Kin selection and sexual conflict shape variation in breastfeeding duration

Juan Du* 1 2, Ilaria Pretelli3 , Min Niu1 ,Yaming Huang1, Liqiong Zhou 1, Yuan Chen 2, Ruth Mace *2 3

1. State Key Laboratory of Grassland and Agro-Ecosystems, College of Ecology, Lanzhou University, 222 Tianshui South Road, Lanzhou, Gansu 730000, PRC
2. Department of Anthropology, University College London, 14 Taviton Street, London WC1H 0BW, UK
3. Institute for Advanced Study in Toulouse, Toulouse School of Economics, and University of Toulouse Capitole, 31080 Toulouse Cedex 06, France

*Corresponding authors: juan.du.13@ucl.ac.uk and r.mace@ucl.ac.uk

Abstract

Breastfeeding provides substantial benefits to infants, yet mothers frequently cease breastfeeding earlier than health guidelines recommend. In cooperative breeding systems, maternal decisions such as the duration of breastfeeding are influenced not only by her own costs and benefits, but also by those of other household members, which are weighed by their relatedness to the child and the parents. We take advantage of variation in post-marital residence patterns among Tibetan communities in southwest China to examine how kinship structure shapes breastfeeding. Analysing feeding histories of 580 children across four residence types (patrilocal, matrilocal, duolocal, and neolocal), we show that average relatedness to co-resident family members is systematically associated with breastfeeding duration. Children and mothers who are more closely related to household members experience longer breastfeeding, while higher paternal relatedness is linked to earlier cessation. These patterns are consistent with conflicts of interest predicted by inclusive fitness theory: parent–offspring conflict and sexual conflict between mothers and fathers. Our findings highlight how family structure within households influences parental investment and co-operation in the family.

Keywords: cooperative breeding; average relatedness; bargaining power; breastfeeding cessation; patriarchy; residence patterns

Introduction

Human females can hardly reproduce and raise offspring successfully without the support of others—such as partners, grandmothers, or other family members—who contribute to cooperative care (Hrdy, 2009; Mace & Sear, 2005). This dependence is especially pronounced during the crucial early stages of life, when infants are inherently reliant on caregivers for nutrition (Andreas et al., 2015), of which breast milk is the most important component (Binns et al., 2016). Breastfeeding mothers rely on allocare to sustain themselves, care for older children, and maintain household subsistence during this energetically costly period. However, kin influence is not always beneficial to mothers. In some cultures, mothers-in-law or husbands may prioritise high fertility, exposing women to higher reproductive costs (Leonetti et al., 2005; Leonetti et al., 2007; Emmott & Mace, 2015; Rempel et al., 2017). Kin selection theory (Hamilton, 1964) provides a useful framework for understanding how conflicts of interest among family members shape reproductive decision-making, including parent–offspring and sexual conflicts (Croft et al., 2021; Trivers, 1974; Haig, 1993). Informed by this framework, we investigate whether the relatedness of mothers, fathers, and children to co-resident family members influences breastfeeding practices in ways consistent with maximising inclusive fitness.

Human societies show a diversity of kinship and residence patterns. The choice of residence after marriage—i.e., post-marital residence patterns—significantly influences individuals’ relationships within their households, affecting both kin support and competition (Du et al., 2023). Women often face resource disadvantages in patrilineal societies, and men in matrilineal contexts (Hill et al., 2011; Marlowe, 2004). These residence patterns shape the sexual division of labour, bargaining power, social networks, and child-rearing practices (Chen et al., 2023; Ember & Ember, 1971; Korotayev, 2003; Prall et al., 2018; Ji et al., 2014). In this study, we take advantage of the natural variation in household organisation across Tibetan communities, where four distinct post-marital residence patterns—patrilocal, matrilocal, duolocal, and neolocal—structure kinship in contrasting ways. Patrilocal households situate mothers with their husband's relatives, while in matrilocal households they remain with their own kin. We leverage the variation in genetic relatedness generated by different residence systems as a proxy for bargaining power within households. Under patrilocal residence (where women disperse at marriage and men remain philopatric), mothers are less related to the group than fathers or children. Under matrilocal residence (where men disperse and women are philopatric), the opposite holds: fathers are less related to the household than mothers and children. In duolocal residence, neither men nor women disperse, remaining with their natal kin throughout life. Fathers and mothers thus live apart, and children reside with their mothers. In such households, fathers' relatedness to the child's household is very low, mothers' relatedness is very high, and children's relatedness lies between the two, as they are surrounded mainly by maternal kin. In neolocal residence, couples establish independent households apart from both natal families. Here, children have high average relatedness to their co-residents because their mother, father, and full siblings are all likely to be present, yielding a mean relatedness close to 0.5.

