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Human monogamy in mammalian context

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Monogamy has been argued to have played an important role in human evolution and, across animals more generally, evolutionary transitions to highly cooperative societies have been far more likely to occur in monogamous species, raising the possibility that this may have also been the case for humans. However, the extent to which we can consider monogamy to be the typical human mating system is subject to debate. Here, I provide comparative context on human mating behaviour by comparing the distribution of sibling types (full siblings versus half-siblings) across more than 100 human societies with equivalent data from 34 non-human mammal species. While cross-culturally variable, rates of full siblings in humans cluster closely with rates seen among socially monogamous mammals and fall consistently above the range seen in non-monogamous mammals. Although the human data is demonstrative of considerable cross-cultural diversity in marriage and mating practices, the overall high frequency of full siblings is consistent with the characterization of monogamy as the modal mating system for humans.

1. Introduction

Evidence from birds [1], mammals [2] and insects [3,4] all suggest that transitions to eusocial or cooperative breeding systems are more likely to occur in monogamous species, raising the possibility that the evolution of highly cooperative social behaviour in humans was also preceded by the evolution of monogamy [5,6]. Additionally, many derived features of human biology and behaviour have been hypothesized to have coevolved with a monogamous mating system, including increased paternal care [7], extended post-reproductive lifespans [8] and the recognition of extensive networks of kin [9].

Despite the hypothesized importance of monogamy in humans, the extent to which monogamy can be regarded our species-typical mating system has been subject to debate [5,6,10]. Although reduced sexual dimorphism [11], reduced testes size [12] and concealed ovulation [13] in humans have all been argued to be indicative of a transition to reduced levels of polygyny during hominin evolutionary history [6], our ability to reconstruct mating systems from the fossil record is limited and focus has instead been on making inferences from the ethnographic record.

Among contemporary or recent pre-industrial human societies, there is considerable diversity in marriage and mating norms and practices. For example, polygynous marriage (where a man is married to more than one woman at the same time) is permitted in approximately 85% of a representative sample of pre-industrial societies [7,14], leading some to suggest that the predominance of monogamous marriage across much of the world today is an evolutionary novelty and a consequence of recent and rapid cultural change [10]. Others have argued that monogamy is the typical human mating system [15] and point out that even within societies that permit polygynous marriage, the majority of marriages are still monogamous [14,16]. Further complexity is added to human mating and marriage practices by the occurrence of serial monogamy [17], polyandrous marriages [18] (where a woman is married to more than one man), partible paternity beliefs [19] and extra-pair reproduction, which is usually estimated to be less than 5% [20] but can be much higher [21].

An alternative but largely overlooked approach to assessing patterns of human mating is to consider the relative frequency of full siblings, maternal half-siblings and paternal half-siblings across populations [22]. At one extreme, exclusive lifetime reproductive monogamy (i.e. where individuals only ever reproduce with one other) would result in only full siblings, while random mating would result in many half-siblings and very few full siblings [23]. Ellsworth *et al*. [22] show that across a sample of small-scale societies the majority of siblings were full siblings, that there were modest differences in sibling proportions across subsistence types, and that high rates of polygynous marriages are correlated with more paternal half-siblings [22]. However, this analysis does not situate human patterns in broader interspecific perspective, making it difficult to determine whether the rates of siblings seen across human societies are what would be expected for a monogamous species. Furthermore, recent analysis of genetically derived kinship data from archaeological sites [24–30] allow for the possibility of adding valuable temporal depth to the human sample. Additionally, while it is clear that deviations from exclusively monogamous mating will increase rates of half-siblings, the nature of the relationship between the degree of monogamy and sibling proportions requires further investigation. Here, I place human sibling proportions in mammalian perspective by comparing data from a global sample of 103 human populations (n = 197 658 sibling dyads in total) and compare this with a dataset of 34 non-human mammal species (n = 61 163 sibling dyads). The results show that the proportion of siblings that are full siblings across the human sample clusters closely with rates seen in socially monogamous mammals and consistently exceeds rates seen in non-monogamous mammals.

