skull was female. The skull was dolichocephalic (cephalic index of 73; 131.5/180), with a post-bregmatic depression, rectangular orbits, wide interorbital distance, low nasal root, absent nasal spine, nasal guttering, moderate prognathism, wide palate, rounded mandibular border, and shallow coronoid notch. These details were found to be consistent with an individual of sub-Saharan African ancestry. Though, it was emphasised that any such determination is difficult given the wide variation in cranial morphology seen both within and between populations (Cartmill, 1998; Sauer, 1992).

This would make BHW one of the earliest individuals with recent sub-African ancestry identified thus far in Britain. Population movement from Northern Africa into Britain during the Roman period has been well established, both on an individual and military unit level. This is evidenced by inscribed altars, tombstones and military diplomas (Eckardt, 2014, pp. 67–77, Fig. 3.3). During the Roman period, North Africa was a culturally complex region characterised by centuries of mixing of Phoenician, Italian, Berber and African populations (Shaw, 2014; also Brett and Fentress, 1996; Mattingly and Hitchner, 1995, pp. 171–174). Sub-Saharan Africans were known as 'Aethiopians' and are depicted quite frequently in Roman art, with the cultural significance of these figurines, vessels and other objects still much debated (e.g Bell, 2022, with extensive references to earlier work). Given military recruitment and trading patterns, individuals of African descent buried in Roman Britain are perhaps more likely to come from the mixed populations of North Africa than the sub-Saharan region.

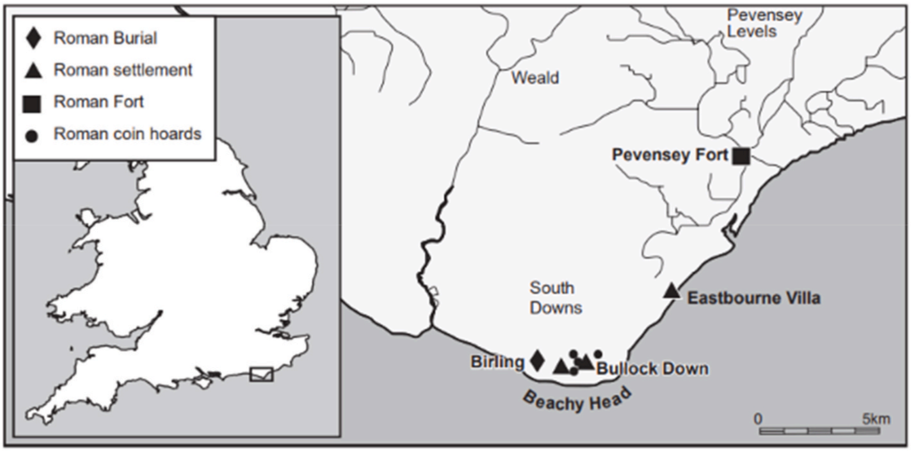

**Fig. 1. Location of Beachy Head and notable Roman sites surrounding the area.** Map produced by Sarah Lambert-Gates.

### *1.4. Facial reconstruction*

Alongside the 2013 craniofacial analysis, a 3D facial depiction of BHW was produced at the University of Dundee (for original report see *S.1.2*). This followed the Manchester method (Wilkinson, 2004; Wilkinson and Rynn, 2012) with facial feature shape determined using published anatomical and anthropometrical standards (Fedosyutkin and Nainys, 1993; Gerasimov, 1955; Rynn et al., 2010; Wilkinson and Mautner, 2003). Facial features were estimated based entirely on skeletal detail using standards that were not reliant on ancestry/population affinity (Rynn et al., 2012).

When performing facial reconstruction from archaeological remains, the most likely hair, skin and eye pigments are determined from the bioanthropological determination, and relevant historical and contextual data. Given the uncertainty regarding any historical phenotype and the variation in pigmentation both across and within populations, researchers chose pigments that are represented in sub-Saharan populations, but also frequently occur across other global populations. Thus, dark eye and hair colours, wavy hair type and a mid-tone skin pigment were depicted. Plastic eyeballs with brown iris colour were mounted in the head model and the skin was painted using acrylic paints. A dark brown wig with long, loose curls was attached to the model (SI figure S1.2.8).

### *1.5. Bulk isotope analysis*

In 2013, as part of the EAP, several samples from Anglo Saxon inhumations from the Eastbourne area, including BHW, were submitted to the NERC Isotope Geosciences Laboratories (NIGL) for carbon and nitrogen analysis ($\delta^{13}$C and $\delta^{15}$N) of collagen (dietary reconstruction), and strontium and oxygen isotope ($^{87}$Sr/$^{86}$Sr and $\delta^{18}$O) analysis of tooth enamel (geographical location during childhood).

