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Review

Family in Medieval Society: A Bioarchaeological Perspective

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Abstract: One of the periods with the greatest social, cultural, and religious changes was, without a doubt, the European medieval period. The concept of "*Family*" was one of the fields that gradually evolved, from individuals who shared the same biological lineage, to members of the same "*House*". One of the ways to study the concept of "*Family*" in ancient periods is through a bioarchaeological perspective, where both anthropology and genetics have proven to be essential disciplines for studying "*Families*". Through burial rituals, observing whether the graves were single or multiple, as is carried out in the study of human remains, we discuss the profound contribution of anthropology to the "*Family*" investigation, through mobility studies, the investigation of biological sex, observing certain congenital anomalies or, even, the study of certain ancient infectious diseases. Concerning genetics, the study of bones or teeth allows us to determine whether individuals were from the same close family or if they belonged to the same lineage through the maternal and paternal sides, being one of the only scientific ways of proposing social relationships between individuals, such as that created through adoption.

Keywords: family; bioarchaeology; Middle Ages; anthropology; genetics

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1. Introduction

One of the periods of greatest cultural and social exchange was the European medieval period (the 5th century A.D. to the 15th century A.D., approximately). Europe, the scene of profound previous transformations, from the Neolithic period to the Bronze Age (Bloxam 2023), during and after the Roman period in the West (Maschek 2024), was faced with social transformations brought about by different cultures, such as Jews and Muslims, during the medieval period. One of the reasons for our interest in studying the concept of "family" in medieval Europe is precisely the possibility that it was one of the social areas where human beings experienced the most changes. From the concept and form of "marriage", through the concepts of "being the son of" and "house of societies" developed by Lévi-Strauss (1984, 1987) and Lévi-Strauss and Modelski (1999), the concept of "family" was shaped in medieval European society, in a context where the word of religion was gaining increasing prominence.

According to Johann Bachofen, in the 19th century, the first humans were organized into matriarchal family groups. Potentially, "*the father figure*" later replaced "*the Mother*" as the leader of society (Allen 1999), as the "*Man, the hunter*", and as a central figure leaving "*the family*" and "*maternal*" perception (Maynes and Waltner 2012), although this perspective may be more of a result of the interpretation of scientists and does not really correspond to the reality of that time (Anderson et al. 2023). Concerning the Neolithic period in Europe, it is probable that the vision of the "*group*" changed, since now it searches for permanence

and prosperity (Maynes and Waltner 2012). The evidence about the Bronze Age does not demonstrate substantial contrasts between women and men, indicating possible equality within the "*family group*" already from infancy (Whitehouse 2006). Two important periods to consider just before Medieval Europe were those of Greek society and the Roman Empire. In both civilizations, the "*family*" was already considered the "*social unit*" (Moulton 1998).

1.1. Defining Family in the Middle Ages

The family was a plastic concept, since before the mid-17th century, when "*baptism certificates going back to grandparents*" began to be available, belonging to a lineage depended largely on oral tradition. On the other hand, according to Casey and Hernández-Franco (1997), in the conditions of pre-industrial society, it is crucial to emphasize raising someone in someone else's home, since King Alfonso the Wise himself indicated that "*raising someone within your home, was a relative or not, it is one of the greatest "blessings" that one person can give to another*", and that the lucky one "*must honour the one who raised him in all things and has reverenced him well as if he were his father*" (Casey and Hernández-Franco 1997). According to Herlihy (1983), what distinguished families in the medieval world were three different ideas, based on "*a particular composition, a particular structure, and a particular set of emotional ties binding the members*", indicating that households were generally uniform in medieval societies, whether in urban or rural areas, or "*up or down the scale of wealth*".

1.2. Religion and the Family "Construction"

The European "medieval world" was multi-cultural, comprising an extensive range of geographical regions, from the Mediterranean to the Baltic Seas, and from the Atlantic coast of North Africa to the Central Asian Mongolian Khanate of the Golden Horn (Mitchell 2007). Traditionally, four cultures were considered predominant: the Roman–Germanic culture in Western Europe, the Byzantine Empire in the eastern Mediterranean, the Muslim culture of the southern Mediterranean, and that of Jews. Although Jews have always been distinct from other cultures in terms of their customs, they have always been found together with the previously mentioned cultural practices (Mitchell 2007). Religion is an essential piece in the medieval life puzzle. On the one hand, although Muslims and Jews have their proper customs, in European medieval societies, they lived more or less following the laws of each country or region, especially regarding polygamy, which was prohibited in most medieval European societies.

In practically most medieval European societies, Roman-Christian precepts were followed, especially concerning "family morality". It was probably not until the 12th century that the Catholic Church proposed a structured *Canon Law* of marriage. Previously, *Secular Law*, Roman legislation, or the "barbarian" codes had guided the conduct of Christians concerning marital and domestic issues. Indeed, the 6th century *Corpus Juris Civilis* of Emperor Justinian permitted divorce, similarly to Roman law. Until the 12th century, the Church limited its interferences in matrimonial concerns due to issues of *sin* and *penitence* (Herlihy 1987). Marital contracts, dowry, bride wealth, and inheritance were *secular* issues. Indeed, according to Herlihy (1987), the Church "*looked upon the state of matrimony as distinctly inferior to virginity and even to widowhood*" (McNamara 1983). However, Christian doctrines exerted an intense effect on aptness for marriage (Ozment 1983), assuming the requirements of Roman law concerning the age of the subjects of marriage (twelve completed years for girls and fourteen for boys) and sexual maturity (Herlihy 1987).

One of the fields in which the Church deeply intervened was that of the "*incest question*", in response to which it increased the prohibitions to the full seven degrees, coinciding with ancient Jewish law (Goody 1983). On the other hand, the Church's insistence on monogamy encountered fierce opposition among the European elites, as several scholars have shown (Wemple 1981). According to Herlihy (1987), incest prevention meant that "*after the death of her husband, the widow cannot marry any male already in her household—not her father-in-law, not a brother-in-law, not a stepfather, or stepbrother*".

In general, the Church developed some general principles of significant implication in the future. For example, sexual morality had to be the same for both sexes (McNamara 1983), all nationalities, and all social classes. Furthermore, the union of husband and wife was both "*privileged and permanent*". Indeed, based on Ephesians 5.21-33, there is an analogy between the conjugal union and the relationship of "*Christ to the Church*".

In this sense, the history of medieval religion is deeply bonded with the history of the *family*. The monogamy regulation (Ozment 1983) and the incest prohibition somehow homogenized household units within this medieval society. According to Herlihy (1987), no other motivations so strongly influenced the behaviour of medieval society as "*family interests*" and "*religious commitments*".

The Marriage

Marriages in early medieval Europe resembled the earlier 'barbarian' model, where men and women were roughly the same age at their first marriage, and they married in their middle or late twenties (Herlihy 1985). The dominant form of marital *transfer* in early medieval Europe, from the barbarian movements until the 12th century, was the inverse dowry (Herlihy 1983, 1985). In terms of both the age of marriage and the terms of marriage, "barbarian" or late ancient practices, rather than the customs of classical Rome, provided the basic models of marriages in the early medieval West (Herlihy 1985).