Therefore, depending on household composition, the interests of different family members can have a major impact on breastfeeding duration. We propose two main hypotheses and a composite hypothesis to explain these dynamics.

- *Hypothesis 1 Parent–offspring conflict:* children benefit from prolonged breastfeeding, whereas parents balance current against future reproduction. Thus, when children are more related to other household members, breastfeeding should be extended, but when parents are more related to other household members, breastfeeding will be shorter.

- *Hypothesis 2 Sexual conflict:* mothers generally favour longer breastfeeding to maximise child survival and well-being, while fathers gain more from shorter breastfeeding and higher fertility. We would therefore expect maternal and paternal relatedness to predict breastfeeding in opposite directions.
- *Hypothesis 3* Both mechanisms: both processes may act together in shaping breastfeeding duration, such that children's and mothers' relatedness are associated with longer breastfeeding, and fathers' relatedness with shorter breastfeeding. In this case, we would expect most of the breastfeeding falls somewhere between the optimum for the mother and the optimum for the father. Note that the correlation between child-parents relatedness and with co-resident family members may introduce complexity when testing these hypotheses, see our inferential approach in SI section 2 and 3).

In this study, we test these hypotheses using demographic and reproductive histories data from 580 Tibetan children raised under four different residence patterns. This unique variation generates predictable differences in how mothers, fathers, and children are related to other household members, providing a natural experiment for examining how kin selection and sexual conflict ultimately influence breastfeeding decisions—either by providing support that facilitates prolonged breastfeeding or by introducing conflicts that may lead to earlier weaning.

Undersatnd why these patterns matter requires returining the significance of breastfeeding itself. The broad endorsement of breastfeeding by the global healthcare community underscores its significance (WHO, 2003; 2014). For infants, breastfeeding acts as a protective shield, reducing mortality from infectious diseases and ensuring better development (Duijts et al., 2010). For mothers, breastfeeding mitigates the risks of postpartum depression, although it may also contribute to other physical challenges

(Chowdhury et al., 2015; Rivi et al., 2020; Page et al., 2021). However, while the World Health Organization (WHO) recommends at least six months of exclusive breastfeeding and two years before cessation, most mothers do not follow these recommendations (Hoddinott, 2014; Theurich et al., 2019). By linking residence pattern, average relatedness, and breastfeeding duration, we ask whether kinship structure shapes the balance of cooperation and conflict in early childcare. In doing so, we place breastfeeding within the broader framework of cooperative breeding, where reproductive decisions emerge not only from mothers but also from the wider set of kin who share the household.

Results

Cox regression model

We employed three Cox regression models to examine predictors of breastfeeding duration. Model 1 looks at the influence of key covariates—mother's birth cohort, household size, and the child's sex and birth order. Model 2 assessed the association between post-marital residence patterns and breastfeeding duration, including all control variables from model 1 except household size (which acts as a confounder; see Supplementary Information 3.2). Model 3 examined how the relatedness of children, mothers, and fathers to other household members predicts the timing of breastfeeding termination, while controlling for the same covariates. Our main inferences are drawn from Model 3, which follows a causally principled framework based on Directed Acyclic Graphs (DAGs). To check that these models can distinguish between the three hypotheses considered here, we make use of synthetic-data simulations (see Methods and Supplementary Information 3.3). We further employ a simulation approach to evaluate whether the qualitative direction of effects observed in the empirical data aligns with data generated in silico under parameter sets reflecting the three hypotheses (H1–H3), thereby assessing how plausibly the observed patterns could arise under each scenario.