The NIGL report (full methods and results in S.2) plots the strontium and oxygen isotope results for the EAP individuals including BHW alongside data from Ringlemere Anglo Saxon individuals (Brettell et al., 2012) and a previous study of Anglo Saxons from Eastbourne (Millard et al., 2005) (Fig. 2a). The strontium and oxygen isotopes for all EAP individuals, including BHW, are consistent with an origin on the south coast of Britain (BHW: $^{87}\text{Sr}/^{86}\text{Sr} = 0.709100$; $\delta^{18}\text{O}_p = 17.84$; SI Fig. 2), though the results cannot exclude areas of the continent with similar values (S.2: NIGL report; SI S.2). The carbon and nitrogen isotope data from BHW ($\delta^{13}$C ($-18.8$) and $\delta^{15}$N (10.3)) and the EAP individuals were plotted with published British individuals from the Iron Age (Wetwang Slack) (Jay and Richards, 2006), the Late Medieval but with a high fish diet (Fishergate) (Müldner and Richards, 2007) and Anglo Saxon sites (Berinsfield) (Privat et al., 2002) (Fig. 2b). The EAP individuals, including BHW, had higher nitrogen isotope ratios than both the Iron Age farmers and the (inland) Anglo Saxons, suggesting a greater marine component in her diet, which would be consistent with coastal living. Relative to the other individuals, BHW had an unusual $\delta^{13}$C bulk value ($-18.8^{\circ}/_{00}$) suggesting a comparatively increased contribution of C4 plants in her diet.

### *1.6. Ancient DNA analysis*

In 2017, preliminary ancient DNA (aDNA) analysis on BHW was conducted by researchers from the Natural History Museum. The low-level sequencing carried out at this time generated an insufficient amount of data based on the number of reads/nuclear DNA to analyse the DNA to publication standard. The results, however, were suggestive that she did not have recent sub-Saharan African ancestry but was more likely to be of east Mediterranean origin. Along with the isotope data, the proposal at this time was that she may have been born in Cyprus and moved to Eastbourne as a young child. Whilst these preliminary results were not published in a scientific journal they were subsequently reported in the media.

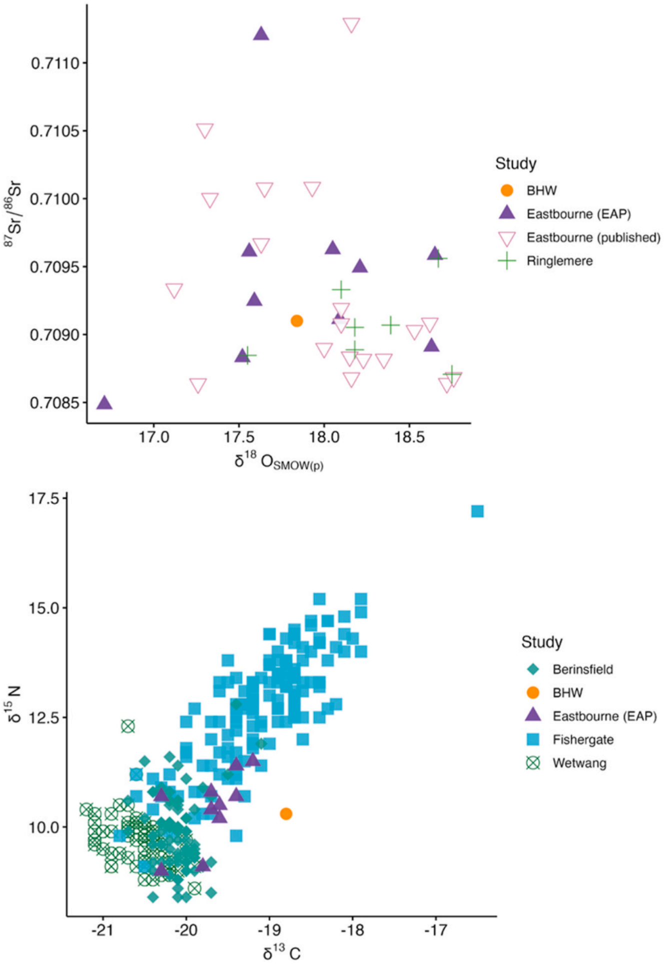

**Fig. 2. The isotopic profile of Beachy Head Woman.** (a) Sr and O ratios plotted to indicate mobility patterns and (b) C and N plotted against one another to indicate dietary profile. Isotopic results from individuals incorporated into the wider Eastbourne Ancestors Project (EAP) from coastal South England, alongside individuals from Roman-era Britain are plotted alongside BHW for context.

