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Tracking the origin of worked elephant ivory of a medieval chess piece from Belgium through analysis of ancient DNA

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Running title: Tracking the origin of elephant ivory of a medieval chess piece

Keywords: Africa, archaeogenetics, artefact, Mediterranean Sea, Swahili Corridor, trade routes

Abstract

The morphological identification of raw biological material used to produce archaeological artefacts is sometimes difficult or even impossible. In recent years, newly developed biochemical techniques have allowed more reliable identification of exploited animal species, even for otherwise taxonomically undiagnostic fragments, and thus can help pinpoint the geographical origin of the raw material. However, in addition to being costly, these techniques involve destructive sampling. This explains why they are rarely applied to archaeological artefacts, especially those made of precious, imported raw material or those representing intact works of art. Here, we analysed the ancient DNA (aDNA) of a medieval chess piece made of ivory of unknown origin, recovered from a medieval settlement in Jambes (Namur), Belgium. This chess piece was broken during excavation. We took this unfortunate event as an opportunity to perform aDNA extraction, to try to answer three questions: 1) What Proboscidean species does the ivory come from?; 2) Can we establish the geographic origin of the ivory more precisely?; and 3) Does doing so help our understanding of (part of) the trade route followed by the ivory? We sequenced two short fragments of the mitochondrial genome and compared them with publicly available DNA data. This enabled the identification of the raw material as an African elephant (genus *Loxodonta*). Although the results cannot exclude that the ivory comes from a forest elephant, the recovered DNA sequence is currently found only among savanna elephant DNA records. The ivory likely originates from an eastern or southern African country and was therefore probably transported along the African trade route passing through the Swahili Corridor. However, the precise itinerary followed by this ivory from the African shore of the Mediterranean Sea to Europe, and then to the archaeological site from which it was recovered, remains unknown. Such identification contributes to documenting past trade networks and long-distance exchange.

1. Introduction

The use of Proboscidean ivory for figurative carving has a long tradition in Europe, dating back to the early Upper Palaeolithic (Conard, 2003). With the contraction of the range of the woolly mammoth (*Mammuthus primigenius*), which became restricted to Siberia from around 12,000 BC onward (Stuart et al., 2002), ivory was no longer available as a local resource, except as fossilised material. However, between the disappearance of the mammoth and the use of fossil mammoth ivory recovered from the Siberian permafrost, mostly exploited for crafts from as late as the 19th century AD onward (Raubenheimer et al., 1990; Rijkelijkhuisen, 2008), Proboscidean ivory was nevertheless used for carving in Europe, as for more than two millennia, elephants were the prime source of ivory. Other mammals were also exploited, mainly marine mammals, such as sperm whale (*Physeter macrocephalus*), walrus (*Odobenus rosmarus*) and narwal (*Monodon monoceros*), in a European context, or hippo (*Hippopotamus amphibius*), around the Mediterranean Sea (MacGregor, 1985). Whatever its geographic origin, from the Holocene onwards, ivory exploited in western Europe had to have been imported, either from northern regions, in the case of marine mammals, or from eastern or southern climes, in the case of elephant ivory. As a luxury product tied to long-distance exchange, ivory long remained an exclusive product reserved for the upper classes. In this context, the import of ivory, either as raw material or as a finished object, constitutes powerful evidence for tracing ancient, long-distance trade routes.

Extant elephants are divided into two genera, encompassing the African elephants (genus *Loxodonta*) and the Asian elephant (genus *Elephas*). Modern DNA analyses, including more comprehensive genomic analyses, support the distinction of two African species, which were formerly considered subspecies of the same species: the African forest elephant (*Loxodonta cyclotis*) and the African savanna elephant (*Loxodonta africana*) (Rohland et al., 2007; Shetty & Vidya, 2011). Nowadays, both species inhabit territories south of the Sahara (Figure 1), with the African savanna elephant mostly found in the eastern and southern parts of Africa and the African forest elephant mostly found in the western and central parts (Wittemyer, 2011). However, the current distribution does not necessarily reflect historical distributions. In addition, African savanna elephants have been reported from Central and West Africa, in transitional environments between forest and savanna where the two species can overlap and potentially interbreed (Mondol et al., 2015). Potential hybrids ($P > 0.95$; Figure 1) have been detected by means of genetics in the Garamba region of the north-eastern part of the Democratic Republic of Congo; along the border between Uganda and the Democratic Republic of Congo; in the northern part of the Central African Republic; and along the border between Benin and Burkina Faso (Mondol et al., 2015).

Although the African elephant was once present in North Africa (Figure 1), it went extinct as a consequence of Roman overexploitation, probably well before 600 AD (see Guérin, 2013, for a summary) and perhaps starting as early as the 2nd century AD (Ogata, 2017). The taxonomic status of this extinct North African elephant, frequently named *Loxodonta africana pharaoensis*, remains unclear.

The Asian elephant (*Elephas maximus*) ranges west to east from India to southern China, and south into Indonesia, where it mostly occurs as isolated populations. Formerly, it has been proposed that the natural range of the Asian elephant extended even farther westward, into Mesopotamia, i.e., modern Iraq, Syria and southern Turkey (e.g., Olivier, 1978), where it would have formed a relict population described as the Syrian elephant (*Elephas maximus asurus*; Deraniyagala, 1955). However, this hypothesis of a natural occurrence of the Asian elephant in Mesopotamia has been questioned by several scholars, from both a biological and an archaeological standpoint (Caubet & Poplin, 2010; Lister et al., 2013; Vila, 2014).