2. Methods

(a) Human dataset

The human sample includes sibling proportions data from 103 human populations derived from archaeological or ethnographic data. The archaeological data are based on ancient DNA (aDNA) analyses of kinship from nine archaeological sites including four Avar-period cemeteries and one Early Bronze Age burial ground from Central Europe [26,27,29], a major Neolithic settlement in Anatolia [30], an Early Neolithic long cairn tomb from Great Britain [25], a Neolithic non-monumental grave site from Western Europe [28] and a Bronze Age barrow necropolis from the Southern Urals [24] (electronic supplementary material, table S1). To assemble this dataset, I conducted a literature search of journal articles on Web of Science with the search terms '(kinship OR relatedness OR genealogy) AND (aDNA OR ancient OR archaeological)'. I considered all papers returned up to and including July 2025 that included an arbitrary sample size threshold of at least 15 sibling dyads. This resulted in a sample of seven publications, two of which contained data on two separate archaeological sites with more than 15 sibling dyads: Wang *et al.* [29] included data from Avar-period cemeteries at Leobersdorf (90 sibling dyads) and Mödling-An der Goldenen Stiege (294 sibling dyads) while Gnecchi-Ruscone *et al.* [26] contained data from Rákóczifalva cemetery (165 sibling dyads) and Kunszallas-Fulopjakab cemetery (71 sibling dyads). Sibling relationships were calculated through assembling parentage lists from genealogical diagrams provided in the publications (electronic supplementary material, table S1). Only sibling relationships between sampled (rather than genealogically inferred) individuals were included.

The ethnographic data are built on genealogies compiled by ethnographers from a global sample of 94 pre-industrial human societies engaged in a range of subsistence types. Data on numbers of siblings for 78 of the 94 societies were included in the analysis by Ellsworth *et al.* [22], who compiled data through the open access *kinsources* database (kinsources.net), with additional information from two other publications [31,32]. Two of the societies included in Ellsworth *et al.* (Hare and Pemon) were excluded here for having fewer 15 sibling dyads. I use the sibling proportion data tabulated by Ellsworth *et al.* [22] as well as sibling numbers for an additional 16 societies based on analysis of kinship datasets that have been made available through the *kinsources* project since 2016 (electronic supplementary material, table S2). I followed Ellsworth *et al.* in excluding individuals who had missing parentage data. The results are robust across alternative approaches for dealing with missing data (electronic supplementary material, figure S3). Although genealogical data are based on reported paternities, which may be misattributed, the proportion of full siblings for the human genetic (n = 9, mean full siblings = 65.1%) and genealogical data (n = 94, mean full siblings = 65.9%) do not suggest a major discrepancy, and additional analyses simulating extra-pair paternity suggest the results are robust to misattributed paternity (see electronic supplementary material). The categorization of subsistence types was based on literature review and cross-referencing the society names with the DPLACE ethnographic database [33]. Although categorical distinctions between subsistence types are often somewhat arbitrary [34], such categories are used here only to give an indication of economic diversity within the sample, rather than to test hypotheses about the relationship between dominant subsistence mode and sibling proportions. While the ethnographic sample includes societies from all major regions, it includes an over-representation of societies from the Americas (52 of 94, 55%). Since the mean proportion of full siblings across the societies from the Americas (65.8%) is close as those from the rest of the world (66.0%), this is unlikely to be skewing the overall mean (see electronic supplementary material, figure S2 for further details).

(b) Non-human mammal dataset

While the mating systems of many of the approximately 6000 mammals species have been qualitatively classified [35], data on sibling proportions requires genetic parentage analysis to have been conducted, something which has been done for a much more modest number of species. To restrict the sample to mammal species for which genetic data have been collected and where sibling data might therefore be available, I compiled a list of species that had been included in recent comparative studies of mammalian reproductive skew [36] and kinship composition [37,38] based on genetic data (n = 70 species in total). For each of these candidate species, I followed up the references provided in the prior studies and complemented this with a Web of Science search for '[relevant species binomial] AND (siblings OR kinship OR paternity)'. These searches yielded 34 species for which sibling numbers could be determined, either because they were directly reported or because a parentage list was provided from which sibling distributions could be estimated (electronic supplementary material, tables S3 and S4). In all cases, data come from a single study population with the exception of chimpanzees (*Pan troglodytes*) for which data were available for four populations (electronic supplementary material, table S3; the species-level sibling numbers for chimpanzees are the sum of the numbers across these four populations). For 15 of the 34 species, sibling or parentage data is available for adults and juveniles across the study population or pedigree. For the other 19 species, sibling or parentage data is provided for juveniles only. However, in all these cases, sampling extends across multiple cohorts of offspring. This is important because sibling proportions within a single reproductive cohort could be skewed by high male reproductive skew within a single breeding season and, in monotocous species, would preclude maternal siblings [39–41]. For categorical data on whether a species was socially monogamous, a plural or singular breeder, and monotocous or polytocous, species names were cross-referenced with published comparative analyses of plural breeding and monogamy in mammals [35,42].