## Part 2 Recent Analysis: 2024–2025

## 2. Methods and Analyses (2024-2025)

### *2.1. Ancient DNA*

#### *2.1.1. Laboratory methods (2017 and 2024)*

DNA extraction and initial library building were carried out in 2017. Forty six mg of bone powder was drilled from the petrous bone of BHW using a Dremel™ high powered drill in the ancient DNA lab of the Natural History Museum; a dedicated aDNA facility following standard protocols (reviewed in Orlando et al., 2021). DNA extraction method followed Dabney et al. (2013), modified so that the Zymo-Spin V columns were replaced with Roche High Pure Viral Nucleic Acid Large Volume spin columns, and two final elution steps of 50 μl TET buffer (total 100 μl) were performed. Double stranded library build was implemented (20 PCR cycles) using dual indexes (Meyer and Kircher, 2010). The library was screened on a NovaSeq550 2x75BP; Mid-Output at the Natural History Museum.

In 2024, a human specific DNA capture method (TWIST Biosciences) that was specifically designed for degraded human material, and targeted variable sites on the human nuclear genome (Rohland et al., 2022) was employed. Laboratory methods followed the default protocol and used a bead-based DNA isolation method to replace the standard drying down protocol, prior to the hybridization reaction. The suggested number of PCR cycles for highly degraded DNA (n = 23) were performed post hybridization. The captured amplified library was quantified using Tapestation 4200, High Res. and sequenced on a NovaSeq X Plus system (10B; 150x2 PE; Novogene, Cambridge).

### 2.1.2. *Computational analysis - alignment and authentication*

Paired end reads were demultiplexed and transferred onto the NHM high performance computing (hpc) cluster and the CropDiversity hpc cluster (Percival-Alwyn et al., 2024). We trimmed read adapters and collapsed paired end reads (adapterremoval 2.0; Schubert et al., 2016). Dual index combinations were checked, with collapsed reads showing more than two nucleotide index mismatches discarded. Collapsed reads were aligned to the nuclear human reference genome hg38 (Schneider et al., 2017) and the Revised Cambridge Reference Sequence (rCRS; NC_012920) (Andrews et al., 1999) using BWA 0.7.17 (Li and Durbin, 2009), relaxed parameters (-q 10) and a random seed (-l 1024). Aligned reads were subsequently sorted, filtered for mapping and base quality ($Q \geq 30$), and duplicate reads removed using samtools (Danecek et al., 2021). This produced the final filtered bam file used for all subsequent computational analysis.

Mapping statistics (SITable 1; Supplementary Data 1) for the nuclear and mitochondrial reference genomes were calculated using samtools and qualimap (Okonechnikov et al., 2016), and aligned reads visually inspected using Tablet (Milne et al., 2013). mapDamage 2.0 (Jónsson et al., 2013) was used to assess DNA damage patterns using default settings. PMDtools (Skoglund et al., 2014) was used to further authenticate DNA, with reads filtered for a PMD score >3. Initial analyses used both filtered and unfiltered datasets to check for modern human contamination. To allow for comparison between BHW and local populations of the same time period, we downloaded recently published rural British Roman-era genomes (n = 96) (Scheib et al., 2024) from the ENA database, and processed them in the same manner as above. The final bam file was imputed with GLIMPSE2 (Rubinacci et al., 2023), using the 1000 Genome Project Phase 3 reference panel (Auton et al., 2015).

### 2.1.3. *DNA preservation and authentication*

DNA was found to be well preserved in BHW, with an endogenous content of ~13 % from initial whole genome screening (WGS) data (SI Table 1). DNA capture and sequencing resulted in over 80 % of variable 1240k SNP sites being covered by 5 or more unique reads (Table 1). DNA damage patterns seen for both WGS and capture data are in keeping with the provenance of the material (SI Fig. 3). PMD filtering of the readset shows a high proportion of retained reads (45 %; Skoglund et al., 2013), and similar results of ancestry analyses when using filtered and unfiltered readsets (SI Table 1). Schmutzi (Renaud et al., 2015) was run to estimate mitochondrial contamination, giving a contamination estimate of between 1 and 3 % (SI Fig. 4). As this was an acceptable range, all subsequent analyses used the unfiltered readset.