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3 Recently, Çakırlar & Ikram (2016) reviewed the available evidence and proposed that this
4 local population of the Asian elephant, or Syrian elephant, was not endemic but was instead
5 introduced to Mesopotamia by humans; captive animals eventually returned to the wild to
6 form naturally breeding populations, between approximately 1800 and 800/700 BC.
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9 Macroscopic traits generally enable the distinction between ivory from Proboscidean and
10 other animal groups because Proboscidean ivory displays a characteristic ‘chevron’ pattern
11 visible in cross-section. This pattern is created by intersecting lines called Schreger lines
12 (Espinoza & Mann, 1992). Measuring the angles formed by these lines generally allows the
13 separation of mammoth (*Mammuthus primigenius*) from elephant (*Loxodonta* sp. and
14 *Elephas maximus*) ivory, as Schreger lines form acute angles in mammoth and obtuse angles
15 in living species, although some overlap exists between 90° and 115° (Espinoza & Mann,
16 1992). More research is needed to assess the potential of Schreger angles for distinguishing
17 between African elephants *lato sensu* and Asian elephant (Trapani & Fisher, 2003). Inner
18 Schreger angles, which are those formed close to the pulp cavity, are poorly visible and
19 should be avoided as diagnostic features; taxonomic distinction should be made using the
20 angles of the outer Schreger lines only (Espinoza & Mann, 1992). During study of these
21 artefacts, these characteristics are sometimes difficult to assess, in particular in small or thin
22 objects, depending on how the piece was extracted from the tusk.
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26 As it is not possible to attribute elephant ivory to species using morphologic characteristics,
27 identification tools employing spectrometry (which is also non-destructive) and biochemical
28 analysis (which is destructive) have been tested. Among these non-destructive techniques, X-
29 ray fluorescence has been shown to be effective in differentiating between African elephant
30 and Asian elephant (Buddhachat et al., 2016), and near-infrared Fourier transform Raman
31 spectroscopy (NIR FT-Raman), in distinguishing between ivory from mammoth and ivory
32 from elephant, but also between ivory from African forest elephant tusks, sometimes called
33 ‘hard ivory’, and that from African savanna elephant tusks, termed ‘soft ivory’ (Shimoyama
34 et al., 1997; Shimoyama et al., 2003). Destructive biomolecular techniques, including those
35 involving the study of isotopes, proteins, and DNA, can allow the identification of the taxon
36 from which the ivory derives and thus help pinpoint the geographic origin of the ivory more
37 precisely. These destructive biomolecular techniques were primarily used to help fight
38 elephant poaching, through the identification of ivory sold on the international market in
39 recent times. Both large mitochondrial DNA fragments and nuclear loci (microsatellite data)
40 were used to investigate the geographic origin of ivory seizures (Comstock et al., 2003;
41 Ishida et al., 2013; Mailand & Wasser, 2007; Wasser et al., 2015; Wasser et al., 2007).
42 Today, the ivory trade is tightly controlled.
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46 Biomolecular techniques have also been applied to archaeological ivory material. Isotopic
47 analyses were successfully conducted on hippo and elephant ivory from the 14th-century BC
48 shipwreck at Uluburun, Turkey (Lafrenz, 2004); on elephant ivory from a 17–18th century
49 AD site in Amsterdam, the Netherlands (Rijkkelijkhuizen et al., 2015); and on elephant ivory
50 from a 19th century AD site in East Africa (Coutu, Lee-Thorp, et al., 2016). Combined
51 analyses of isotopes and peptides have also proved successful, on 7th–10th-century AD
52 elephant ivory from KwaZulu-Natal, South Africa (Coutu, Whitelaw, et al., 2016). More
53 recently, broad genomic data collected from a post-medieval unmodified ivory tooth found in
54 Portugal, as well as from the raw ivory of the Portuguese *Bom Jesus* shipwreck, provided
55 evidence for historical ivory trade between West Africa and Portugal (de Flamingh et al.,
56 2021; Psonis et al., 2020). However, aDNA analysis is seldom applied to archaeological
57 artefacts to track raw material sources.
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Researchers are inhibited from applying such destructive techniques to intact archaeological objects made of ivory for two main reasons. These are rare finds in the archaeological record, frequently carved into works of art that are precious testimonies of past human cultures. This pitfall was noted by François Poplin (2012), who nevertheless recognised at the time that aDNA studies are key to future research into raw materials. In addition, the proteins and ancient DNA are oftentimes degraded, and the success of the analysis is therefore not guaranteed. Since then, a combination of short mitochondrial and nuclear DNA sequences has been shown to be useful for identifying elephant species from old tissue samples (Cappellini et al., 2014; Ngatia et al., 2019). There are few reports of DNA analysis on worked ivory in the scientific literature, especially of archaeological worked ivory. A few communications by wildlife forensic investigators (e.g., the U.S. Fish & Wildlife Service Forensics Laboratory) used DNA extracted from recent ivory carvings or idols to identify elephant species (Gupta et al., 2011). Recently, Ewart et al. (2020) optimised DNA extraction protocols on both raw and worked elephant ivory and demonstrated that powdering the ivory directly with a drill, as well as short decalcification times (2 hours), produces results comparable to sample powdering in liquid nitrogen and a longer decalcification time (3 days). In addition, sampling the cementum and using a total demineralisation DNA extraction method contribute to minimising the amount of elephant ivory that is necessary in order to recover DNA (Winters et al., 2018). These improvements may encourage more frequent DNA analysis, to better complement the other biomolecular approaches that are already available for worked archaeological ivory.

We had the opportunity to study a finished chess piece made of ivory dating to before the 13th century AD, found in a medieval context during an archaeological rescue excavation conducted in Jambes (Namur, Belgium). The piece was slightly damaged during excavation, which allowed us to sample small fragments of the inner part of the object that could not be refit during the restoration process. They were tested for the presence of aDNA in the hope of identifying the Proboscidean species from which the ivory originates and, additionally, to try to establish the geographical origin of the ivory, as this could help reconstruct medieval trade routes.