In the 12th century, Pope Alexander III (1159–1189) affirmed that the spoken consent of the eligible partners alone made the marriage valid and binding. The Church asserted that "*no one and no institution can interfere with the right of a man and a woman, otherwise eligible, to marry or not to marry*" (Herlihy 1985). Feudal lords lost control over the marriages of their serfs, and even the Church saw its authority diminish since it no longer needed the blessing of a priest (Herlihy 1983). In northern European countries, the bride's endowment "in the face of the church" was the main proof that a legitimate marriage had taken place (Herlihy 1985). Perhaps most decisively, the principle challenged the authority of the parents, fathers specifically, who might seek to arrange, or prevent, the marriages of their offspring (Herlihy 1985, 1987).

Throughout medieval Europe, the terms of marriage were gradually modified to shift the burden of the matter onto the bride and her family. Italy is an example of the clear change, where documents refer to the *dos* in its classical sense of the bride's dowry (Herlihy 1985). Outside of Italy, the wealth of local traditions, their uncertainties, and the restricted number of surviving marriage arrangements make it difficult to trace a firm evolution, but, according to Herlihy (1985), there is much evidence that the treatment of women in marriage agreements was deteriorating from the late 12th century.

On the other hand, the Iberian kingdoms maintained the "older practices" of grooms giving money to brides the longest, until the 13th century. According to Herlihy (1985), some possible factors could respond to this different reality in early medieval Iberia. Women were probably valued members of the household. At the aristocratic level, they performed important administrative functions, from managing estates to making annual rewards to the knights at court. At lower social levels, women played a central role in many production processes, such as the manufacture of cloth, including such skilled operations as dyeing. During the Middle and Late Middle Ages, women lost some of these roles. The growth of administrative firms and departments limited their value as administrators (Herlihy 1985).

1.3. Kinship Models in the Middle Ages

How medieval families organised themselves and how they were structured depended significantly on socio-economic factors and, perhaps to a lesser extent, on geography and location (Mitchell 2007). Wealthy families lived in much more peaceful environments, without being exposed to a lack of food shortages or poor hygiene conditions, which allowed them to grow and prosper. On the other hand, comparing the urban environment with the rural one, rural families lived in constant uncertainty, as they depended directly on the level of harvests and what each season of agriculture provided them. Despite the profound differences between wealthy families and those without resources, between

urban and rural families, the family model was generally similar. The family was usually based on "*tradition*" and "*biology*". The society referred to as "Old Europe", of Christian Europe, was to some extent structured around lineages and/or kinship ties (Casey and Hernández-Franco 1997). From Ireland to Genoa, Tuscany or Naples, from Portugal, Castile, and Aragon to Poland or Lithuania, the family structure adopted both forms of organization. Anthropologists and historians have shown, over the centuries, the relationships of consanguinity and filiation that can be established within the *family* (Franco 2001). The literature shows that kinship models according to genealogy—*genealogical models*, emerged for the first time in European society, during the medieval period (Johnson and Paul 2016). For example, as early as the 11th century, Christian scholars were devoted to validating the genealogy of the ancestors and family of Jesus Christ as a tree (Klapisch-Zuber 1991, 2000), later adopted as the "*family tree*,". By the 16th century, the representation of families according to the concept of a family tree was quite popular throughout Europe (Johnson and Paul 2016).

Alongside this reality of kinship, the researchers also specify the existence of another type of kinship, spiritual or ritual, organized around principles such as loyalty, friendship, recognition, or even patronage (Casey and Hernández-Franco 1997). The structure of spiritual kinship consisted of biologically artificial fraternities that bound individuals together within the framework of vassalage, but it counted for at least as much as *blood* kinship (Casey and Hernández-Franco 1997).

While royal authority prevailed until the 10th century, from that century onwards the ties of ritual kinship established around the royal house gave way to ties of blood kinship organised around norms of agnation, maleness, and virility, as well as the veneration of the founder of an aristocratic house (Casey and Hernández-Franco 1997). It was the family structure of the lineage, and it was much more "secure" for the continuity of the unilineal descent group in a lordly world.

The current idea is that in the society of "*Old Europe*" the idea of descent was the result of a form of kinship organization reduced almost exclusively to members of high society, with a greater hierarchy of power and property. Second, in this society, the idea of lineage was perceived as a symbolic form of a trunk, an ordered line of unilineal descent that originated with a *reputed founder* and through which the honour and status of the initiator of the lineage was transmitted to successive generations of the lineage: "*from good men, others like them will be born*." Thirdly, lineage was not only a characteristic that conferred rank within the social structure, but also allowed the family name and the *House* to be perpetuated over generations—its name, its property, and its distinctive deeds.

The Catholic Church itself in the West has in some way contributed to the importance of the family in society by implementing norms for the constitution of what could be called "*the true family*" (Franco 2001). An example of this is the rule that marriage should be exogamous, which made cases of incest difficult and allowed the circulation of wealth between different families (Franco 2001). Towards the end of the 11th century and the beginning of the 12th century, a ritual between the betrothed, *the wedding*, began to appear more frequently and become obligatory from the 16th century with the Council of Trent. In general, the wife became a member of her husband's family after marriage (Franco 2001).

Finally, the concept of "*House societies*" developed by Lévi-Strauss is quite relevant to medieval society, where kinship may not be biological but based on the social relationships of those who live in the same home (Lévi-Strauss 1984, 1987); Lévi-Strauss and Modelski 1999). The "*House*" is seen as a significant space that would serve as a link for social formation between individuals. On the other hand, this type of relationship between individuals could be studied throughout the generations, since a record (symbols, brands, designs) was left in the different objects that belonged to the individuals (clothing, war material, objects of the house, etc.) (Johnson and Paul 2016) and later those belonging to the same family, or "*House*", are included in the family trees.

2. The Bioarchaeological Perspective

According to Johnson and Paul (2016), archaeological studies of ancient familial burials reflect modern society's interest in understanding what the concept of "*Family*" has ultimately meant throughout history and whether or not people have behaved according to the same rituals and social concepts. According to these authors, there is a "*fascination*" with ancient "*family burials*". Indeed, the image of a (small) unit of individuals, buried and interpreted as a "*family*", immediately captures the attention of modern society, because of the immediate inclination for compassion and empathy due to the similarity of behaviour between contemporary and ancient society.

Herlihy (1983) describes what a 4th-century wool weaver, Severus, wanted to have inscribed on his tombstone and is very clear about what family meant for an individual of that time: *"Since we in this world had a life in common, so let us have a common tomb".*

Concerning infants, in specific locations, burial practices for infants were carefully specified in certain places. Lucy (1994) suggests that in the early Anglo-Saxon period, children may have been buried elsewhere, and that the apparent lack of infant burials in certain sites cannot be attributed solely to poor preservation. Over time, particularly in the later Anglo-Saxon and medieval periods, the inclusion of children in communal cemeteries led to observable clusters. However, these clusters did not follow a universal pattern. For example, at St Andrews Fishergate in York, 76% of under-5s were found in the western third of the cemetery (Stroud and Kemp 1993). At St Olav's monastery in Trondheim, Norway, a reserved burial area near the choir was dedicated to infants, constituting 45% of the remains (Sellevold 2008). Similarly, at Hamar Cathedral, Norway, 57% of recovered remains from the southwest of the cemetery were children, in contrast to only 8% in the west (Sellevold 2008). The pattern extended to Taunton (Somerset) in England, where 85% of non-adults were located at the western end of the cemetery, with only three children excavated from the east (Rogers 1984).