In our control model (Model 1), we found no effect of child sex on breastfeeding duration: sons (LHC = 0.021, 89% PI: −1.098 to 1.146) and daughters (LHC = −0.027, 89% PI: −1.161 to 1.104) were equally likely to be weaned. Maternal birth cohort also had no measurable effect: children of mothers born before 1980 (LHC = 0.043, 89% PI: −0.902 to 0.980), between 1980–1990 (LHC = −0.002, 89% PI: −0.958 to 0.938), and after 1990 (LHC = −0.036, 89% PI: −1.009 to 0.923) were equally likely to cease breastfeeding. Birth order showed no difference between firstborn and later-born children (firstborn LHC = 0.069, 89% PI: −1.099 to 1.215; later-born LHC = −0.071, 89% PI: −1.248 to 1.083). Although birth order is often linked to differential parental investment (Wander & Mattison, 2013), this was not observed in our dataset—likely reflecting the characteristics of our sample, which includes mothers giving birth after 2010, a period when compulsory education and family-planning policies had restricted family size (two or three children, depending on region). In contrast, household size showed a strong negative association with breastfeeding duration, with larger households linked to earlier weaning (LHC = 1.197, 89% PI: 0.437–1.959).

Model 2 indicated that residence patterns were also associated with variation in breastfeeding duration. Duolocal, matrilocal, and neolocal households were all linked to slightly longer breastfeeding than patrilocal households. Although individual residence effects overlapped zero, the contrasts between patrilocality and each of the other residence types were consistently significant: duolocal (LHC = −0.831, 89% PI: −1.251 to −0.391), matrilocal (LHC = −0.449, 89% PI: −0.801 to −0.098), and neolocal (LHC = −0.550, 89% PI: −0.912 to −0.191). Lower log-hazard coefficients indicate longer breastfeeding durations (Fig. 1; SI Table 2.5), and Figure 2 illustrates the corresponding distribution of breastfeeding lengths across residence patterns.

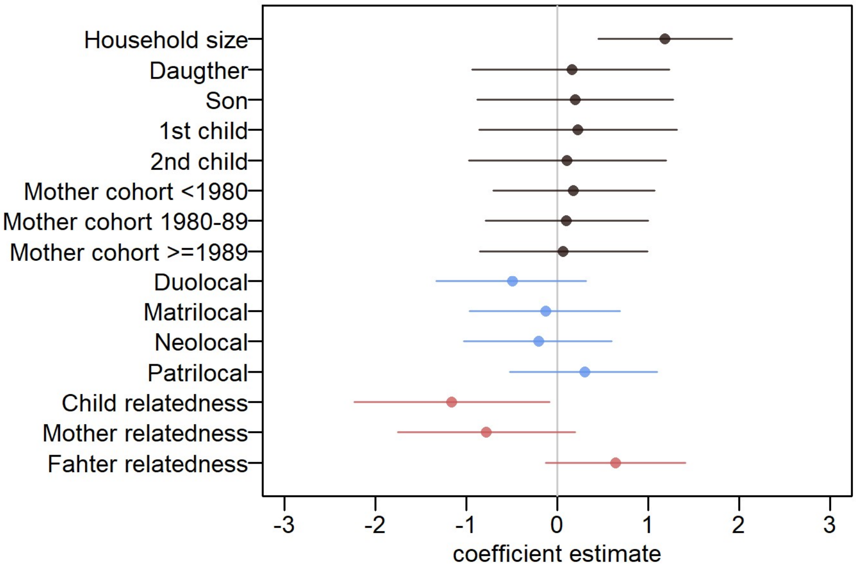

Figure 1: Posterior log-hazard coefficient estimates for the relevant predictors. Negative coefficient estimates indicate longer breastfeeding duration (a positive effect), whereas positive coefficients indicate shorter duration (a negative effect). Black points represent results from Model 1, blue from Model 2, and red from Model 3. Coefficients for patrilocality differ significantly from the other residence strategies, even though the effect of each specific residence pattern on breastfeeding duration overlaps with zero. Differences between strategies are as follows: duolocal vs. patrilocal = −0.831 (−1.251 to −0.391), matrilocal vs. patrilocal = −0.449 (−0.801 to −0.098), and neolocal vs. patrilocal = −0.550 (−0.912 to −0.191). All values refer to the posterior means and 89% credible intervals.