2. Material and methods

Archaeological excavation performed in 2017 along the Meuse River in Jambes, part of the modern-day city of Namur (Belgium; Figure 1), brought to light destruction layers of a medieval building that are associated with a fire event. This building is interpreted as a habitation, possibly including horse stables on the ground floor. Several remarkable finds, such as a coffer key made of copper alloy and the ivory chess piece investigated here, underline the aristocratic status of the inhabitants, who likely belonged to the Namur elite. If the keeping of horses were proven, this would further underline their status (Vanmechelen et al., 2018b).

The ivory chess piece (inventory number NR.17.JAMA.01045.0002; Figure 2) is the first such item to be discovered from a secure archaeological context in Wallonia (the southern half of Belgium). The fire event that destroyed the building where the chess piece was discovered is dated to the beginning of the 13th century AD based on the associated material culture (Vanmechelen et al., 2018a, 2018b). This gives a *terminus ante quem* for the dating of this chess piece. Its schematic, or abstract, shape corresponds to set A of the two style sets established by Anna Contadini (1995) for the collection of the Ashmolean Museum (Oxford). Style set B comprises pieces that represent figures in a more naturalistic way. With the documentation currently available, it is not possible to establish a chronology for these two styles or to know precisely when chess pieces became abstract, since no chess piece older

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3 than the 9th century AD has yet been discovered; but it is likely that both styles co-existed
4 before the Islamic era (Contadini, 1995). Pieces related to style set A are the oldest known,
5 appearing as early as the 9th century AD, but are in use until the 15th century AD. In
6 contrast, the scarcer pieces of style set B appear later (Contadini, 1995). The protrusion at the
7 front of the Jambes chess piece symbolises the horse protome, which identifies the piece as a
8 knight (Contadini, 1995; Grandet & Goret, 2012). Similar though not identical knights have
9 been recovered from other countries in north-western Europe, such as France, at the castles of
10 Rougemont-le-Château (prior to the 13th century AD), Crèvecœur-en-Auge (11th–12th
11 century AD) and Châtenois (11th century AD) (Grandet & Goret, 2012). However, the
12 Jambes knight appears more abstract in shape than these examples.
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15 For the purpose of analysing the DNA, a total of 96 mg of ivory powder was collected from a
16 small ivory fragment from the inner part of the chess piece that was accidentally detached
17 during excavation. DNA extraction was performed in a DNA lab dedicated to ancient DNA,
18 equipped with UV lamps, under positive air pressure to avoid contamination, and where
19 Elephantidae had never before been analysed. Best practices recommended for working with
20 ancient DNA were applied (Gilbert et al., 2005; Willerslev & Cooper, 2005). In particular,
21 UV disinfection was applied before and after each experiment. Clean lab coats, masks, shoe
22 covers, and hair caps were worn for each experiment. Gloves were changed after each tube
23 opening. Contacts with other DNA labs were banned (only sterile material was used, and
24 access to other labs was not permitted before or during the ancient DNA analysis). Extraction
25 negatives (samples treated like all others but without any ivory powder inside) were included
26 in all experiments. For DNA extraction, first the outer layer of the ivory was removed, by
27 scraping off its surface using a structured tooth tungsten carbide cutter attached to a hand
28 rotary tool (8100 8v Max Rotary Tool). After 10 minutes of exposure to UV, ivory powder
29 was collected by drilling inside the ivory fragment, using the hand rotary tool at 5000 rpm,
30 with an engraving cutter (1.6 mm). DNA was extracted from the ivory powder following the
31 protocol of Dabney et al. (2013) and was eluted twice in 45 µl of Tris-EDTA buffer with
32 Tween-20. From this extracted DNA, we attempted to amplify six short DNA fragments (four
33 mitochondrial and two nuclear fragments) by polymerase chain reaction (PCR). The short
34 mitochondrial DNA fragments were selected because they contain diagnostic positions to
35 discriminate between the Asian elephant (genus *Elephas*) and the African elephants (genus
36 *Loxodonta*) and may provide some information on the geographic origin of the ivory
37 (Cappellini et al., 2014). In addition, we tried to amplify two nuclear fragments that contain
38 nucleotide sites that are diagnostic for the two African elephant species, which cannot be
39 identified using mitochondrial data. Indeed, due to hybridisation, some savanna elephants
40 carry the mitochondrial DNA originally found in forest elephants (Ishida, Demeke, et al.,
41 2011; Ishida et al., 2013). Two mitochondrial fragments of 331 and 33 base pairs (bp) of the
42 D-loop region were targeted with the primer pairs AFDL3/AFDL4 (Eggert et al., 2002; Lee et
43 al., 2013) and Ele-CytbF1/Ele-CytbR1 (Cappellini et al., 2014), respectively. One additional
44 mitochondrial fragment of 116 bp of the cytochrome *b* gene was targeted with the primer pair
45 L15123/H15240 (Ngatia et al., 2019). One last mitochondrial fragment of 53 bp of the ND5
46 gene, coding for the NADH dehydrogenase 5 protein, was amplified using the primers Ele-
47 ND5-F3/Ele-ND5-R3 (Cappellini et al., 2014). The nuclear fragments, consisting of 4 and 26
48 bp of the PHK (phosphorylase kinase) and the BGN (biglycan) genes, respectively, were
49 tested using the primer pairs PHK-s1F/PHK-s1R and BGN-s1F2/BGN-s1R2 (Ishida,
50 Demeke, et al., 2011; Ishida, Oleksyk, et al., 2011). Each PCR consisted of a mix of 25 µl
51 with 3 µl of DNA template, 1.5 mM of Mg²⁺, 0.2 mM of each dNTP, 0.5 µM of each primer,
52 0.2 µg/µl of bovine serum albumin, 0.03 units/µl of Platinum Taq DNA Polymerase and 1×
53 PCR buffer (Invitrogen, ThermoFisher). The PCR profiles for the mitochondrial markers
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3 consisted of a first step at 94 °C for 3 min; a second step of 40 cycles at 94 °C for 30 s,
4 primer annealing at 51, 52, 52 and 57 °C (for the primer pairs L15123/H15240, Ele-
5 CytbF1/Ele-CytbR1, Ele-ND5-F3 and Ele-ND5-R3 and AFDL3/AFDL4, respectively) for 30
6 s and 72 °C for 15 s; and a final step at 72 °C for 7 min. For the nuclear markers, a
7 touchdown PCR was applied, with 45 cycles at annealing temperatures of 60, 58, 56, 54, 52
8 and 50 °C for 3, 5, 5, 5, 5 and 22 cycles, respectively. PCR reactions were repeated with the
9 two elutions obtained from the DNA extraction. PCR products were purified using ExoSAP-
10 IT (ThermoFisher) and then sequenced in both directions using the BigDye Terminator v.1.1
11 Cycle Sequencing Kit (Life Technologies) and an ABI 3130xl Genetic Analyser
12 (LifeTechnologies). Chromatograms were visualised using CodonCode Aligner v. 8.0.2
13 (CodonCode Corporation). Base calling and consensus sequence were double checked
14 manually and independently, by two researchers. The Basic Local Alignment Search Tool
15 (BLAST) (Zhang et al., 2000), available on the website of the National Center for
16 Biotechnology Information (<https://blast.ncbi.nlm.nih.gov>), was used to align the DNA
17 sequence obtained here with the public nucleotide collection and to retrieve the most similar
18 sequences (allowing a maximum of 5000 output sequences). In parallel, we aligned the
19 fragments that were successfully sequenced here with elephantid DNA sequences
20 downloaded from GenBank using the tool ClustalW (Thompson et al., 1994), implemented in
21 Mega 7.0.26 (Kumar et al., 2016). We computed all pairwise distances in Mega 7.0.26
22 (Kumar et al., 2016). Finally, we constructed a haplotype network (or reticulated graph) for
23 the DNA marker showing the most variations in order to visualise the relationships among
24 the short DNA sequences available for the elephant genus to which the previous analysis
25 could assign our sample based on our ancient DNA fragment. This analysis was performed in
26 PopART (<http://popart.otago.ac.nz>), using the median joining network method (Bandelt et al.,
27 1999).
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3. Results and discussion