**Table 1**

**Phenotypic analysis of Beachy Head Woman.** Predicted eye, hair and skin pigmentation as calculated using HIrisPlex-S.

| Phenotype | Likelihood | AUC loss |
|---|---|---|
| **Blue eye** | **0.911** | **0** |
| Intermediate eye | 0.057 | 0 |
| Brown eye | 0.032 | 0 |
| Blond hair | 0 | 0.025 |
| Brown hair | 0 | 0.015 |
| Red hair | 0 | 0.102 |
| Black hair | 0 | 0.012 |
| **Light hair** | **0.958** | **0.007** |
| Dark hair | 0.042 | 0.007 |
| Very pale skin | 0.067 | 0.064 |
| Pale skin | 0.136 | 0.012 |
| **Intermediate skin** | **0.706** | **0.025** |
| Dark skin | 0.05 | 0.005 |
| Dark to black skin | 0.041 | 0.003 |

### 2.1.4. *Sexing and MT haplogroup assignment*

Sex classification was performed using Skoglund et al. (2013) and implemented following Anastasiadou et al. (2024). We considered the asymmetrical targeting of X and Y reads seen when performing targeted hybridisation capture (–capture option). As expected, we found BHW to be genetically female (XX chromosomes; SI Table 2).

A consensus mitochondrial genome for BHW was assembled using all unique q30 aligned mitochondrial reads and ANGSD (-do-fasta 2; -min. depth [2 and 3]; -trim 2). Haplogrep v3 (Schönherr et al., 2023) was used to determine her mitochondrial haplogroup, using the latest MT Phylotree (v17 - Forensic Update). BHW was shown to carry a mitochondrial haplotype deriving from the K1a haplogroup (K1a26; Q = 82 %). This haplogroup is associated with modern-day populations from Northern European and the British Isles, and identified in several individuals from rural Iron Age Britain (Scheib et al., 2024; Schiffels et al., 2016).

### 2.1.5. *Population genetic analyses*

Prior to population level analysis, all aligned read data for BHW and all processed rural British Roman-era individuals were trimmed of terminal ends (bamUtils; -n 5). Pseudo-haploid calling was performed at nucleotide positions on the human genome shown previously to be variable across populations (Mathieson et al., 2015) using samtools mpileup (Danecek et al., 2021) and pileupCaller (https://github.com/stschiff/sequenceTools). These data were merged with the Allen Ancient DNA Resource (S. Mallick and Reich, 2023; v62.0), creating a dataset that contained over 20,000 modern and ancient human individuals spanning tens of thousands of years.

Initial analysis to determine the population affinity of BHW was performed using ADMIXTOOLS 2 (Maier and Patterson, 2024). Principal Component Analysis (PCA) was performed using smartpca (Patterson et al., 2006; Price et al., 2006), where a set of modern genomes were used to calculate eigenvectors (allsnps: YES), and BHW subsequently projected. Following the results of this initial analysis, we subset the list of modern genomes to only include those from West Eurasian and repeated the PCA to offer higher resolution. For this analysis, we projected relevant ancient Eurasian individuals alongside BHW.

Outgroup-f3 statistics (*qp3Pop*) were calculated to clarify the genetic affinity of BHW to modern populations. We used global modern genomes as comparative populations and both Chimp and Mbuti as outgroups, before analysis was refined adhoc to include all modern West Eurasians and ancient Eurasian individuals dated to the Roman period and 2000 years prior (SI Table 3). Chimp was used as an outgroup as it is asymmetrically related to all human populations, with Mbuti used for subsequent analysis focused on non-African populations given this population is equally related to all non-Africans.

In order to test the hypotheses, as suggested by previous craniofacial results, of admixture into BHW and to compare her levels of drift with contemporary British individuals we used *qpDstat*'s f4 mode in ADMIXTOOLS 2 (Maier and Patterson, 2024) and ADMIXTURE (Alexander et al., 2009). F4-statistics were used to explicitly test for evidence of recent African admixture in BHW, and to infer the similarity between the ancestry of contemporary Iron Age British populations and BHW when compared to contemporary individuals from Continental Europe and Africa. See SI 3.1 for details of ADMIXTURE and structured modelling in ADMIXTURE analyses including SI Figs. 5 and 6.

Initial f3-outgroup analysis using modern human individuals (*qp3Pop{BHW, modern population, Mbuti/Chimp}*) show BHW to have a strong affinity to modern day Europeans (Fig. 3a), and the highest genetic affinity to modern individuals from Great Britain (Fig. 3b).