Sellevold (2008) proposes that in the medieval period, the demographic composition of burials varied according to the type of church, suggesting distinct congregations. In the later medieval period, the religious doctrines of Protestantism and Catholicism influenced the treatment of infants within cemeteries. Newborns were considered tainted by the original sin, and unbaptized or stillborn infants were often denied burial in consecrated ground (Orme 2001). However, historical records reveal instances, such as a royal license granted to enclose the cemetery to prevent the secret burials of unbaptized infants (Daniell 1997). This practice is exemplified by the discovery of 24 infants buried randomly in an extended section of the cathedral cemetery (Shoesmith 1980), serving as the closest approximation to a child cemetery in medieval England (Daniell 1997, p. 128).

In addition to Protestantism and Catholicism, other religions such as Islam and Judaism influence the burial practices of non-adults, although the details of the organization of these burial sites are less extensively documented in the available literature.

There is no way of knowing exactly what the concept of *family* would have been like in prehistoric societies, as there are no written records. The approach that is often attempted is through the study of funeral practices and burials (Lee et al. 2014; Palomo-Díez et al. 2017; Gomes et al. 2020; Gomes et al. 2021; Rath et al. 2024), trying to understand whether these were related to a certain biological kinship between individuals. In the case of the discovery of multiple graves with non-simultaneous burials (because in this case simultaneous burials, this could be due to epidemics or wars), the absence of biological kinship between individuals allows us to think about other types of "*family*", for example, a concept based on social rather than biological relations between individuals.

Currently, one of the ways to study the concept of family is through the study of human biological remains found in both family graves and medieval necropolises. Two of the disciplines that have contributed the most to the historical and archaeological understanding of family history are undoubtedly biological anthropology and genetics. In the following, the two perspectives and areas of research in which both disciplines have

contributed the most to the study of the origins and history of the *family* are described in detail.

2.1. The Bioanthropological Perspective

The study of family in biological anthropology involves a multidimensional analysis that considers both biological and cultural factors shaping human social organization. In the context of European medieval times, the study of family in biological anthropology intersects with history, archaeology, and related fields. While direct biological evidence is limited due to the lack of preserved biological remains, researchers use a combination of historical documents, material culture, and anthropological methods to infer aspects of family life during this period.

2.1.1. Mobility

The study of human mobility is a multidisciplinary field that can combine genetics, anthropology, archaeology, and other scientific disciplines to understand the movement and migration of human populations over time. When analysed side by side, these methods provide a more comprehensive picture of people's movements (e.g., Krzewińska et al. 2018).

Stable isotope analysis (SIA), particularly of elements like strontium, can help to identify the geographic origin of individuals (see an in-depth review of this topic in Alexander Bentley 2006). Strontium stable isotopes in teeth reflect the geological composition of the region where an individual lived during their childhood, providing information about migration, if their skeletons are found in a place with a different strontium stable isotope ratio or if samples from tissues formed later in life, such as the third molar, have a different isotopic composition (e.g., Hrnčíř and Laffoon 2019). Permanent teeth begin to form at around 7 months of age, and the third molar can be fully formed by the age of 23 (AlQahtani et al. 2010), providing a significant insight into the mobility of these individuals during their youth. These analyses can also be used to study mobility patterns by sex, age, or family group. Oxygen isotopes in dental enamel can also provide insights into long-distance migration, as the isotopic composition of water sources varies with geography (see an in-depth review of this topic in Pederzani and Britton 2019).

In medieval Europe, extended families were common. Several generations often lived together in a household, including parents, children, grandparents, and sometimes even aunts, uncles, and cousins (Herlihy 1985). Mobility studies can potentially help to understand the families' dynamics and those who were not local within the families. The medieval social structure was often patriarchal, with the father serving as the head of the household (Hanawalt 1986). Marriages were often arranged for strategic and economic reasons, and considerations of social status and alliances played a significant role. Social class played a significant role in determining family structures and dynamics. Nobility and peasants exhibited different family patterns. The former often prioritised lineage and inheritance (Reynolds 1994). As inheritance and property rights were traditionally passed down through the male line, and marriages were frequently arranged, it is intriguing to investigate which genders were more mobile and the distances from which new family members could originate.

SIA is more affordable than genetics, therefore a research strategy to identify nonlocal individuals in cemeteries can start with the analysis of geographically sensitive stable isotopes such as strontium and oxygen. The combination of SIA and genetics, even if more common in studying pre-historic populations (e.g., Bentley 2006), can also be applied to medieval communities to better understand if families include non-locals and if they more frequently tend to be males or females (e.g., Haak et al. 2008). Some studies have been able to identify outsiders who were outliers both genetically and isotopically (e.g., Dupras and Schwarcz 2001).

Stable isotopes, such as carbon, nitrogen, and sulphur, can be analysed in human remains to reconstruct dietary patterns (e.g., Pederzani and Britton 2019; Nehlich 2015; Alexander Bentley 2006). This allows an effective approach to study the subsistence strategies and dietary behaviour between groups and families. An example of this is the

research of Paladin et al. (2020) that studied the dietary patterns, subsistence strategies, changes in socio-economic structures, and mobility of the early medieval groups living in the different valleys of the Italian Alps. A later study (Coia et al. 2022) also shows differences in the genetic and mobility patterns between individuals from different parts of the Italian Alps, suggesting genetic exchanges with allochthonous people in one of the groups, probably linked to high mobility and geomorphological, historical, and socio-cultural factors.

Genetic and stable isotope analyses can be combined to cross-validate findings and gain a more nuanced understanding of past population movements. These methods offer complementary information, addressing questions about genetic relationships, ancestral origins, and the geographic mobility of past human populations.

2.1.2. Sex and Gender in Past Societies

Understanding how past societies conceptualized and organized gender has implications for contemporary discussions on gender equality, feminism, and LGBTQ+ rights (e.g., Springate 2020). Sex and gender studies are crucial in archaeology for creating more precise and comprehensive narratives of the past, promoting inclusivity, and contributing to broader discussions on gender and identity. Artefacts, burials, and symbols can provide insights into how gender identities were constructed and expressed and if they correspond to sex. To investigate gender in past populations, it is essential to determine the sex of the individuals. Even though sex can be estimated in skeletonized remains, these methodologies do not give 100% correct estimations, especially when the most dimorphic bones, such as the *os coxae*, are fragmented or absent. The difficulty of estimating the sex based on osteology increases in intersex individuals. Recently, a 1000-year-old case of Klinefelter's syndrome was published (Roca-Rada et al. 2022), highlighting the importance of genomics to sex and gender studies in past populations. Sex estimations are even more problematic in non-adults; thus, in this field, genomics plays a determinant role by providing sex chromosome information, even in fragmented human remains.