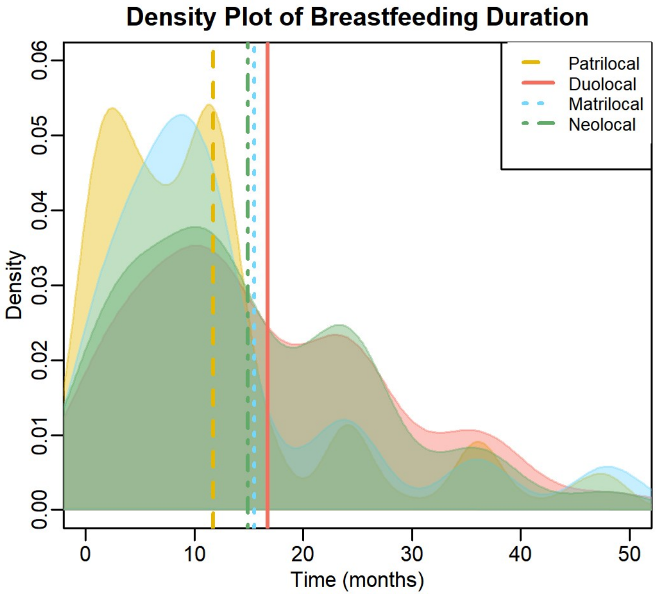

Figure 2: Density plots of individual children's breastfeeding duration under different residence patterns. Colours indicate residence type (yellow = patrilocal; red = duolocal; blue = matrilocal;

green = neolocal). Vertical lines represent mean breastfeeding duration for each residence pattern (solid = duolocal; dashed = patrilocal; dotted = matrilocal; dot–dash = neolocal).

Across different residence patterns, infants and parents varied in their average genetic relatedness to co-resident household members (Fig. 3). In Model 3, although the posterior densities overlap with zero, most of the posterior mass lay consistently on one side, indicating a clear directional trend. Specifically, the proportion of the posterior density that crosses zero is 0.043 for child's relatedness (≥ 0), 0.101 for mother's relatedness (≥ 0), and 0.090 for father's relatedness (≤ 0). These results suggest that the model is reasonably confident about the direction of effects: higher maternal and child relatedness to household members is associated with prolonged breastfeeding, while higher paternal relatedness predicts earlier weaning. Together, these findings point to the joint operation of parent–offspring and sexual conflict in shaping breastfeeding duration (see Fig. 1 and SI Table 4).

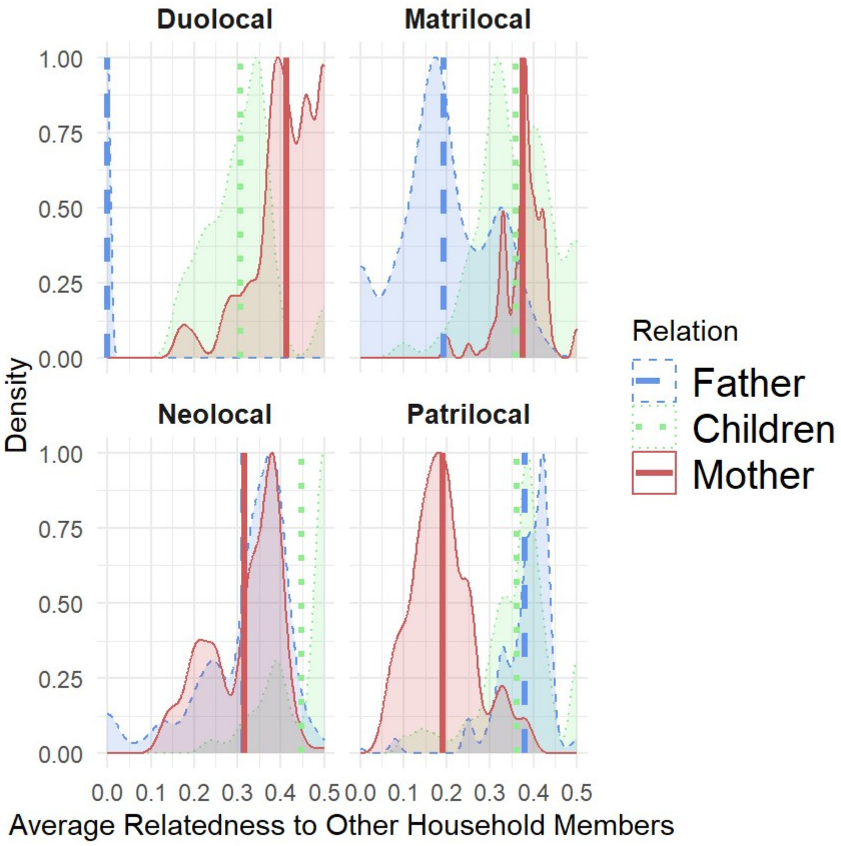

Figure 3: Density plots of individuals' average relatedness to other household members under different post-marital residence patterns. Colours indicate family members (blue = father; red = mother; green = child). Lines represent mean relatedness for each individual type (solid = mother; dashed = father; dotted = child).