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35 A macroscopic examination verified that the raw material used to shape the medieval chess
36 piece from Jambes is Proboscidean ivory (Goffette & Pigière, 2017). The piece was carved in
37 the axis of a tusk, and its base, cut transversally to the axis, shows a polished cross-section,
38 allowing observation of the characteristic Schreger lines (Espinoza & Mann, 1992; Locke,
39 2008; Raubenheimer et al., 1990). However, these lines and the angles they form are difficult
40 to distinguish on the Jambes piece, even with the aid of a photocopier machine, which usually
41 yields a good reading of these lines. The angles measured fall within the overlap between
42 Asian and African elephant, but also within that between elephants and mammoth (mean of
43 103°, measured on 10 angles), which precludes reliable identification of the species involved
44 based on morphological features.
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48 DNA sequences were obtained from the ivory powder for two of the six fragments targeted:
49 33 bp and 53 bp of the mitochondrial D-loop and the ND5 gene, respectively (GenBank
50 accession numbers MZ374757 and MW557501). They correspond to the two smallest
51 mitochondrial fragments of our experiments, suggesting that the DNA in our sample was
52 degraded to a point that prevented the amplification of nuclear fragments or of mitochondrial
53 fragments longer than ca. 100 bp. This observation contributes to authenticating the ancient
54 origin of the DNA fragments sequenced here. Sequences obtained from independent PCRs
55 with the two elutions of the DNA extraction as template and using the same primer pairs were
56 identical. The BLAST search retrieved public nucleotide sequences that matched exactly
57 (100% coverage and 100% identity) the sequences retrieved here for D-loop and ND5. For D-
58 loop, the 5000 exact matches that were displayed were from *Loxodonta* and other species (but
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not *Elephas maximus*; Data S1) while for the ND5 gene (Data S2), the exact matches were DNA sequences that are exclusively from African savanna elephants (*Loxodonta africana*), all of which have been identified to the species level using nuclear data (microsatellites or nuclear markers) (Ishida et al., 2013; Lei et al., 2008; Murata et al., 2009). The alignment obtained here for the 33 bp D-loop fragment (our sequence and published D-loop sequences of *Loxodonta*; Data S3) showed only two variable sites. Two of the three most frequent haplotypes (representing 92% of the sequences and including the haplotype obtained here; Data S4) were from both *Loxodonta africana* and *Loxodonta cyclotis*. Compared with other elephantids, the ND5 sequence obtained here showed zero to six nucleotide differences with other sequences from *Loxodonta africana* (African savanna elephant), six to seven differences with *Loxodonta cyclotis* (African forest elephant) and six to twelve differences with *Elephas maximus* (Asian elephant). The alignment based on African elephants comprised only 11 variable sites and 11 different haplotypes (Data S5 and S6). This 53 bp DNA sequence was found in the sequences occurring exclusively in the savanna elephant (Figure 3A) and, more precisely, in the African ‘savanna-wide’ subclade (belonging to ‘S’ clade in Ishida et al., 2013), which is distributed in the savanna belts immediately south of the Sahara, as well as across eastern and southern Africa. It is also found in Cameroon (Figure 1), in a single area that is disconnected from the remnant of the known distribution of the subclade. We have to note that the geographical distribution of all elephants sequenced so far represents a partial view of their current and past distribution. For example, individuals from the ‘savanna-wide’ subclade may exist but may not yet have been reported in the geographic region connecting the spot in Cameroon to the remainder of its distribution. Based on current knowledge, the ‘savanna-wide’ subclade represents the vast majority of the haplotypes found in Kenya and Namibia (Ishida et al., 2013). Among all ND5 sequences covering the 53 bp fragment analysed here, available for contemporary African elephants with a known geographic origin, 281 of 689 matched our ancient DNA sequence. They were represented in most specimens originating from Namibia (98%), Kenya (79%) and Tanzania (56%) (cf. haplotype ‘I’ in Figures 3A and 4, respectively). These 281 records were from six African countries: 124 from Kenya, 59 from Namibia, 46 from Tanzania, 28 from Botswana, 16 from South Africa, seven from Zimbabwe and one from Cameroon (Figure 3B). Since hybridisation has been demonstrated to occur between savanna and forest elephants (Ishida, Demeke, et al., 2011; Ishida, Oleksyk, et al., 2011), we cannot exclude that our ivory comes from a forest elephant carrying the mitochondrial DNA of a savanna elephant. However, based on the data currently available, the ‘savanna-wide’ subclade is carried only by savanna elephants. As for the geographic origin of the ivory, there is only one report of the ‘savanna-wide’ subclade outside of southern and eastern Africa. Again, based on the data currently available, which comes from 21st-century samples, the vast majority of the elephants showing the ND5 DNA sequence recovered from our ancient ivory live in southern or eastern Africa. Therefore, the ivory analysed here seems likely to stem from those regions.