Knowing the sex of non-adults in archaeological research enhances our understanding of childhood diet and health in past populations. It allows for nuanced investigations into the complex interplay of biological, cultural, and socio-economic factors that shaped the experiences of children in ancient societies. This involves considering how cultural norms and practices related to gender roles may have affected children's access to resources and care. Mortality patterns that differ by sex among non-adults provide information about potential gender-related vulnerabilities or protective factors.

Incorporating sex-specific information on non-adults into life course reconstructions allows tracking changes in health and diet throughout different developmental stages. Sex-differentiated investigations of non-adults provide a basis for understanding variations in childhood care and health practices across regions and periods. This is particularly relevant for patriarchal societies such as medieval Europe, where inheritances were passed down through male lines and the Catholic Church had a strong influence on family life, including attitudes towards childbirth and the role of women within the family (Brown 2017). There is also evidence of differential parental investment in male versus female offspring in European Islamic medieval populations (Jiménez-Brobeil et al. 2021). Differential care provided to non-adults based on their gender may cause growth disruptions, which are associated with a significantly increased risk of adult mortality, especially if they happen during late childhood/early adolescence (Watts 2015).

Gender-based social inequalities may impact access to food resources, as gender roles often influence dietary patterns, impacting nutritional health. Most diet estimations based on stable isotopes analysed from the bone collagen of individuals who lived in Europe during the medieval period suggest no differences in the foods eaten by both sexes in Christian (e.g., Olsen et al. 2018; Walter et al. 2020) and Islamic (e.g., Jiménez-Brobeil et al. 2021) populations, but that was not the case across all archaeological sites. In Northern Italy, the diets of low-status males differed from those of females (both status groups)

and high-status males. However, these differences only became apparent in adulthood (Reitsema and Vercellotti 2012). In the 11th to 12th century in Giecz, Poland, men consumed more animal products (meat or dairy) than did women (Reitsema et al. 2010). Isotopic data suggest a difference in food access between females and children compared to males in medieval Islamic Lisbon, Portugal (Toso et al. 2019). Various studies have compared diets between sexes, but there has been little exploration of this within and between families. This gap in the literature is likely due to the need for genetic analysis alongside stable isotopes. Future studies combining these two methodologies will greatly improve our understanding of the household dynamics of medieval families.

2.1.3. Congenital Anomalies and Kinship

Congenital anomalies, also referred to as birth defects or congenital disorders, are structural or functional abnormalities that are present at birth. These anomalies can affect various organs or parts of the body and may result from genetic, environmental, or multifactorial causes. The degree of relatedness between individuals within a family or population, known as kinship, plays a role in the occurrence and understanding of congenital anomalies.

Not all congenital diseases manifest in the skeleton; only those impacting skeletal development and potentially certain haemolytic anaemias can be observed. Skeletal anomalies, if asymptomatic, may go unnoticed in newborns whose skeletons are still developing. On the other hand, non-skeletal anomalies are not discernible in the skeleton, posing a challenge in comparing their frequency between the present and the past. Another constraint arises from the scarcity of data on the prevalence of congenital anomalies in historical populations, with the majority of references focusing on case studies of particular pathologies (e.g., Curto and Fernandes 2022; Fernandes and Costa 2007). Even in medical records, the registration of the frequency of congenital anomalies is not widespread, except for specific cases (e.g., Marcão et al. 2018; Sousa et al. 2014). Many congenital anomalies have multifactorial causes, involving both genetic and environmental factors. Some congenital anomalies have a clear genetic basis and can be directly linked to alterations in an individual's DNA (Webber et al. 2015). These genetic anomalies can be inherited from one or both parents. Consanguinity, which refers to the mating of closely related individuals, increases the likelihood of sharing genetic material, including deleterious recessive alleles. Consequently, the offspring of closely related individuals have a higher risk of inheriting autosomal recessive disorders, such as genetic haemolytic anaemias.

Genetic haemolytic anaemias are mutations of the erythrocyte's membrane, enzymes, and/or the haemoglobin protein (Andolfo et al. 2016). Haemoglobin malformations disrupt oxygen transportation, inducing haemoglobinopathies (HGs) such as β-Thalassemia (β-Thal) and sickle cell disease (SCD), which have been the most prevalent in the Mediterranean Basin over centuries (Angastiniotis et al. 2021). The fixation of HGs alleles in the populations is associated with migrations (De Sanctis et al. 2017), consanguineous marriages and intermarriage, and the selective pressure against malaria (e.g., Denic et al. 2008). The palaeopathological record of malaria and HGs remains elusive due to the absence of bone lesions in mild-to-moderate mutations (β-Thal minor or intermedia), the high comorbidity of these conditions (HbS/β-Thal), the sharing of similar changes between conditions, and early mortality in severe mutations (β-Thal intermedia or major).

The first aDNA study supporting a palaeopathological diagnostic of a congenital anomaly was published in 2017 (Boer et al. 2017) and detected a mutation of the FGFR3 gene in tooth material from a museological achondroplastic skeleton. Since then, the number of genetic studies on human skeletons with genetic disorders has been increasing (e.g., Shaw et al. 2019; Roca-Rada et al. 2022).

Kinship can influence the probability of shared genetic susceptibility within families. Families with a history of certain congenital anomalies may be at an increased risk, indicating a genetic predisposition. The study of kinship and familial patterns of congenital anomalies can contribute to population-level research. Researchers may investigate the

prevalence of specific congenital disorders in certain families or populations to identify potential genetic markers. For a more in-depth review of ancient DNA analysis of genetic bone disorders, see Maixner et al. (2021).

In summary, understanding the occurrence and inheritance patterns of congenital anomalies requires an appreciation of kinship. Family history, consanguinity, and the study of familial patterns can provide valuable insights for both clinical and research purposes due to the genetic basis of these anomalies. Genetics is a strong ally for paleopathologic studies of congenital anomalies by identifying specific genetic factors, tracing their prevalence across populations and generations, and offering insights into evolutionary patterns. This interdisciplinary approach combining genetics, anthropology, and archaeology enhances our understanding of the historical and cultural aspects of these anomalies.

2.1.4. Morphological and Morphometric Skeletal Variability

Non-metric skeletal traits are used to gain insights into the biological and evolutionary aspects of human populations, contributing to a better understanding of human history and diversity (Buikstra and Ubelaker 1994). These traits are usually divided into dental, cranial, and post-cranial traits. Even though these traits are mainly used to study populations' affinities (Hauser and De Stefano 1989; Hanihara 2008) and help to identify people in forensic cases (Palamenghi et al. 2023), since they are genetic, they can also be used to study families and their affinity.

Non-metric methodologies categorise traits into two distinct trait categories: morphoscopic traits, which assess shape; and discrete traits, which are classified as either present or absent. The inventory of non-metric skull traits is extensive, with Hauser and De Stefano (1989) documenting over 200. Examples of morphoscopic features include suture shape and palate shape, while prominent examples of discrete traits include Wormian bones and the metopic suture.