(c) Estimating sibling proportions and reproductive monogamy

Sibling proportions were estimated by calculating the numbers of individuals of known parentage who shared two parents (full siblings), a mother but had different fathers (maternal half-siblings) or a father but different mothers (paternal half-siblings). Reproductive monogamy was calculated as the proportion of reproducing individuals (i.e. those who were represented in the dataset as the mother or father of at least one individual) who had reproduced with only one other individual who had themselves only reproduced with the focal individual. For this analysis, the sample was necessarily restricted to those populations or species for which parent lists were available (16 of 94 ethnographic datasets, 19 of 34 non-human species datasets). While the non-human data all come from studies that span at least two reproductive cohorts, not all studies have complete lifetime reproductive success for all individuals. Where this is the case, rates of reproductive monogamy may be overestimated.

(d) Modelling sibling proportions

The computational model was written in R [43] using custom code. The model starts by considering a group containing N_f females who produce k offspring and then varying the extent to which they produce these offspring with one male versus multiple males. When $e = 0$ there is exclusively monogamous mating and all siblings are full siblings. When $e = 1$ males and females are randomly paired to reproduce and full siblings are rare. At intermediate rates ($0 < e < 1$), we start as in the exclusively monogamous condition and the father identity of each individual is then sampled to a random male with probability e. At low values, the parameter e can be interpreted as the introduction of extra-pair paternity into a lifetime monogamous mating system (e.g. $e = 0.05$ would reflects 5% extra-pair paternity). However, this interpretation is stretched at higher levels of e, and since extra-pair paternity is not the only driver of individuals switching reproductive partners (e.g. this would also occur under serial monogamy), I describe the parameter simply as 'deviation from monogamy'. The model assumes a balanced sex ratio of potential mothers and fathers as well as all paternities falling within the group (though for relaxation of this assumption see electronic supplementary material, figure S4). Estimation of e in the empirical data is based on taking the proportion of full siblings observed in each population/species and finding the simulation results that produced a proportion of full siblings within 2 percentage points of the observed proportion and taking the average value of e for those simulations.

3. Results

The proportion of siblings that are full siblings rather than half-siblings varied greatly across the human sample, from 26% among individuals excavated from an Early Neolithic site in Britain [25] to 100% of siblings in four populations, including a Neolithic cemetery from northern France [28]. Across the entire human sample, the average proportion of siblings that are full siblings (66%) was comparable with the rates seen in socially monogamous non-human mammals (mean = 70.6%, range = 45.2% to 100%, n = 10) and consistently exceeded the range seen in the non-monogamous non-human mammals (mean = 8.6% of siblings are full siblings, range 0–22%, n = 24, figure 1). As such, human mating patterns produce sibling distributions that very clearly cluster with socially monogamous species such as meerkats (*Suricata suricatta*, 59.0% full siblings) and African wild dogs (*Lycaon pictus*, 85.0% full siblings) rather than non-monogamous species such as chimpanzees (*Pan troglodytes*, 4.1% of siblings).