The African origin of the ivory used to produce the Jambes chess piece fits the general pattern of people exploiting African elephant instead of Asian elephant for ivory craftwork in Europe and around the Mediterranean Sea. African elephant ivory was more desired than Asian elephant ivory for craftwork, at least for the production of large artefacts, since the Asian elephant grows smaller tusks (Guérin, 2013). In addition, only male Asian elephants have tusks, which reduces the number of tusks produced compared with African elephants, in which both males and females bear tusks. Therefore, in China and India, where indigenous ivory was available and exploited, there was constant demand for imported African elephant tusks during the Middle Ages (Guérin, 2010, 2013). The related export to China and India continued beyond the medieval period, as illustrated by the shipwreck of the *Bom Jesus*, lost

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3 in 1533, while sailing on the India route with more than 100 African forest elephant tusks
4 from West Africa aboard (de Flamingh et al., 2021). African ivory was exported not only to
5 Asia, but also around the Mediterranean basin and farther north in Europe. The hard ivory of
6 the African forest elephant has sometimes been preferred for carving to the softer ivory of the
7 African savanna elephant, such as in post-medieval Japan; however, in China, carvers were
8 not selective (Nishihara, 2012).
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10 From the beginning of the Roman period to the 6th century AD, elephant ivory reaching
11 Europe originated from North Africa and from Aksum, in the Ethiopian Highlands (Horton,
12 1987). At the end of the 6th century AD, the elephant ivory supply to Europe suffered from
13 the decline in Mediterranean trade that resulted from the economic instability that followed
14 the fall of the Western Roman Empire. Between the 6th and the 10th century AD, elephant
15 ivory working around the Mediterranean Sea and in Europe apparently strongly diminished,
16 although existing ivory artefacts may have been re-worked (Horton & Middleton, 2000).
17 Elephant ivory was replaced by other materials, such as walrus ivory (Horton & Middleton,
18 2000). Between the 9th and the 13th century AD, the walrus ivory trade flourished and tusks
19 were imported from the northeast Atlantic and Greenland into Europe (Star et al., 2018), to
20 the point of creating competition with elephant ivory (Dectot, 2018). However, from the 10th
21 century AD onward, elephant ivory was again imported in large quantities in Europe,
22 suggesting that a new source became available, with raw material likely originating in sub-
23 Saharan Africa and passing through the Red Sea (Horton & Middleton, 2000). During the
24 10th century AD, the African ivory trade was controlled by people known today as the
25 Swahili, who occupied 2400 km of the eastern coast of Africa, including the shores of
26 modern-day Somalia, Kenya, Tanzania and Mozambique (Horton & Middleton, 2000). Their
27 ancestors traded tusks with inland, Bantu-speaking people, who obtained elephant tusks from
28 two major sources. The first and most accessible was located in modern-day Kenya, while the
29 second was farther from the coast, in modern-day Zimbabwe, southern Mozambique and
30 South Africa (Guérin, 2010, 2013). The tusks travelled along the East African coast, via the
31 Swahili Corridor, to the Red Sea, before reaching Egypt, which was part of the Fatimid
32 empire starting in 969 AD (Guérin, 2010, 2013; Horton, 1987). In Egypt, tusks were carried
33 to the Mediterranean ports partly through the desert and along the River Nile, to Cairo and to
34 Alexandria, from where they were shipped to Christian Europe. This period, spanning the
35 10th and 11th centuries AD, saw a significant development of ivory carving in Egypt, given
36 its central position in the ivory trade, as well as in parts of Europe where tusks were
37 imported, from Byzantium to Al-Andalus (southern Spain) (Guérin, 2010). During the late
38 11th to 12th centuries AD, the number of tusks traded around the Mediterranean Sea declined
39 because of political instability in Egypt, resulting in a dearth of elephant ivory in northern
40 Europe (Guérin, 2010).
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47 At the same time, an alternative trade route was in use that brought ivory from another
48 African source. This trans-Saharan commercial route connected the Mediterranean world
49 with sub-Saharan Africa via a network of caravan routes across the Sahara Desert, led by
50 Amazigh merchants. Although primarily used to transport gold from the rich mines located in
51 present-day Mali and Guinea, then ruled by the Ghana Empire, the trans-Saharan caravans
52 also transported ivory of West African elephants (Guérin, 2013). From 909 AD onward, the
53 part of the Mediterranean coast of North Africa called Ifrīqiya, which covered present-day
54 Algeria, Tunisia and Libya, was under the control of the Fatimid dynasty, which took
55 advantage of the pre-existing trans-Saharan route network (Guérin, 2013). After reaching the
56 Mediterranean shore, ivory was shipped from Ifrīqiyan ports to Europe, the closest being
57 those located in southern Italy, such as in Sicily, Salerno or Amalfi (Guérin, 2013). It is
58 therefore no surprise that Italy is identified as the most likely entry point of chess into
59 Europe (Guérin, 2010).
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3 Europe, together with Al-Andalus, where the game was imported by Islamic traders shortly