Hefner and Ousley (2014) advanced the field by introducing optimised summed scoring attributes (OSSA). Recognising that a singular trait or combination of traits fails to precisely delineate a population, there arose a necessity to establish a method for assessing the threshold at which an individual could be categorized within a specific geographic group. OSSA quantifies the likelihood of an individual belonging to a particular population (Hefner and Ousley 2014). The authors devised a scoring sheet wherein each trait receives a score, and the cumulative score determines the ancestral group.

For dental traits, Scott et al. (2018) introduced rASUDAS, a novel web-based application for ancestry estimation using dental casts from the Arizona State University Dental Anthropology System (ASUDA). This tool, available on the Osteomics platform (http://osteomics.com/, accessed on 8 January 2024), utilises the crown and root morphology of the dentition. The reference sample comprises 21 traits derived from the ASUDA and encompasses approximately 30,000 individuals from seven distinct geographic regions.

The metric approach is a traditional method, and recently, new software has been developed using different statistical approaches. For instance, FORDISC (Ousley and Jantz 2013) uses up to 34 cranial and 39 postcranial measurements to calculate discriminant functions. Additionally, the application of geometric morphometrics techniques has enabled a comprehensive analysis of cranial shapes utilising three-dimensional coordinate data (Slice and Ross 2009). Geometric morphometrics involves the statistical examination of form using Cartesian landmark coordinates. The postcranial methodologies are less explored and have more limited applications (Liebenberg et al. 2019).

Even if less common, there are also a few studies conducted with medieval osteological collections (Česnys and Tutkuvienė 2007), particularly reporting the frequency of specific traits. Partiot et al. (2023), for example, found no differences in non-metric variations, in individuals who died during the perinatal period, between Nubian and Western European samples. Springs Pacelli and Márquez-Grant (2010) registered the frequencies of crown morphological variants from Ibiza, Spain, and Tomaszewska and Kwiatkowska (2019) registered the frequency of 38 non-metric cranial and 9 post-cranial traits in Wrocław, Poland.

While these methodologies have found substantial application in pre-history and forensic anthropology in recent times, described for example by (Vach and Alt 1993; Pilloud and Larsen 2011; Esparza et al. 2017 or Fowler 2022), or in modern societies, as described by (Case et al. 2017 or Cvrček et al. 2018), there remains considerable scope for their exploration in medieval contexts. Nevertheless, their potential as invaluable tools for studying familial relationships during the Middle Ages should not be overlooked.

2.1.5. Disease Susceptibility in the Family

The skeletal record may not provide a complete representation of the historical prevalence of infectious diseases in a population. Certain infections, such as cholera, smallpox, and enteric dysentery primarily affect soft tissues, leaving no visible traces on bones. Additionally, individuals may succumb to the infection before sufficient time elapses for skeletal lesions to manifest. Therefore, the absence of skeletal lesions does not necessarily indicate the absence of infections during an individual's lifetime (Wood et al. 1992; DeWitte and Stojanowski 2015). Distinguishing an individual who succumbed rapidly to an infectious disease, without developing bone lesions, from someone who never contracted the disease is a challenging task (Wood et al. 1992). Additionally, even when skeletal lesions are present, most of the time they are not specific to a particular infectious disease. Attributing certain bone lesions solely to infectious agents can be challenging due to various non-infectious causes.

Genetic analysis of genomes from ancient pathogens provides distinctive insights into the agents responsible for and the evolutionary dynamics of infectious diseases. This advancement enables the identification of pathogens, including bacteria and viruses, providing insights into disease transmission patterns and the evolution of strains over time (e.g., Drancourt and Raoult 2005; Tsangaras and Greenwood 2012). Genetic analysis can reveal population susceptibility, immune responses, and the complex dynamics of co-infections in ancient societies. Researchers use these data to engage in a form of paleoepidemiology, reconstructing the historical epidemiological landscape.

In the field of bioarchaeology, numerous studies investigate infectious diseases and individuals' susceptibility to them. However, this has not been related to family groups. A few examples have focused on variables related to sex, age, social status, and skeletal indicators of health (e.g., DeWitte and Hughes-Morey 2012; Gowland 2015; Roberts and Brickley 2018; Godde et al. 2020). In the future, studying infectious diseases within familiar groups in past populations may provide insights into historical outbreaks and how infectious diseases spread within specific groups, their impact, and the responses of communities and societies. Studying infectious diseases within specific families or comparing families based on the frequency or types of infectious diseases can provide valuable insights into the genetic, environmental, and behavioural factors that influence disease susceptibility (e.g., Cooke and Hill 2001; Jirtle and Skinner 2007). By comparing the occurrence of infectious diseases among family members, we might identify genetic factors that may contribute to increased or decreased susceptibility to specific infections. Families often share similar environments, hygiene, lifestyles, diets, and living conditions. Studying infectious diseases within families enables researchers to assess the impact of common environmental exposures on disease transmission. This information is crucial for understanding how living conditions and behaviours within a family setting can contribute to the spread of infectious agents. Families often have close contact and frequent interaction, creating an environment that is conducive for the transmission of infectious diseases. Some individuals may also carry infectious agents without showing symptoms, acting as carriers within a family. Family studies can provide insights into the immunological responses to infectious diseases, particularly across generations within families. This longitudinal perspective can help in understanding how infectious diseases may affect different age groups and influence health outcomes over time.

2.2. The Genetic Perspective

Nowadays, genetics is a valuable tool for finding solutions in historical, anthropological, and archaeological fields (Gomes et al. 2021). Geneticists can provide answers to questions such as infants' biological sex, biogeographical origin, or external phenotype. In some cases, genetics is the only instrument capable of solving archaeological puzzles, such as determining relationships between individuals buried separately or identifying unrelated individuals buried together. In historical cases, genetic studies have special relevance as they can confirm or even reveal cases of adoption (Lozano-García et al. 2023).

The genetic analysis and its contribution to a family hypothesis are also of great interest, even when this possibility seems non-existent. For example, a woman dies at 20 years of age, leaving behind a male-born child. This individual passed away 50 years later, being buried next to his mother. From an anthropological perspective, it is possible to determine that the burials were not simultaneous. Furthermore, it is also possible to know that the man would have reached a higher age than that of the woman at the time of her death. At a social level, since there is no type of written or oral record, it could be thought that the two are not related, given the discrepancy in ages, which includes the fact that the man was the father of the woman. Genetic analysis without a priori information, for example, without access to ages or morphological degradation aspects of cadavers, would allow us to verify, or at least propose, all previous kinship hypotheses, including *maternity*.