A similar pattern emerged when comparing the empirical results with simulated data. The synthetic datasets that most closely reproduced the real outcomes were those generated under a combination of positive effects for child and maternal relatedness and a negative effect for paternal relatedness. As shown in Figure 4, the simulations consistent with these parameter combinations correspond to Hypothesis 3 (H3), indicating that both parent–offspring and sexual conflict jointly shape breastfeeding duration.

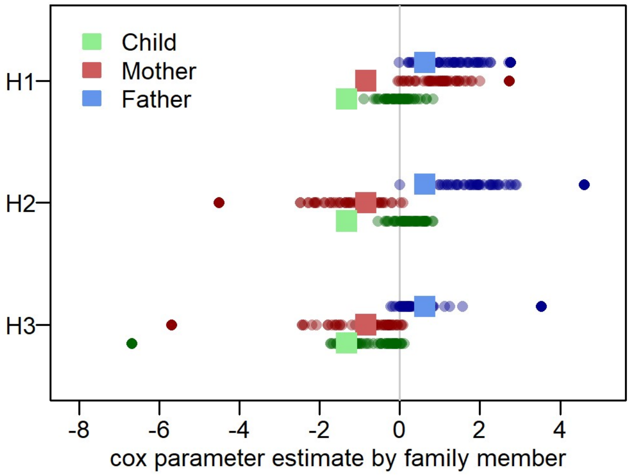

Figure 4: Comparison of log-hazard coefficients from Cox regression Model 3 fitted on the real dataset (light-coloured squares; N = 580) and on 50 simulated datasets (darker circles) generated under different hypotheses (H1–H3). Colours indicate the predictors: green = child's relatedness effect, red = mother's relatedness effect, and blue = father's relatedness effect. Simulations show that the pattern most consistent with the empirical data corresponds to H3, reflecting combined parent–offspring and sexual conflict.

We further identified the set of generative parameters that produced simulated data most closely matching the empirical results from Model 3. Comparing this "best-fitting" parameter set to our causal hypotheses revealed a consistent pattern: positive coefficients for child and maternal relatedness and a negative coefficient for paternal relatedness (Table 1). This configuration aligns with Hypothesis 3 (H3), supporting the interpretation that both parent–offspring and sexual conflict contribute to shaping breastfeeding duration.

Table 1: Descriptive statistics for a distribution of 250 parameter values that generate simulated data best matching the real data (cox model results from the real data are compared to those from 300 simulated datasets, and the generative parameters for the most similar dataset are retained. This process is repeated 300 times to obtain a parameter distribution that can be interpreted in the framework of the hypotheses described above. See supplementary information for more details).

	Intercept	Child	Mother	Father
Mean	-0.21	0.97	0.67	-0.59
5%	-2.41	0.00	-0.26	-2.60
94%	1.01	4.19	3.39	0.00

Table 2: Reasons given for weaning by 44 women under 3 different residence patterns.

Category	Neolocal	Patrilocal	Matrilocal
physical costs	3 (19%)	2(14%)	2(14%)
opportunity costs	5(31%)	8(57%)	3(21%)
social norms	4(25%)	2(14%)	6(43%)
Others	4(25%)	2(14%)	3(21%)

Self-reported reasons for weaning (Table 2) reveal that behaviours increasing the time and energy demands on women—such as breastfeeding—are often constrained by competing work responsibilities. Breastfeeding is a highly demanding maternal behaviour rather than a simple healthcare practice. Among respondents, opportunity costs—cases where women ceased breastfeeding due to conflicts with work or subsistence labour—were the most frequently cited reason (36%), followed by social norms (27%) and physical difficulties (16%). Although the sample size is limited, notable residence-specific differences emerge: in patrilocal households, opportunity costs were cited most frequently (57%), while in matrilocal households, social norms predominated (43%). These patterns suggest that women's breastfeeding decisions are influenced by both economic constraints and normative pressures. Some may follow community expectations to avoid social criticism rather than consciously weighing costs and benefits.

Across all five regions, household income primarily depends on agricultural or pastoral labour. Accelerometer data from the same population, published elsewhere indicate that women, especially in duolocal and patrilocal systems, engage in significantly more fieldwork and animal husbandry than men (Chen et al., 2023), intensifying the trade-off between breastfeeding and economic productivity. While the small sample size limits statistical power, these qualitative findings reinforce that breastfeeding decisions are shaped by labour demands, social expectations, and kinship structure.