4 before 1000 AD (Murray, 1913). The game of chess then spreads rapidly to central and
5 northern Europe, reaching Germany and France within a few decades, whereas it took about
6 two centuries to reach northern Scotland and Scandinavia (Bourgeois, 2012, 2015; Murray,
7 1913).
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10 Although the Jambes chess piece is small and did not require a large tusk for its production, it
11 fits in the general pattern of exploiting African rather than Asian elephant ivory for craft
12 purposes. The benefit of our results lies in suggesting the source of the ivory within Africa.
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14 Having established the origin of the ivory of the Jambes chess piece, we can contribute to
15 determining the route that was followed at the time to distribute African ivory to Europe. The
16 ivory tusks transported via the trans-Saharan route was mainly of West African origin
17 (Guérin, 2013). In contrast, the ivory tusks transported along the Swahili Corridor mostly
18 originated from South and East Africa, within the current boundaries of Kenya, Mozambique,
19 Zimbabwe and South Africa (Guérin, 2013; Horton, 1987). The ‘savanna-wide’ haplotype
20 detected in the aDNA of the ivory of the Jambes chess piece has so far not been detected in
21 contemporary elephant populations living to the west of Cameroon (Ishida et al., 2013),
22 seemingly excluding a West African origin for the Jambes ivory. Instead, the fact that the
23 ‘savanna-wide’ haplotype is widespread in eastern and southern African countries (Ishida et
24 al., 2013) indicates that the ivory used to make the chess piece from Jambes was likely
25 transported to Egypt via the Swahili Corridor and the Red Sea, from where it entered Europe.
26 Guérin (2013) suggests that before the conquest of Egypt by the Fatimids in 969 AD, ‘ivory
27 came from West Africa and not through the Swahili coast’. On this basis, given that the ivory
28 used to produce the Jambes chess piece likely transited through the Swahili Corridor, we
29 argue that this chess piece was probably crafted between the end of the 10th century and the
30 beginning of the 13th century AD, which is the *terminus post quem* based on the dating of the
31 archaeological context from which the chess piece was recovered.
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35 It remains unknown how this chess piece reached Jambes, or through which port it entered
36 Europe and in what state, that is, carved or uncarved. Indeed, the place where the chess piece
37 was carved is unknown. Workshops in Mediterranean Europe mostly produced figurative
38 ivory chess pieces (style set B) comparable to various finds from northern Europe, such as the
39 so-called Charlemagne chess set, produced in southern Italy. Comparable figurative pieces
40 made of red deer (*Cervus elaphus*) antler were recovered in France from the castle of Loisy
41 (10th–11th century AD) (Grandet & Goret, 2012). In contrast, the schematic style of the
42 Jambes knight (style set A) was most popular in the Islamic world. However, this chess piece
43 need not necessarily have been produced in, or even close to, the Islamic world, as schematic
44 representations had a strong influence on the types of medieval chess pieces that were
45 produced in Europe (Contadini, 1995). This is illustrated, for example, by the abstract chess
46 pieces made of cervid antler recovered from the castle of Châtenois (11th century AD)
47 (Grandet & Goret, 2012). Both styles co-existed in the productions of north-western Europe,
48 where intermediate, partly figurative pieces were also carved (Bourgeois, 2012). Given the
49 diversity of shapes in the pieces produced in north-western Europe, the Jambes chess piece
50 may be a European imitation of an Islamic form.
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54 **4. Conclusion**

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56 This study successfully demonstrates the effectiveness of aDNA analysis as a tool to identify
57 the source of ancient ivory. We used very small fragments of the object recovered during an
58 archaeological excavation, which were unusable for the purpose of restoration, to extract and
59 analyse aDNA to identify the species. Although macroscopically it is obviously Proboscidean
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3 ivory, the morphometric criteria observed on this chess piece preclude an accurate taxonomic
4 identification, as they fall within the overlap between extant African (*lato sensu*) and Asian
5 elephants and the now-extinct woolly mammoth. The recovered DNA identifies an African
6 elephant (genus *Loxodonta*) as the source of the raw ivory. The finding that the ivory from
7 which this chess piece was made likely comes from an African savanna elephant from a
8 region where the 'savanna-wide' haplotype is represented suggests that this ivory reached
9 Europe via the Swahili Corridor, the Red Sea, and Egypt.
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27 constructive comments, as well as Suzanne Needs-Howarth for copy editing the English text.
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30 31 **Supporting information**

32 Supporting information is available online (in the Supporting Information section at the end
33 of the article), including the best-matching public DNA sequences retrieved from the BLAST
34 searches (Data S1 and S2) and the alignments and the haplotype compositions of the D-loop
35 (Data S3 and S4) and ND5 (Data S5 and S6) DNA fragments analysed here.
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38 39 **Conflict of interest**