PCA (Fig. 3b) shows BHW is most similar to modern populations

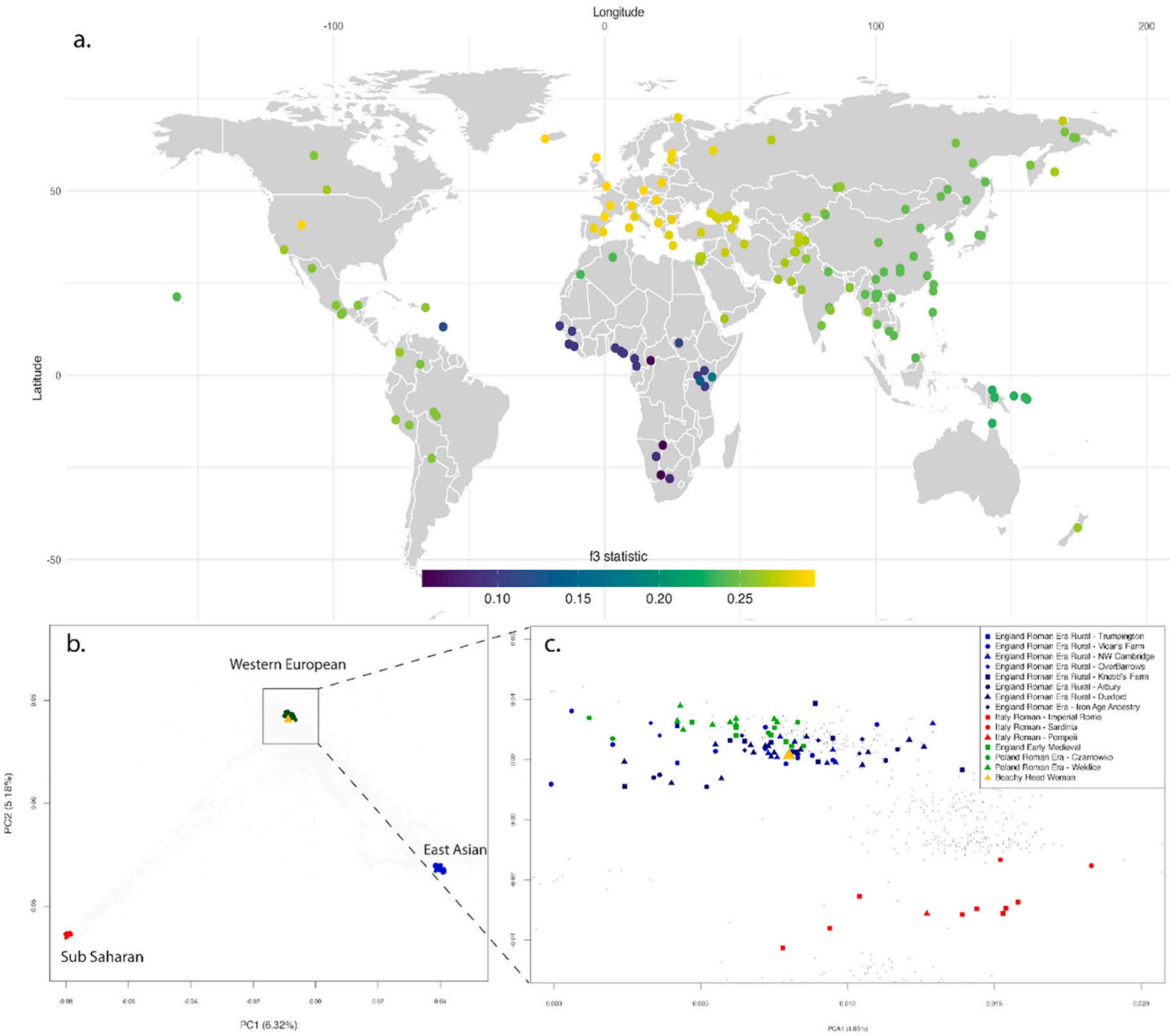

**Fig. 3. The genetic affinity of Beachy Head Woman.** (a) World map with global populations coloured by outgroup-f3 statistic value when: f3{Beachy Head Woman, modern population, Chimp}. Lighter colour denotes a greater genetic affinity between BHW and the population in question. Principal component analysis (PCA), with Beachy Head Woman (golden triangle) projected onto eigenvalues calculated using (b) modern global genomes, and (c) modern Eurasian genomes. In figure (b), populations representative of sub-Saharan African (i.e. Mbuti; Red), West Eurasian (i.e. French; Green), and East Asian (i.e. Han Chinese; Blue) ancestry are highlighted. Several relevant genomes dating to the Roman period (Scheib et al., 2024) are projected onto modern West Eurasian populations in figure (c). (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

from Western Europe, with no attraction towards sub-Saharan Africans. The projection of additional Roman-era individuals (Fig. 3c) highlights the association between the ancestry of BHW and populations from Roman-era Britain and Northern Europe. This ancestry differs from individuals associated with the expansion of the Roman empire (i.e. those of Mediterranean origin) and instead resembles the local and/or rural communities in Germany, Poland, Belgium and the UK (Antonio et al., 2019; Scheib et al., 2024; Silva et al., 2024) during the Roman occupation.