Genetic analysis of ancient human remains is challenging due to the loss of genetic material over time, particularly when biological tissues are not perfectly conserved. One of the fields that have contributed most to the genetic analysis of ancient human remains has been forensic genetics (Capelli et al. 2003; Palomo-Díez et al. 2018; Gomes et al. 2019), through the implementation of various extraction techniques adapted to different burial circumstances, and different amplification techniques, including the "inhibition" factor in addition to the factors of the scarcity and fragmentation of genetic material (Caragine et al. 2013; Gomes et al. 2017; Huang et al. 2021). The development of specific software, which takes into account, for example, allelic dropout, is also an important factor to consider when carrying out the statistical interpretation of ancient data. However, a major issue associated with this statistical interpretation is the lack of specific databases for ancient populations, as explained later. The use of current databases leads to biased probabilistic values, as they do not reflect possible genetic drift events, such as bottleneck or "founder effects", and the current allelic and haplotype frequencies may not correspond at all to those of past societies.

The great potential of genetics comes from the fact that individuals biologically share genetic information located in certain genetic markers. Due to how each genetic marker is inherited, it is possible to determine biological kinship maternally, paternally, or both ways. Compared with other types of information, namely archaeological and historical, it is also possible to determine patterns indicative of adoption.

2.2.1. Inheritance of Recombinant Markers

The study of non-coding recombinant markers, specifically those located on autosomal chromosomes and the X-chromosome, is crucial in determining kinship relationships. (Behl et al. 2022; Gomes and Arroyo-Pardo 2022; Kumar 2022). The name "recombinant" comes from the recombination that can occur between homologous chromosomes during cell divisions. In the case of the X-chromosome, this recombination occurs only in female cells, whereas in the case of male cells, recombination occurs between two small portions between the Y chromosome and the X-chromosome (PAR 1 and PAR 2) (Gomes and Arroyo-Pardo 2022).

(a) Autosomal markers

Both the father and mother transmit one chromosome from each autosomal homologous pair to all their descendants, sons and daughters. That is, each descendant receives 22 autosomal chromosomes from the paternal path and another 22 homologous chromosomes from the mother. This copy that each descendant receives may or may not be the

result of a recombination between the autosomal chromosomes of the father and mother, respectively (Behl et al. 2022; Kumar 2022; Manera-Scliar et al. 2023).

(b) X-chromosomal markers

The specific mode of transmission of the X-chromosome, different from all other human chromosomes (Szibor 2007), is what motivates its use and interest, both at the population level and in complex forensic issues.

In somatic or non-gametic female cells, there is a pair of X-chromosomes that can recombine just as autosomal chromosomes do. However, when referring to a male cell, the X chromosome does not have another homologous chromosome. In these cells, the pair of sex chromosomes is formed by one of the telomeric areas of the chromosomes. However, there is no genetic marker incorporated in commercial kits for forensic genetics located in PAR1. Thus, for forensic studies, it is considered that there is no recombination between the X chromosome and the Y chromosome.

The X chromosome is transmitted peculiarly, since it depends on the biological sex of the individual. A father transmits to all his daughters an entire copy of his X chromosome, without recombination. On the other hand, a mother will transmit to all of her descendants a copy of one of her X chromosomes, and recombination may exist between her homologous X chromosomes (Szibor 2007; Gomes and Arroyo-Pardo 2022).

2.2.2. Inheritance of Lineage Markers

(a) Maternal lineage

Mitochondrial DNA (mtDNA) is one of the most used markers in the analysis of historical and archaeological samples. Inherited solely maternally, this genetic marker is characterized by a high number of copies in each cell when compared to nuclear DNA (Budowle et al. 2003; Palomo-Díez and López-Parra 2022; Manera-Scliar et al. 2023), which is why, consequently, it is an analysis that normally produces results in old samples.

Thus, one of the advantages of this matrilineal marker is its high number of copies in almost all human cells, as well as its ability to relate individuals belonging to the same family maternally (Budowle et al. 2003; Palomo-Díez and López-Parra 2022; Manera-Scliar et al. 2023), as they must all have the same mitochondrial genetic profile. Indeed, complete mitogenomes, the D-loop region, and diagnostic SNPs can be used to infer the affinity between individuals. One major disadvantage of this genetic marker is that it does not allow for individual identification, as all maternally related individuals will have the same genetic profile. It has a null power of discrimination. For example, if there are four individuals in a tomb and all four have the same mitochondrial genetic profile, it is not possible to obtain a higher degree of precision regarding the degree of kinship between them, only that they are related maternally. The belonging of an individual to a given family will also depend not only on the fact that they have the same mitochondrial genetic profile but also on the frequency of that profile in that specific population; the more frequent this profile, the less likely it is to belong to a particular family through the mother's side. Until recently, interpreting results in ancient populations using mtDNA data was challenging due to the unavailability of a database of 'ancient' mitochondrial DNA. At this moment, the AmtDB database (Ehler et al. 2019) allows for estimating lineage frequencies according to the major European historical periods, including the Middle Ages. Although this database contains only around 2500 mitochondrial genetic profiles, it provides a better understanding of the frequency of lineages in each region.

(b) Paternal lineage

The study of paternal lineages is particularly relevant, in the case of medieval families, due to the traditional patrilineal inheritance of inheritances, surnames, and kingdoms. At the genetic level, the paternal lineage is analysed through the study of the Y chromosome, a lineage marker that is inherited exclusively paternally (Palomo-Díez and López-Parra 2022; Manera-Scliar et al. 2023), without changes, over several generations, from the father

to all his male children. For this reason, male individuals from the same paternal biological family must have the same Y chromosome genetic profile.

Studying this genetic marker allows for the possibility of establishing biological relationships between male individuals, both close, such as brothers or father–son, and distant, such as paternal great-grandfather–grandson. Y-STRs and diagnostic Y-SNPs are the most commonly used markers in this case, allowing for the inference of paternal affinity between individuals. However, studying this patrilineal genetic marker has a major disadvantage in that obtaining results from historical and archaeological samples is difficult, and a complete Y chromosome genetic profile is not commonly found in degraded samples.

To belong to a biological family through the father, individuals must have the same Y-chromosome genetic profile. However, in this case, it is much more difficult to determine the frequency of these genetic profiles in ancient populations, as to date there is no database of ancient Y-chromosome information. For this reason, databases of modern genetic profiles continue to be used, despite plausible differences in frequencies due to possible episodes of genetic drift over the centuries.

2.2.3. The Study of the Families' Origin

Both lineage markers allow an approximation of the biogeographical origin of individuals (Palomo-Díez and López-Parra 2022; Manera-Scliar et al. 2023). MtDNA allows a study of biogeographical origin through the maternal route, and the Y-chromosome through the paternal side. To carry out this type of study, it is essential to know the frequencies of each lineage in the past, as well as the distribution of each lineage in the territories. In the case of mtDNA, as previously mentioned, the mitochondrial database of ancient DNA, AmtDB (Ehler et al. 2019), has allowed us to delve deeper and compare data between populations in a given period (synchronic study), as well as in the same territory over different periods (diachronic study). Regarding the Y-chromosome, studies that exist on archaeological and historical samples are not yet available on an online and freely accessible platform, which makes it more difficult to carry out studies on haplotypic frequencies and/or genetic drift of this chromosome in past populations.