40 The authors have no conflict of interest to declare.
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44 45 **[figure captions]**

46 Figure 1. Map showing the location of Jambes (Namur, Belgium) and illustrating the past
47 distribution of African savanna elephant (*Loxodonta africana*) and African forest elephant
48 (*Loxodonta cyclotis*) (Grubb et al., 2000; Furstenburg, 2010). The distribution of the
49 'savanna-wide' haplotype is based on Ishida et al. (2013), and the records of potential hybrids
50 ($P > 0.95$) detected from DNA samples are taken from Mondol et al. (2015). The Swahili
51 Corridor and the main trans-Saharan routes are represented based on Horton (1987), Guérin
52 (2010) and Smith (2015), respectively. Map modified from <http://d-maps.com>
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54 Figure 2. Four views of the ivory chess piece from Jambes (inventory number
55 NR.17.JAMA.01045.0002; photographs R. Gilles © AWaP)
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57 Figure 3. Haplotype networks constructed with the median joining method and representing
58 the ND5 DNA sequences (53 bp) available for African elephants (*Loxodonta* spp) and
59 obtained here from the chess piece. All identical sequences (forming a haplotype) are
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grouped in a circle whose size is proportional to the number of sequences forming this haplotype. The 11 haplotypes are labelled with Roman numerals (I–XI) and are connected by segments representing the minimum number of substitutions from one haplotype to another. The number of short lines on these segments indicates the number of substitutions separating one haplotype from its neighbour. The pie chart inside each circle refers to the species identification (A) or the country of origin (B) of the specimens showing each haplotype

Figure 4. Geographical distribution of the ND5 DNA sequences (53 bp) available for African elephants (*Loxodonta* spp) and analysed here (Data S2 and S6). Colours in the pie charts represent the haplotypic compositions for each country. *: Haplotype I (white) was obtained from the chess piece. The size of the 13 pie charts is proportional to the total number of sequences from each country

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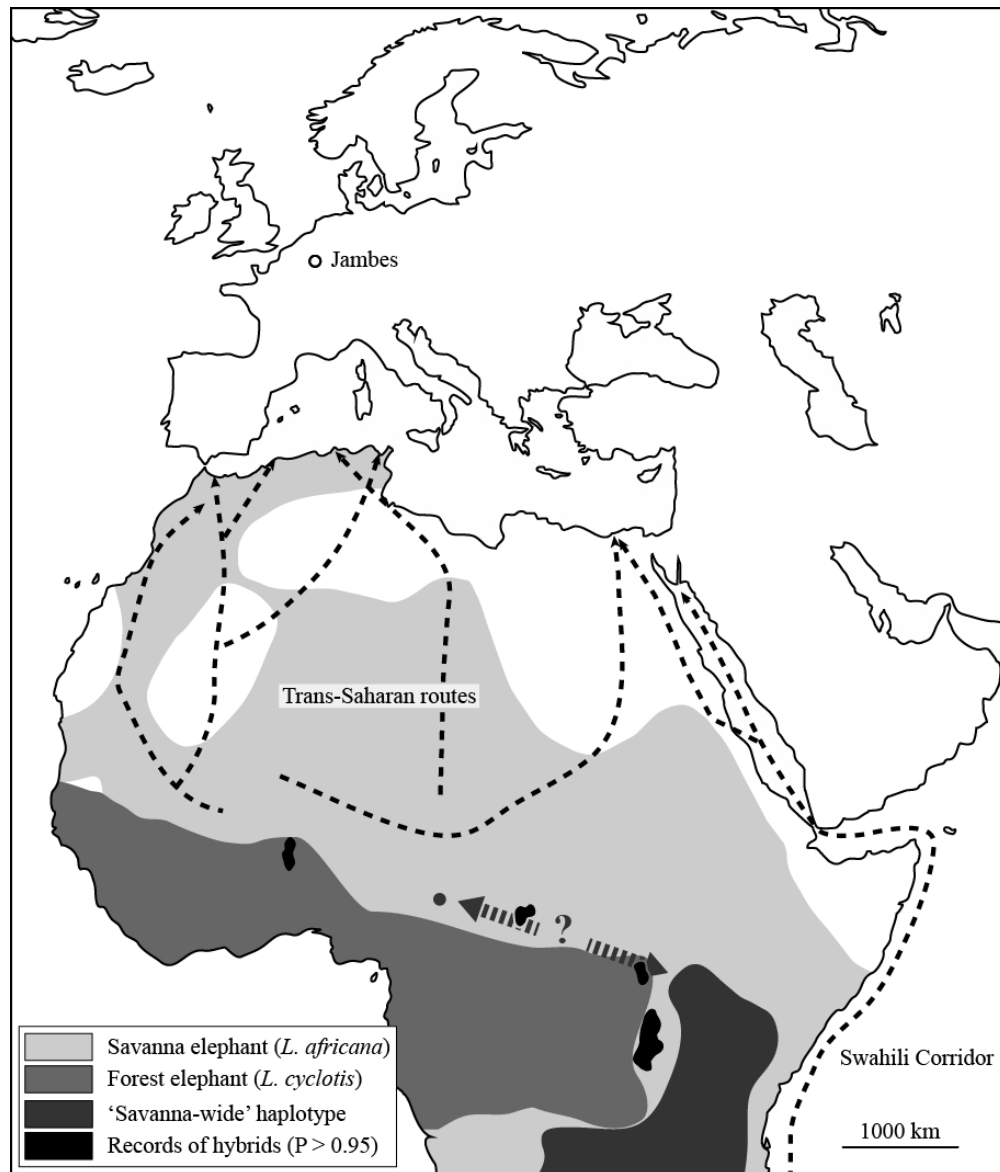
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44 Figure 1. Map showing the location of Jambes (Namur, Belgium) and illustrating the past distribution of
 45 African savanna elephant (*Loxodonta africana*) and African forest elephant (*Loxodonta cyclotis*) (Grubb et
 46 al., 2000; Furstenburg, 2010). The distribution of the 'savanna-wide' haplotype is based on Ishida et al.
 47 (2013), and the records of potential hybrids ($P > 0.95$) detected from DNA samples are taken from Mondol
 48 et al. (2015). The Swahili Corridor and the main trans-Saharan routes are represented based on Horton
 49 (1987), Guérin (2010) and Smith (2015), respectively. Map modified from <http://d-maps.com>