Discussion

Our findings demonstrate that variation in residence patterns predicts breastfeeding duration in ways consistent with both parent–offspring conflict and sexual conflict. Children were breastfed for shorter periods in patrilocal households compared with matrilocal, duolocal, or neolocal households. This pattern supports the idea that the kinship structure of households—by shaping who is related to whom—alters the balance of cooperation and conflict over parental investment.

The effects of relatedness were aligned with our theoretical predictions. Higher relatedness of children and mothers to their co-resident kin was associated with prolonged breastfeeding, while higher paternal relatedness predicted earlier weaning. This pattern suggests that children's and mothers' inclusive fitness interests are often aligned, and both may conflict with paternal interests. In line with H3, breastfeeding duration appears to be shaped by the combined effects of parent–offspring and sexual conflict, with outcomes typically lying between the maternal and paternal optima.

Residence patterns also alter the intensity of conflict. In matrilocal and duolocal households, where mothers remain with their natal kin, maternal bargaining power is greater, and both mother and child are more likely to secure prolonged breastfeeding. In contrast, patrilocal households align fathers more closely with their kin, favouring earlier weaning to increase fertility. These results mirror long-standing predictions from kin selection theory: the distribution of relatedness within households influences who wins reproductive bargaining.

An additional explanation for the observed longer breastfeeding duration in matrilocal and duolocal households, as well as the relatively small effect of maternal relatedness, is the reduced parent-offspring conflict between the mother and the child. Matrilineal societies are associated with weaker marriage ties and higher divorce rates as also observed here (Mattison, 2011; Parkin, 2021, Du and Mace, 2019). That means mother's future offspring are, on average, less closely related to the focal child than in patrilineal societies where marriages are more stable. In other words, because the mother gains less reproductive benefit from weaning early when future offspring are more likely to be half-siblings rather than full siblings, her evolutionary incentive to curtail breastfeeding is reduced, even though the child continues to benefit from prolonged nursing. This prediction on weaning conflict goes back to Trivers original formulation of parent-offspring conflict (Trivers 1974). Bargaining power also differs systematically: women in matrilineal households negotiate reproduction from a position of greater kin support than those in patrilineal households.

One important conflict that exists between the breastfeeding mother and other co-resident household members is that her contributions to the family economy reduce while she is breastfeeding. The significant opportunity costs of breastfeeding are further exemplified by findings that breastfeeding mothers often engage in fewer subsistence and domestic tasks than non-breastfeeding women (Batan et al., 2013; Hawkes et al., 1997; Quinlan & Quinlan, 2008; Chen et al., 2023). Allomaternal care can offset these costs, but its effect depends on the type of support. When kin provide food or labour support, mothers can sustain longer breastfeeding. By contrast, when kin provide direct childcare, opportunity costs may increase, since maternal subsistence work must be combined with frequent separations from the infant (Emmott & Mace, 2015; Emmott, 2023; Emmott et al., 2020a; Myers et al., 2021). These proximate dynamics help explain why maternal relatedness had smaller average effects in our models than those of children or fathers.

Self-reported reasons for weaning provide additional proximate evidence. Opportunity costs were the most frequently cited reason for stopping breastfeeding, particularly in patrilocal households where women face greater labour demands. Social norms were also cited, especially in matrilocal households, suggesting that maternal behaviour is shaped both by ecological and kinship contexts and by culturally transmitted expectations. While the qualitative sample was small, these reports align closely with the evolutionary patterns identified, and this opens the possibility for future research on the proximate motivations for weaning.

Taken together, our results show how inclusive fitness theory can illuminate the dynamics of breastfeeding. Breastfeeding is not solely a maternal choice: it is shaped by kinship structure, bargaining power, and conflicting fitness interests between mothers, fathers, children and other co-resident household members. By linking residence patterns, relatedness, and breastfeeding duration, our study demonstrates that kin selection and sexual conflict together provide a powerful framework for explaining why mothers often cease breastfeeding earlier than health guidelines recommend. Here we show how the family structure, and the relatedness of children and parents to their co-resident household members are shaping breastfeeding duration and It is misleading to interpret reproductive decision-making in the context of mothers alone.