2.2.4. "Adoption" throughout History-the Biological Perspective

At the historical level, there are several cases of adoption, such as in ancient Rome, or ancient Egyptian society (Lozano-García et al. 2023). However, in later historical periods, such as during European medieval times, adoption ceased to be a subject that was openly discussed, moving into the background. At the level of high elites, the succession of kingdoms and feudal lords was typically passed down to male heirs based on biological lineage. Possibly, people from rural areas adopted orphaned or even extramarital children. However, in general, in medieval times, blood lineage began to take precedence, meaning adoption ceased to be a relevant subject in the literature during this period. However, a genetic study conducted on a "family" grave can demonstrate that a certain individual was adopted or did not share the same maternal and/or paternal family lines. This can happen in the case where, for example, in a document or tombstone it appears that "*here lies X, son of A and B*", so a genetic study could demonstrate that, as there is no biological relationship between *X*, *A*, and *B*, the meaning of "*son of*" could be due to a question of adoption. This study involves the use of recombinant markers, both X-chromosome and autosomal, to confirm the absence of identical alleles due to descent between the supposed "parents" and child(ren). Additionally, the study verifies the matrilineal and/or patrilineal lineages. In this way, a genetic study can confirm or refute a written document or the inscription on a funeral tombstone, where there is information that such a person would be someone else's (biological) progeny.

2.2.5. How Genetics Contributes to Medieval Family Perspective

There are more and more studies demonstrating the contribution of genetics to the field of "*family history*" in medieval times (for example, Gamba 2012; Amorim et al. 2018;

Deguilloux et al. 2018; Rott et al. 2018; Rath et al. 2022; Dzehverovic et al. 2023; Rath et al. 2024). Next, we describe some examples.

(a) A triple burial from medieval St. Peter's cemetery (Cölln/Berlin, modern Germany).

Rath et al. (2022). Genetic and isotope analysis of a triple burial from medieval St. Peter's cemetery in Cölln/Berlin.

This study analyses a German cemetery where a necropolis of the ancient medieval city is located. They carried out the study of three individuals who were present in the same grave (Figure 1), with the aim of, on the one hand, checking whether they were related and, on the other hand, knowing the possible biogeographical origin of each of the individuals. The analysis of autosomal markers indicated that the three individuals were not closely related. Concerning lineage markers, mtDNA and Y-chromosome analysis allowed the authors to conclude that two of the three individuals would be local, and one would possibly be from abroad, and these results were also corroborated by isotope analysis. Considering the burial of the individuals (Figure 1), the authors consider that "*maybe the men shared a social bond not related to genetically detectable parameters, or perhaps the circumstance of their death (e.g., location or cause) is the only thing that brought these three unfortunate souls together. The archaeologists assume that the men were killed by more than one assailant, as the injuries that can be seen on each of the skeletons were caused by different weapons.*"

Figure 1. The grave contains the three analysed individuals. Source: Rath et al. (2022). Genetic and isotope analysis of a triple burial from medieval St. Peter's cemetery in Cölln/Berlin.

(b) A simultaneous collective burial in early medieval southern Germany (Bavaria, modern Germany).

Rott et al. (2018). Family graves? The genetics of collective burials in early medieval southern Germany on trial.

This study investigates the kinship between individuals buried together in 13 simultaneous collective graves (Figure 2), in an early medieval necropolis in Aschheim-Bajuwarenring (Bavaria, Germany). Graves were chosen whose individuals or coffins were located on the same burial level, that is, which could be attributed to simultaneous burials. It was found that in small collective burials of up to three individuals, a close genetic relationship might be assumed in most cases. To establish kinship relationships and perform statistical calculations, this study analysed autosomal, mtDNA and Y-chromosome markers. Considering the high number of individuals who died simultaneously and were

related to each other, the authors advance a hypothesis linked to a critical stage of medieval Europe, specifically "The Plague", in this case, the Justinian Plague (541–750 A.D). They also reflect on some forms of burial of individuals, namely when individuals are observed "holding hands", which could lead an archaeologist to think that the individuals were related, and the genetic study shows that they are not.

Figure 2. Example of individuals from a quintuple burial. Source: Rott et al. 2018. Family graves? The genetics of collective burials in early medieval southern Germany on trial.

(c) A kinship study in two early medieval necropolises in Hungary and North Italy.

Amorim et al. (2018). In "Understanding 6th-century barbarian social organization and migration through paleogenomics".

In this study, the analysis of individuals buried in two cemeteries from the high Middle Ages, currently located in Hungary and Northern Italy, was carried out. Despite distinct migration patterns, in both cases, the authors were able to demonstrate that biological kinship relationships "*played an important role in these early medieval societies*".

(d) The King's identity.

King et al. (2014). Identification of the remains of King Richard III.

This work reveals the identity of an individual who had been missing for five centuries: the English King Richard III himself. Although the analysis carried out was not focused on the analysis of family relationships between medieval individuals, it was truly extraordinary, as it made it possible to identify a monarch who died in the 16th century. To complete this identification, the analysis of lineage markers was carried out. On the one hand, the mtDNA of the human remains (Figure 3) was compared with that of a current living descendant, resulting in a complete match. However, the analysis of the Y chromosome brought a surprise, as there was no match with an alleged living paternal descendant. Given this, the researchers assumed that in the course of this paternal lineage, there had been at least one event of false paternity (or possibly some unofficial adoption). It is important to consider that "false" paternity should be interpreted only in a biological concept, since it could be the case of a social kinship, like an adoption.

The skeleton has been identified as that of the English monarch Richard III through comparative genetic analysis of ancient DNA with current maternal descendants, as well as genetic analysis of the external phenotype. The statistical value obtained from this analysis leaves no doubt about the identification.

Figure 3. Bone remains were later found associated with the English monarch Richard III, who died in the 16th century and who had been in an unknown location for almost 530 years. On the right, one of the painted representations of the monarch, used as a source of comparison for the genetic analysis of the external phenotype Source: Watson (2015), https://www.bbc.com/news/uk-england-leicestershire-31642375, consulted on 12 December 2023.

(e) A Medieval burial in medieval Castilla y León (Segovia, modern Spain).

Gamba et al. (2010). Brief communication: Ancient nuclear DNA and kinship analysis: The case of a medieval burial in San Esteban Church in Cuellar (Segovia, Central Spain).

In this study, the authors analyse seven individuals allegedly belonging to an important Spanish lineage, specifically, the Córdoba-Hinestrosa family, possibly related to King Alfonso X. Four graves were studied, one of which was multiple, with the human remains of three individuals. The analysis of the bone and dental remains of these individuals suggests a possible paternity relationship between them. This is significant as the inscriptions on their tombstones do not provide any indication of their possible affiliation. No additional instances of biological kinship were found among the remaining individuals. This suggests that their burial together may have been for social reasons rather than biological ones.

(f) Kinship in a Merovingian burial (France).

Deguilloux et al. (2018). Investigating the kinship between individuals deposited in exceptional Merovingian multiple burials through aDNA analysis: The case of Hérange burial 41 (Northeast France).