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Figure 2. Four views of the ivory chess piece from Jambes (inventory number NR.17.JAMA.01045.0002; photographs R. Gilles © AWaP)

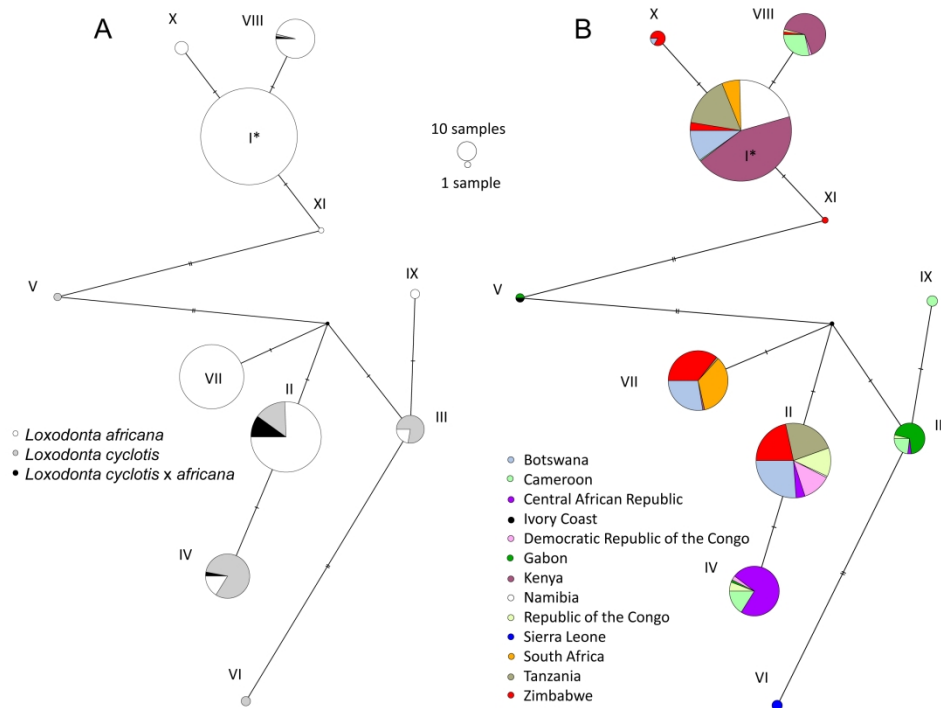


Figure 3. Haplotype networks constructed with the median joining method and representing the ND5 DNA sequences (53 bp) available for African elephants (*Loxodonta* spp) and obtained here from the chess piece.

All identical sequences (forming a haplotype) are grouped in a circle whose size is proportional to the number of sequences forming this haplotype. The 11 haplotypes are labelled with Roman numerals (I–XI) and are connected by segments representing the minimum number of substitutions from one haplotype to another. The number of short lines on these segments indicates the number of substitutions separating one haplotype from its neighbour. The pie chart inside each circle refers to the species identification (A) or the country of origin (B) of the specimens showing each haplotype

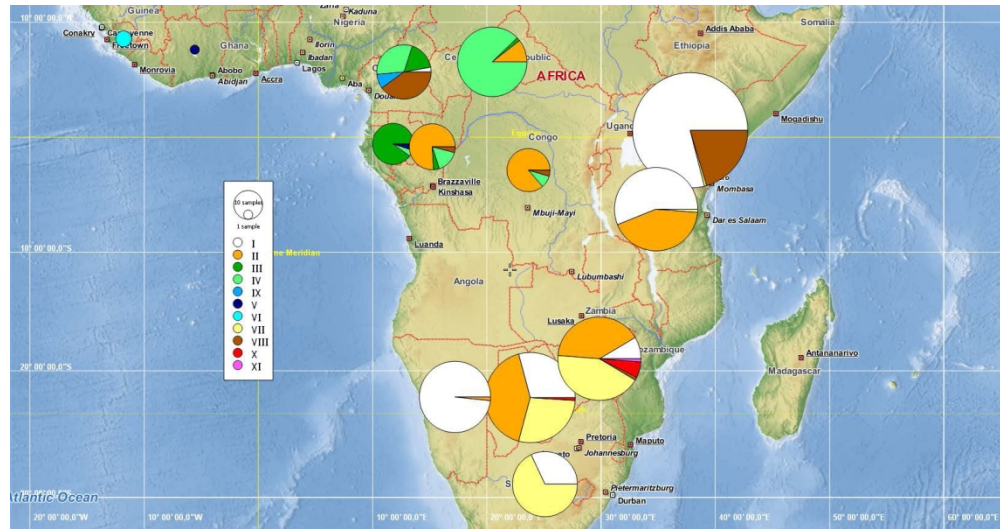


Figure 4. Geographical distribution of the ND5 DNA sequences (53 bp) available for African elephants (*Loxodonta* spp) and analysed here (Data S2 and S6). Colours in the pie charts represent the haplotypic compositions for each country. *: Haplotype I (white) was obtained from the chess piece. The size of the 13 pie charts is proportional to the total number of sequences from each country