Although it is clear that random mating will result in very few full siblings and that exclusively monogamous mating will result in only full siblings, the nature of the relationship between the proportion of full siblings and the extent to which mating is monogamous is not obvious. In order to better understand this relationship, I constructed a computational model in which I varied rates of mating within a simulated population between exclusive monogamy ($e = 0$) and random mating ($e = 1$) (§2). Varying rates of e in this scenario produces a nonlinear negative relationship between e (characterized as 'deviation from monogamy') and the proportion of full siblings (figure 2a), with relatively modest deviations from monogamy having a

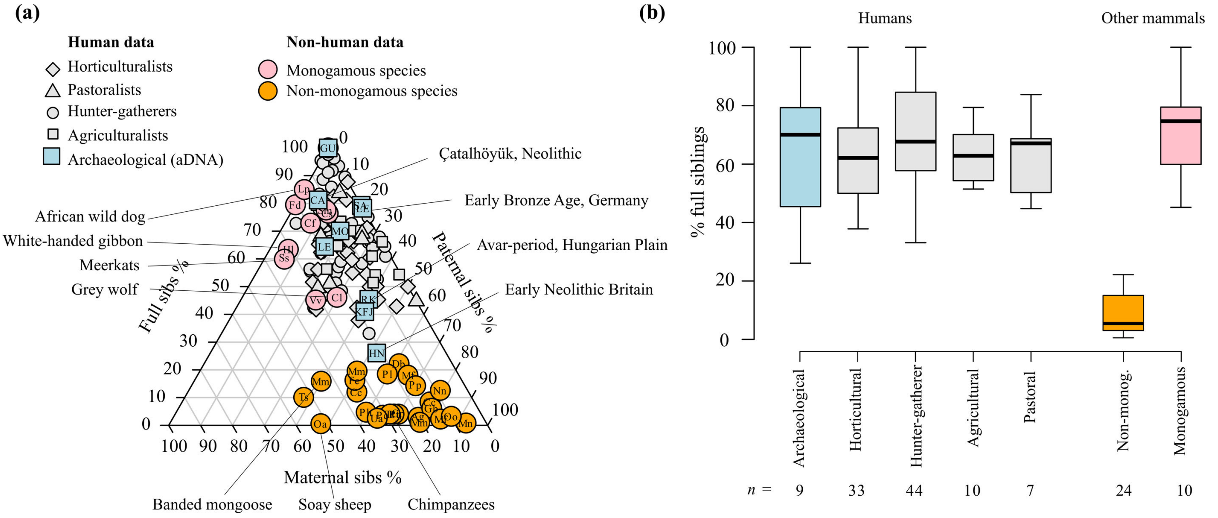

Figure 1. Human sibling proportions in mammalian context. (a) Ternary plot showing the proportion of full siblings, maternal half-siblings and paternal half-siblings across the sample of human societies and non-human species. (b) Boxplot showing the proportion of full siblings across the sample of human and non-human species. Boxplots show median values, 50th percentile values (box outline) and range (whiskers). Colours correspond to ancient human data (blue), ethnographic human data (grey), non-monogamous non-human mammals (orange) and monogamous non-human mammals (pink). Letters in circles are abbreviated species names (e.g. Oa = *Ovis aries*, Soay sheep, see electronic supplementary material, tables S3 and S4, noting that some species share the same abbreviation). Letters in squares identify the data from archaeological sites (electronic supplementary material, table S1).