In this case, the authors study a grave (Figure 4), with four individuals, something very uncommon during the Merovingian period in Northern France. In the specific case of this grave, the presence of an adult woman buried together with two children and a teenager is curious, raising the question of the possible relationship between them. Through the study of autosomal and mtDNA markers, it was possible to determine a maternal relationship between the adult woman and the two infant individuals. However, from a biological perspective, there is no genetic relationship between the adult woman and the adolescent individual. Therefore, it is important to consider other types of social relationships, such as maternal relationships through adoption.

(g) Kinship investigation between 11 people from the medieval city of Travnik (Bosnia and Herzegovina)

Dzehverovic et al. (2023). Kinship analysis of skeletal remains from the Middle Ages.

In this case, the authors analysed the dental remains of 11 individuals buried in three medieval cemeteries in Travnik (Bosnia and Herzegovina). To carry out this study, the researchers carried out the study of autosomal markers, as well as Y chromosome markers.

The results demonstrate that of the 11 people, 2 would be related as "brother–sibling"; the authors also state that all male individuals belonged to the same Y chromosome lineage, J2a, an interesting result as this lineage is rare in the current population of Bosnia and Herzegovina.

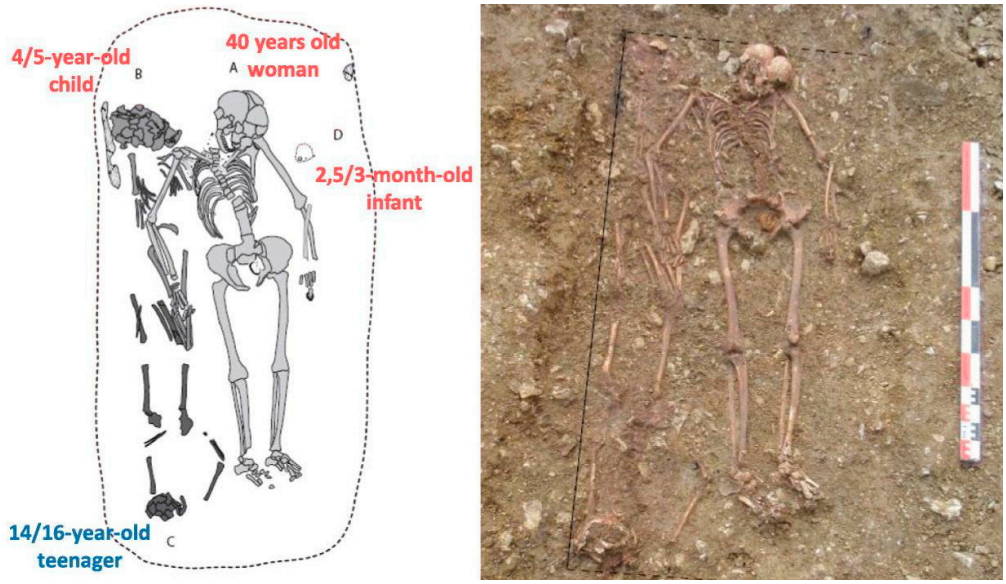

Figure 4. Illustration and photo of the burial, with the adult woman in the centre, and the children and the teenager on both sides. Source: Deguilloux et al. 2018. Investigating the kinship between individuals deposited in exceptional Merovingian multiple burials through aDNA analysis: The case of Hérange burial 41 (Northeast France).

3. Discussion

The concept of family seems to have changed over time and across regions and human history from prehistoric, presumably matriarchal societies to today's cultures where the concept of family can be social (Bamford 2004; Leach 2004; Astuti 2009; Viveiros de Castro 2009) or biological, depending on the society or community. During the medieval period, biological issues and genealogy were important, but social kinship also played a significant role. Studying this era is advantageous due to the abundance of written records available to researchers. The study of population mobility is one of the ways of understanding family dynamics, for example, allowing us to understand the migratory flow at higher social levels, e.g., in certain marriages; or at less favoured levels, through migration for work reasons, or to understand the existence of a migratory flow of foreign slaves. Associated with mobility, the study of isotopes makes it possible to determine the dynamics of medieval populations, allowing us to understand the extent to which social levels at the time differed in terms of diet. Not only at a social level but also within the "family", this study allows us to recognize what the reality of the nutrition of the *wife*, *husband*, *older children*, and *infants* would be. It enables us to determine whether an individual's sex and social status are decisive factors in matters of nutrition.

On the other hand, one of the increasingly relevant studies regarding the investigation of medieval populations is related to the determination of physical characteristics possibly associated with pathologies. The study of individuals in bioanthropology allows us to understand the extent to which physically demanding work was associated with specific demographics, such as males or females, lower social classes, or enslaved populations. This study also allows us to determine the evidence of injuries associated with military situations, thus corroborating many of the historical sources that indicate that this individual died in combat. The study of individuals' physical health allows us to comprehend the overall health status of a population. This is primarily linked to the examination of their diet, as mentioned earlier.

At a genetic level, there are a growing number of projects aimed at understanding the functioning of medieval European societies; however, compared to other historical periods (for example, Lee et al. 2014; Marcus et al. 2020; Bloxam 2023; Cox et al. 2023; Modi et al. 2023; Popović et al. 2023; Sirak 2023; Vitezović 2023; Whittle et al. 2023; Linden 2024), the number of published studies is not abundant enough to allow a generalization of the observations. For instance, research on medieval Iberian societies is limited, making it difficult to determine the correlation between historical sources and bioarchaeological observations.

The seven cases presented here show us different realities. For example, whereas in case (c) there is a strong component of biological kinship in the burial of individuals, in case (a) there is no biological relationship between them; this also occurs in case (d). In these cases, the hypothesis of possible kinship at a social level can be proposed, such as adoption. In the case of (e), (f), or (g), there are buried related individuals and others unrelated. This situation is also curious since although biological ties between individuals are not the most common, a family burial can still be proposed, for example, mother–child(ren)–paternal grandmother. In this example, the paternal grandmother has a biological bond with her grandchild(ren), but not with her daughter-in-law.

Finally, one of the major fields where genetics is increasingly gaining importance is the study of microorganisms from the past (paleopathology) (for example, Economou et al. 2013; Brickley et al. 2020; Alves-Cardoso et al. 2022; Dutour 2023), allowing us to determine cases where a considerable number of individuals are buried together not due to biological kinship factors but rather to a general epidemic.

Bioarchaeological studies are an ideal tool to understand population dynamics in medieval times, rather than to modify them. The article highlights the complexity of defining the concept of family. It was a crucial aspect of life in medieval times, encompassing arranged marriages, the involvement of the Church, and the inheritance of kingdoms or empires. Recognising that an individual may have been buried with another person not because they were biological relatives but because of a social bond (such as adoption) helps us to understand the workings of a society. Although we have a significant amount of written information, we have very little bioarchaeological information.

4. Conclusions

In general, bioarchaeological studies allow us to confirm or at least propose new hypotheses not mentioned in the historical record. The absence of biological links between individuals can often be explained by some form of social kinship, from adoption to other familiar figures who are not expected to have a biological link, such as a father-in-law or daughter-in-law, among others.

As a future perspective, it is necessary to extend the bioarchaeological study to other populations where historical sources are abundant, but bioarchaeological studies on samples from this antiquity are practically absent.

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