D-statistics (f4-statistics) consistently show no evidence of recent gene-flow between BHW and sub-Saharan Africans, with highly similar results obtained when gene flow between local and/or rural Roman-era individuals from Britain and sub-Saharan Africans are also calculated (Fig. 4 & SI Fig. 7). Ad-hoc D-statistics found *Roman-era British* individuals share elevated levels of drift with BHW (and vice-versa) over non-British Iron Age individuals (SI Fig. 8; f4{*Mbuti/Chimp, BHW; Roman-era British, European/MENA/African Roman era individuals*}). Results of both unsupervised (K = 6) (SI Fig. 9) and supervised (K = 6) admixture (SI Fig. 11) modelling shows BHW to have the most similar pattern of ancestry with Iron Age northern Europeans.

### 2.1.6. Phenotypic traits

HIrisPlex-S (Shirk and Cushman, 2011; Walsh et al., 2014, 2017) was used to predict the hair, eye and skin pigmentation of BHW. Variable sites targeted by TWIST and shown to be associated with phenotype (n = 32) were filtered and individually inspected. Of the 32 sites used by HIrisPlex-S, 27 were covered by 5 or more bases, with any nucleotide positions with less than 5 unique reads covered set as empty (N/A) to avoid issues with low-coverage data. Genotype likelihoods were calculated (ANGSD); at all sites exceeding this threshold, allowing for the homo- ($0.2 \geq$ maf) and hetero- (maf $>0.2$) zygosity at each to be determined. These calls were input into HIrisPlex-S and eye, skin and hair pigmentation predictions assessed, with skin pigmentation (intermediate), eyes (blue), and hair (light) could be predicted (Table 1). Further, manual investigation highlighted that SNP rs1426654 was covered by 10 unique reads and homozygous (A) for the allele state strongly associated with the *SLC24A5* gene and light skin pigmentation (Lamason et al., 2005; C. B. Mallick et al., 2013). These results were confirmed with the imputed data that produced diploid calls at all targeted phenotype positions (n = 32) used for assessment by HIrisPlex-S (Supplementary Data 3).