Methods

Descriptive Statistics

This study draws on data on 353 female respondents (mothers to 580 children for whom complete information were available for analysis) collected from five regions in western China, each differing in ecology, economy, and culture but sharing a common religion and political administration (Figure 5; SI Tables 2.1 and 3.1). The study sites include two areas in the Gannan Tibetan Autonomous Prefecture of Gansu Province (Zhuoni and Maqu), two in the Garzê Tibetan Autonomous Prefecture of Sichuan Province (Zhaba and Lugu), and one in the Diqing Tibetan Autonomous Prefecture of Yunnan Province (Shangrila). Within each region, data were collected from multiple villages clustered by language, cultural identity, and ecological context (Figure 5). This area is distinctive for the coexistence of four post-marital residence patterns—patrilocal, matrilocal, duolocal, and neolocal—among neighbouring Tibetan communities of farmers and herders. These contrasting kinship systems generate marked variation in the average relatedness of children and parents to their co-resident household members (Figure 3; SI Table 1).

The main sources of household income vary across regions. In Maqu, yak and sheep herding provide the principal livelihood, with crops largely reserved for household or livestock consumption (Du & Mace 2018; Gelek 2006). The seasonal collection of *yartsa gunbu* (caterpillar fungus) supplements income but has declined in recent decades (Xing & Wang 2023). Zhuoni families engage in both barley cultivation and livestock rearing, earning cash income through herding, farming, or temporary wage labour in nearby towns (Zhou et al. 2022). In Zhaba, Lugu, and Shangrila, most families rely on farming, supplemented by limited herding, foraging for mushrooms and medicinal fungi, or occasional tourism work. Income from wage labour and tourism is irregular and fluctuates annually, and salaried or office-based employment remains rare in all five regions (Chen et al. 2023; Huang et al. 2025).

Despite shared Buddhist traditions and other cultural similarities, these Tibetan populations differ in kinship organisation and post-marital residence. Maqu and

Zhuoni, inhabited by Amdo Tibetans, follow patrilineal descent and predominantly patrilocal residence (Zou 2006). Zhaba and Lugu, in contrast, are matrilineal societies practising duolocal residence (Chen et al. 2023; Jiao & Zhong 2017). Shangrila, located in the Diqing Tibetan Prefecture and inhabited by Kang Tibetans, is characterised by matrilineal descent and matrilocal residence (Du et al. 2023). These regional contrasts provide a unique opportunity to examine how variation in kinship and household composition shapes breastfeeding practices within a single ethnolinguistic population.