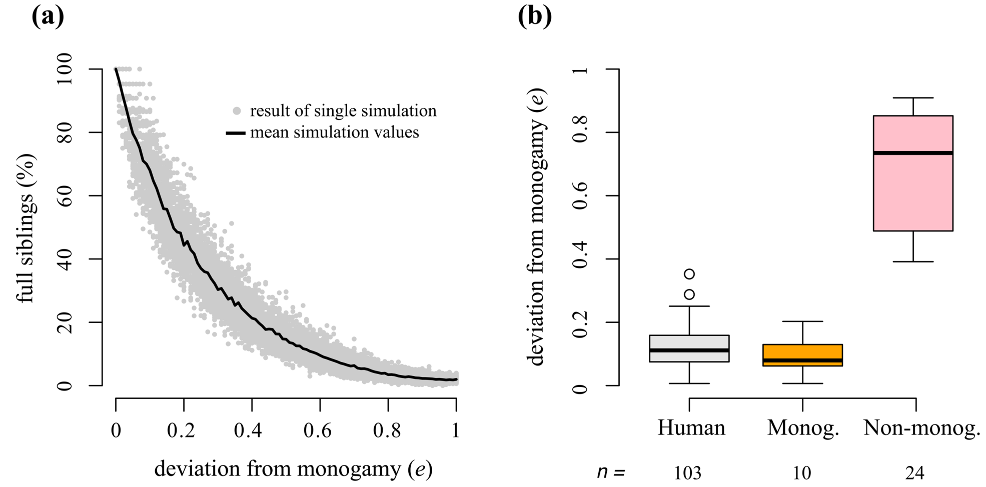

Figure 2. Estimating deviation from monogamy from proportions of full siblings. (a) Simulation results to estimate the proportion of siblings that are full siblings given varying levels of monogamous mating. (b) estimated *e* for human and non-human mammal samples based on extrapolating observed sibling proportions through the predictions of the theoretical model.

disproportionate effect on the production of half-siblings. For example, at $e = 0.25$ only approximately 40% sibling dyads will be full siblings, while at $e = 0.5$ approximately 15% of siblings will be full siblings (figure 2a). Although the exact relationship between deviation from monogamy and full sibling proportions is also influenced by group size, parity and extra-group mating, the relationship is largely robust to these differences (see electronic supplementary material, figure S4). Extrapolating back from the observed rates of full siblings, we can estimate e across the human sample to vary from 0 to 35%, averaging 12% (figure 2b). Mean estimated rates produced for the monogamous and non-monogamous species are 9.9% and 68.1%, respectively (figure 2b).

A final means of comparing reproductive behaviour in humans with that of other species is to estimate rates of reproductive monogamy directly. This is here defined and measured as the proportion of reproductive individuals who have only reproduced with one individual and where that individual has themselves only reproduced with the focal individual. This is possible for a sub-sample of the total dataset for which parentage data are available (see §2). An average of 63.3% of individuals across the ethnographic human datasets were reproductively monogamous ($n = 16$ societies). These rates are higher than seen in the non-human monogamous species (38.6%, $n = 5$) and much higher than seen in non-monogamous species (6.7%, $n = 13$).

4. Discussion

It has been hypothesized elsewhere that monogamy has played an important role in human evolution [5,9,44,45], as well as in the evolution of highly social animal societies more broadly [1–4]. While previous work has relied on inferences from the fossil record [11], or cross-cultural comparisons of marriage norms [14,46], I here focus on measuring the outcome of mating systems: the relative proportion of full and half-siblings born into a population; a direct, theoretically salient, but relatively overlooked approach [22]. Although the variation in sibling composition across the human dataset is demonstrative of the obvious fact that humans are not universally monogamous, the finding that human rates of full siblings overlap with the range seen in socially monogamous mammal species and are consistently higher than those observed in non-monogamously mating mammal species lends weight to the broad-stroke characterization of monogamy as the modal mating pattern for our species.

If we can regard humans as a monogamous species, then we join the estimated minority of approximately 9% of mammals that are socially monogamous [35]. However, where humans deviate from the vast majority of socially monogamous mammal species is that we live in social groups in which multiple females breed: socially monogamous mammalian species tend to either live in groups containing only the breeding pair and their offspring, or in singular breeding groups where only one female of many reproduces [2]. Although monogamous pairs sometimes aggregate in a few species, the only other species of mammal that has been suggested live in stable multi-male multi-female groups containing multiple monogamous pairs is the Patagonian mara (*Dolichotis patagonum*), where large numbers of monogamous pairs may share a warren [35,47]. Humans also differ from most socially monogamous species in being monotocous [42] (i.e. typically producing single offspring per pregnancy rather than litters); all of the monogamous mammal species in the present sample, with the exception of the white-handed gibbon, are litter-bearing (polytocous) species (electronic supplementary material, table S4). Therefore, while humans are not unusual among mammals in producing large numbers of full siblings through monogamous mating, we are unusual in doing so while being monotocous and living in plural breeding multi-male multi-female groups. Given that all other African great apes live in groups and have either polygynous or polygynandrous mating systems, it is probable that human monogamy evolved from a non-monogamous group-living state, a transition that is highly unusual among mammals more generally [35] and which suggests different pressures selected for the evolution of monogamy in humans as compared with other species, possibly related to the energetic demands of our large brains and slow growth [48,49].