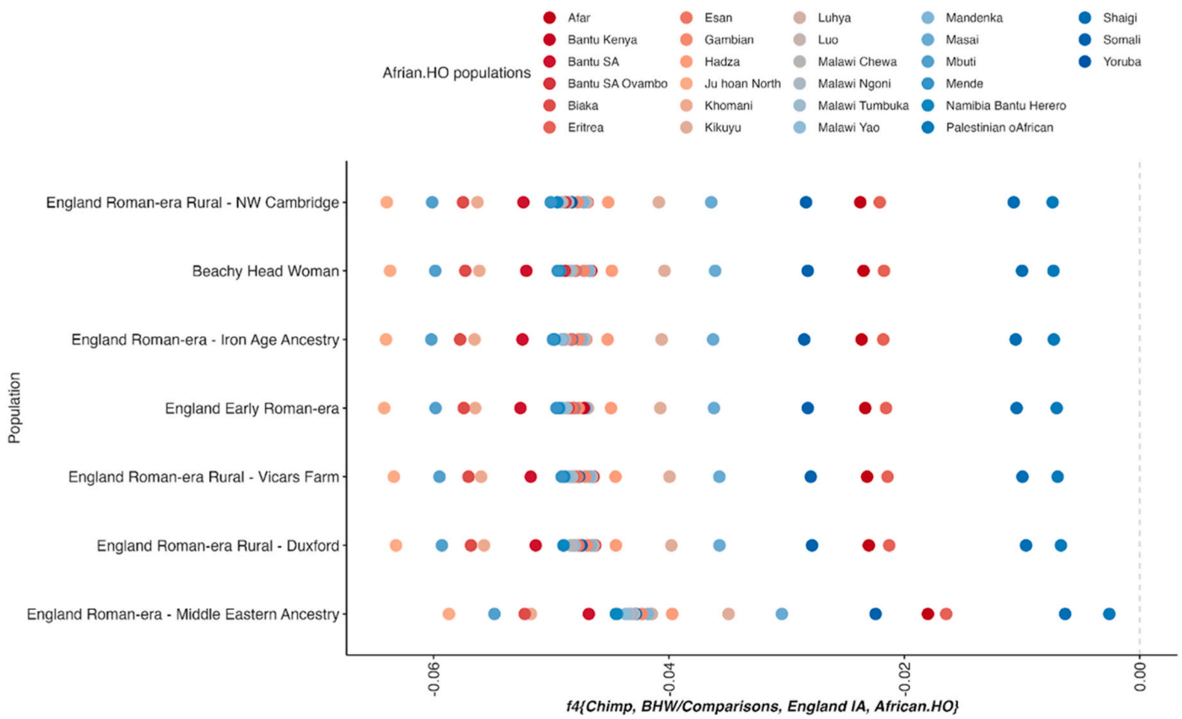

**Fig. 4. A comparison of shared genetic drift between Beachy Head Woman and sub-Saharan Africans using f4 statistics, with the shared genetic drift observed between other Roman Era British individuals and sub-Saharan Africans.** BHW and contemporary British individuals modelled with African populations from the Human Origins dataset and Iron Age England as a clade. Of note is the difference between BHW and the Middle Eastern individual found in Yorkshire included in Martiniano et al. (2016)

### 2.2. *Updated facial depiction*

In 2025, the original facial reconstruction of BHW (produced in 2013) was scanned using an Artec Space Spider™ handheld 3D scanner (see Fig. 5a). This scan then was imported into UnReal Engine 4.26, and MetaHuman Creator (https://MetaHuman.unrealengine.com/) used to create a digital model of BHW that matched the facial morphology of the original reconstruction. Intermediate skin pigmentation, blond hair and blue eye colour, as informed by ancient DNA results, were selected to create the fully pigmented and textured digital 3D depiction (Fig. 5b).

## 3. Discussion

The decade-long investigation into Beachy Head Woman's origins has centred around how her story has shifted over time and has sparked important debates about diversity and how we portray individuals from our past. The results presented here will no doubt add to this, but the story of the investigation into BHW is not out of the ordinary. All science

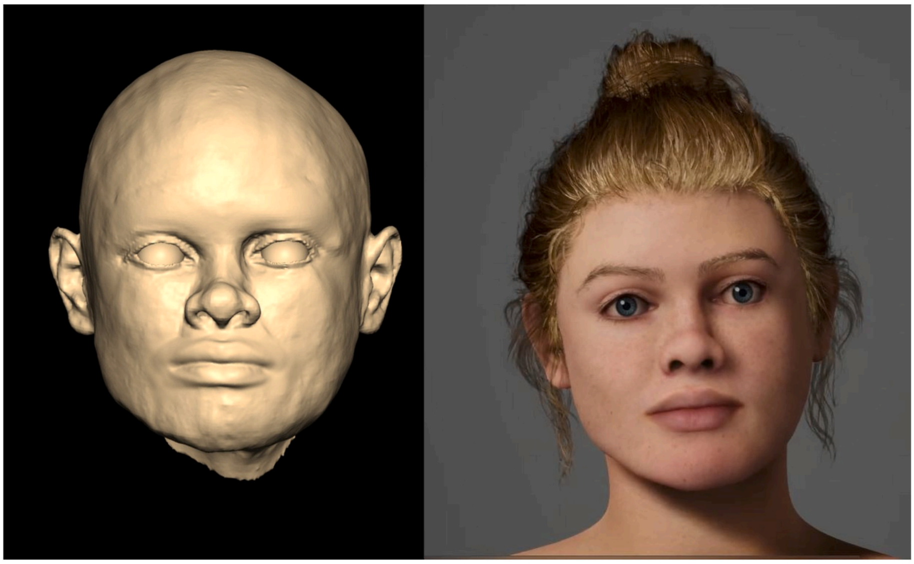

**Fig. 5. Second iteration facial reconstruction of BHW.** (a) 3D scan of the iteration #1 facial reconstruction - physical model (b) Iteration #2 of the facial depiction of Beachy Head Woman. MetaHuman version with hair, skin and eye textures as suggested by the DNA analysis. Both images courtesy of Face Lab at Liverpool John Moores University.

is an iterative process and BHW represents a case study in how as methods and technologies evolve, so can the conclusions we draw from them. The case of BHW does, however, raise important questions as to how methods previously commonly applied in bioanthropology classify human diversity, and how these can be combined with multiproxy biomolecular analysis.

The field of bioanthropological classification has seen significant changes over the last 15 years, and has been moving away from the traditional morphological and anthropometrical methods of ancestry estimation due to their origins in 19th century biological classification of humans along racial hierarchies (Albanese and Saunders, 2006; Brace, 1982; Haller, 1971; Sauer et al., 2016; Williams et al., 2005). These traditional methods of ancestry estimation using cranial metrics can help reify outdated notions of the biological reality of race (Goodman, 1997; Johnson, 2016; Ross and Williams, 2021). Classifying individuals into discrete racial categories overlooks the continuous nature of most human variation, as seen in genetic data (e.g. Prugnolle et al., 2005), blood groups (e.g. Howes et al., 2011), and skin pigmentation (e.g. Jablonski, 2012). In addition, skeletal traits often have as much variation within as between ancestry groups, and do not cluster into discrete categories (Manica et al., 2007). There has been much discussion of how to take this into account in anthropological ancestry estimation and the visualisation of ancient peoples (Armstrong-Fumero, 2014; Caspari, 2010; Edgar and Hunley, 2009; Ousley et al., 2009; Warren et al., 2018; Wilkinson, 2020). Although certain morphological features are still considered to identify populations, this is being increasingly carried out with an understanding of the clinal variation in these features and the invalidation of the biological concept of race (Adams & Piloud 2021; Hefner et al., 2024; Navega et al., 2015; Spradley and Weisensee, 2013).

The case of BHW demonstrates the errors associated with traditional anthropology methods and explains why they are no longer used to establish ancestry estimation. Anthropologists have noted (Dunn et al., 2020; Edgar and Pilloud, 2021; Parsons, 2021) that whilst they may detect discrete biological traits believed to correlate with geographic origin, there are inherent scientific, theoretical, and structural challenges associated with these methods, due to overlapping classifications, unrepresentative datasets and inflexible interpretation. It is important to stress that anthropology methods are not unique in evolving, genomic data generation and analyses have changed considerably over the last 20 years. Next generation sequencing (NGS) radically changed the field of ancient DNA and arguably most notably the field of ancient human DNA. This is due to the large quantity and low cost of data that can be produced with NGS, but also the ability to bioinformatically authenticate genuinely ancient DNA from modern DNA, a process that was not possible using the older methods of Sanger sequencing Polymerase Chain Reaction (PCR) products. Whilst the genomic results reported here were all generated from authenticated NGS data, the shift in ancestry from that of a possible Cypriot background when using low level sequencing data to English/northern continental Europe when deeper sequencing effort was achieved further highlights the importance of generating sufficient high resolution genomic data to more accurately determine an individual's ancestry. The results of this paper suggest that previous archaeological cases reliant on anthropological ancestry estimation, and/or non-authenticated genomic data from older studies, may need reassessment using multi-proxy biomolecular methods. For Roman archaeology, specifically, the results offer an opportunity to reassess bioarchaeological work carried out over recent decades, while still acknowledging the strong historical and epigraphic evidence for migration into Britain during this period.

## 4. Conclusions

The research presented here spans over a decade of technological advancements and highlights progressive analyses in osteological, morphometric and biomolecular techniques that have been applied to BHW. Although initial analysis using traditional anthropological morphometric techniques deemed the remains of BHW to be likely of sub-Saharan origin, the results from recent genetic analysis indicate that she shows a close affinity to individuals from modern day England and contemporary Roman-era Iron Age individuals in England and Northern continental Europe. When combined with $^{87}$Sr/$^{86}$Sr isotope results, which indicated BHW shared similar early-life mobility to individuals also excavated from the south coast and dated to the Roman-era Iron Age and early medieval periods, this suggests BHW likely came from the south coast of England. The decade-long investigation into BHW not only helps clarify her origin but also illustrates this iterative work in practice. By reporting each analysis conducted on BHW, even those whose conclusions we no longer support, we highlight how these efforts can lead to both more equitable and more accurate science.

## CRediT authorship contribution statement

**Andy Walton:** Writing – review & editing, Writing – original draft, Methodology, Investigation, Formal analysis. **William Marsh:** Writing – review & editing, Methodology, Investigation, Formal analysis. **Alex Strang:** Writing – review & editing, Methodology, Formal analysis. **Jonathan Seaman:** Writing – review & editing, Resources, Conceptualization. **Kelly Van Doorn:** Writing – review & editing, Resources. **Hella Eckardt:** Writing – review & editing. **Caroline Wilkinson:** Writing – review & editing, Writing – original draft, Resources, Methodology, Formal analysis. **Ian Barnes:** Writing – review & editing, Supervision, Conceptualization. **Selina Brace:** Writing – review & editing, Writing – original draft, Supervision, Investigation, Conceptualization.

## Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

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## Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.jas.2025.106445.

## Data availability

DNA sequence data generated for this project has been deposited in the European Nucleotide Archive under project accession number PRJEB102740.

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