The ‘monogamy hypothesis’ holds that the evolution of highly cooperative social behaviour is more likely to occur in species in which parents mate monogamously and produce full siblings [4]. The relevance of full siblings is that, in diploid species, individuals can expect to be as genetically related to their full siblings as they would be to their own offspring ($r = 0.5$), more readily favouring altruistic behaviour towards kin and helping parents to raise younger siblings by ‘helping at the nest’. The theoretical predictions about the relationship between monogamy and full sibling production shown here offer a refinement to this hypothesis because the theoretical results suggest that even modest deviations from monogamy can have a large influence on diluting the proportion of siblings that are full siblings (e.g. approx. 25% extra-pair paternity would lead to approx. 40% siblings as full siblings, though noting that the overall number of siblings of any kind also increases). This could go some way to explaining why, for example, the proportion of birds that are cooperative breeders (approx. 9%) is so much lower than the proportion that are socially monogamous (approx. 90%) [50]: it is not uncommon for socially monogamous birds to have estimated rates of extra-pair paternity exceeding 20% [51]; this may sufficiently reduce relatedness to make transitions to cooperative breeding unlikely.

In humans, the majority of the half-siblings are paternal half-siblings rather than maternal half-siblings [22]. This is indicative of higher levels of male reproductive skew than female reproductive skew in humans [22,36] and is consistent with polygynous marriages being much more commonly permitted across human societies than polyandrous marriages, which are rare [14,52]. Since the ethnographic data are collected through self-reported parentage rather than genetic analysis, it is possible that there is some misattributed paternity within the ethnographic human dataset. However, the general consistency between genetic and ethnographic datasets in the frequency of full siblings suggests the effect may not be great, and where extra-pair paternity has been estimated in human societies it is typically well under 5% [20]. Although a recent finding has reported 46% extra-pair paternity among Himba pastoralists [21], this is a considerable outlier and was also accompanied by high paternity confidence; men were able to correctly identify whether they were the biological father of their spouse’s children in approximately 75% of cases.

It is important to note that what has been measured by analysing sibling proportions is patterns of reproduction, rather than patterns of mating, and is therefore an assessment of reproductive monogamy, rather than monogamy in mating. In most mammals, mating and reproductive patterns will usually be tightly linked. In humans, this link will be diminished in part by birth control; not just the highly effective contraceptives developed over the last century but also ‘natural’ birth control methods and cultural practices to control fertility that are a consistent feature cross-culturally [53,54]. Further to this, serial monogamy can result in turnover in reproductive partnerships (and the production of half-siblings) while still providing conditions for the increased paternity certainty that is argued to be necessary for the increased paternal investment important in the evolution of human life history [5,9,17,48]. The same is true for polygynous marriage; whereas polygynous mating systems in most mammals see regular turnover in male dominance between reproductive cohorts [40] and result in limited numbers of full siblings [39,41], human polygynous marriages can be very stable, resulting in a mix of full and paternal half-siblings and providing favourable conditions for paternal investment. As such, it is arguably the evolution of pair-bonding in general, rather than monogamy in particular, that is important for the evolution of paternal care.

Human marriage and mating practices are highly variable, and there has been much interest in explaining this variability from an evolutionary perspective [10,55,56]. Here, I place this variation in mammalian context, concluding that monogamous mating is the modal mating system of *Homo sapiens*. This result increases the plausibility of hypotheses that have situated monogamy (or, more generally, pair-bonding) as a core human characteristic that has coevolved with various aspects of our biology and behaviour [8,9,48,57] and facilitated the establishment of the extended kinship networks (through the identification of paternal and affinal kinship [15,58,59]) that provided the first step in building large-scale societies and networks of cultural exchange that have been crucial to our success as a species [60].

Ethics. This work did not require ethical approval from a human subject or animal welfare committee.

Data accessibility. All data and code are available on GitHub (https://github.com/mdyble/siblings) and have been archived in Zenodo [61]. Supplementary material is available online [62].

Declaration of AI use. I have not used AI-assisted technologies in creating this article.

Author's contributions. M.D.: conceptualization, data curation, formal analysis, investigation, methodology, project administration.

Conflict of interest declaration. I declare I have no competing interests.

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