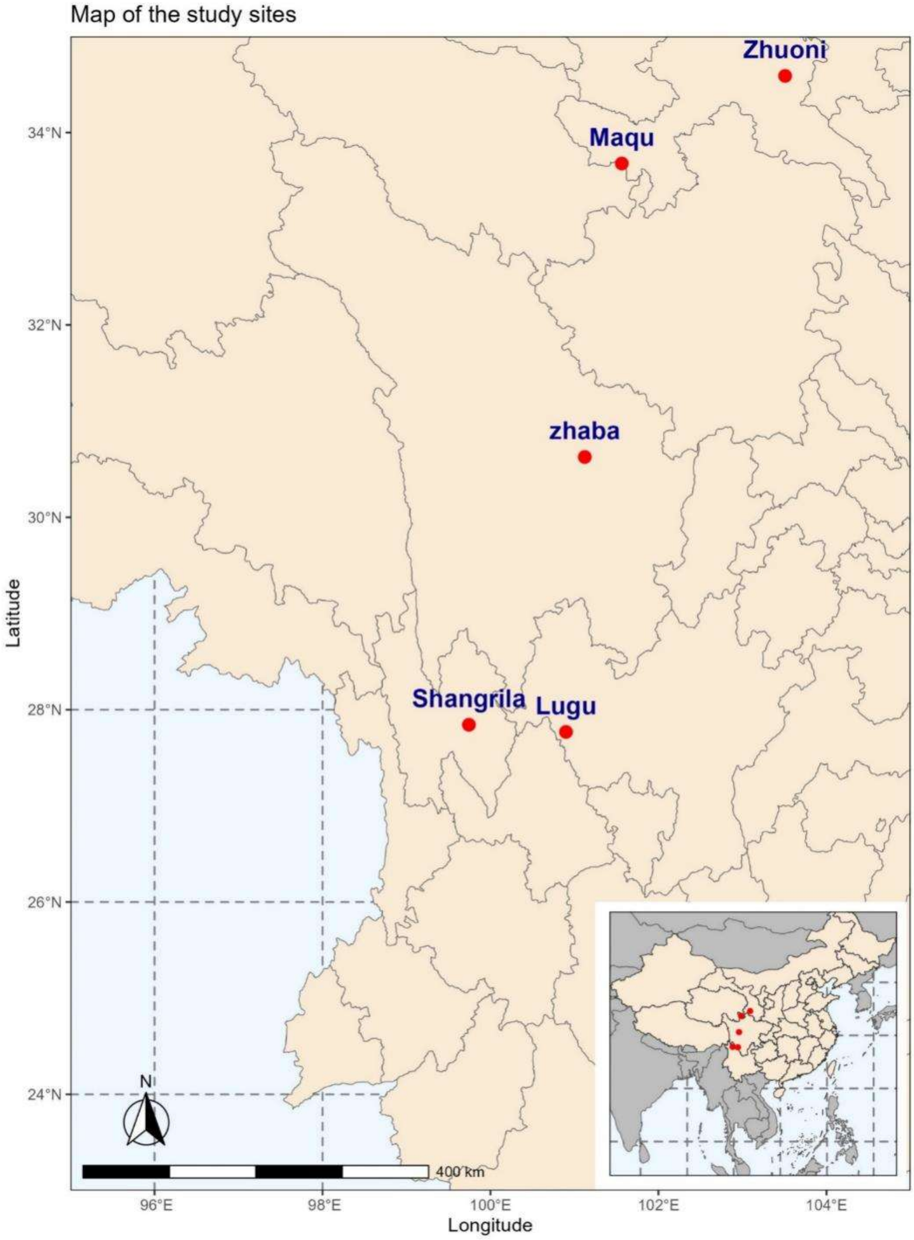

Figure 5: Map of the study sites. 5 different regions were indicated on the map with red dots, note that in each region, there are different villages where we collected data. The border was shown based on the provincial level in China.

We conducted household surveys in five regions of western China, walking from one household to another accompanied by local assistants in each area. The survey consisted of two sections: household structure and individual details. For household data, we collected sociodemographic information from the household head or another knowledgeable adult when the head was absent. These data included all co-resident members' years of birth and marriage, parental identities, dispersal histories, frequency of residence in the household, financial status, and primary subsistence activities.

Individual questionnaires were administered separately to adult men and women and recorded marital histories, sibling composition, and reproductive histories. Female respondents provided detailed information on each child's birth date, delivery method, breastfeeding duration, supplementary feeding practices, and reasons for weaning. Although demographic data were collected for all adult household members, this study focuses on families with children born after 2010 to ensure accurate recall of breastfeeding histories and residence arrangements. This yielded complete breastfeeding data for 580 children (284 daughters and 296 sons; SI Table 2). Breastfeeding cessation was defined as the termination of all suckling and censored at 24 months, because of low reliability of longer reported duration and consistently with the physiological relevance of the behaviour, as per with WHO health recommendations (WHO 2023).

Households were categorised into four post-marital residence patterns: patrilocal (wives disperse to husbands' households), matrilocal (husbands disperse to wives' households), duolocal (neither spouse disperses), and neolocal (both disperse to form new households). Although residence typically corresponds to prevailing descent systems in each region, exceptions occur—for example, matrilocal families within predominantly patrilineal communities. The distribution of residence patterns varied: duolocal residence was most common in Zhaba (53.4%) and present at lower frequencies in Lugu (16.5%), while patrilocality predominated in Zhuoni (63.1%) and Maqu (48.8%). In Shangrila, matrilocality was the dominant pattern (47%) (SI Table 1). Neolocal families exist in all locations (Lugu 35.9%, Maqu 28.9%,Shangrila 16.9%, Zhaba 16.8%, Zhuoni 16.9%).

Genetic relatedness was defined as the average coefficient of relatedness of each focal individual (child, mother, or father) to all other co-resident household members. Relatedness was calculated from pedigree data collected during household interviews using standard methods (Hamilton 1964; Wright 1922). For each individual i, we summed the genealogical relatedness of i (Wright, 1922) to each other members of household j and divide by the number of other household members (excluding i), n (Figure 6). This measure captures the individual's average genetic connection to their household, reflecting how kinship structure may influence cooperation and conflict over childcare (Figure 6).

$$\bar{r}_i = \frac{\sum_{j=1}^{n} r_{i,j}}{n}$$

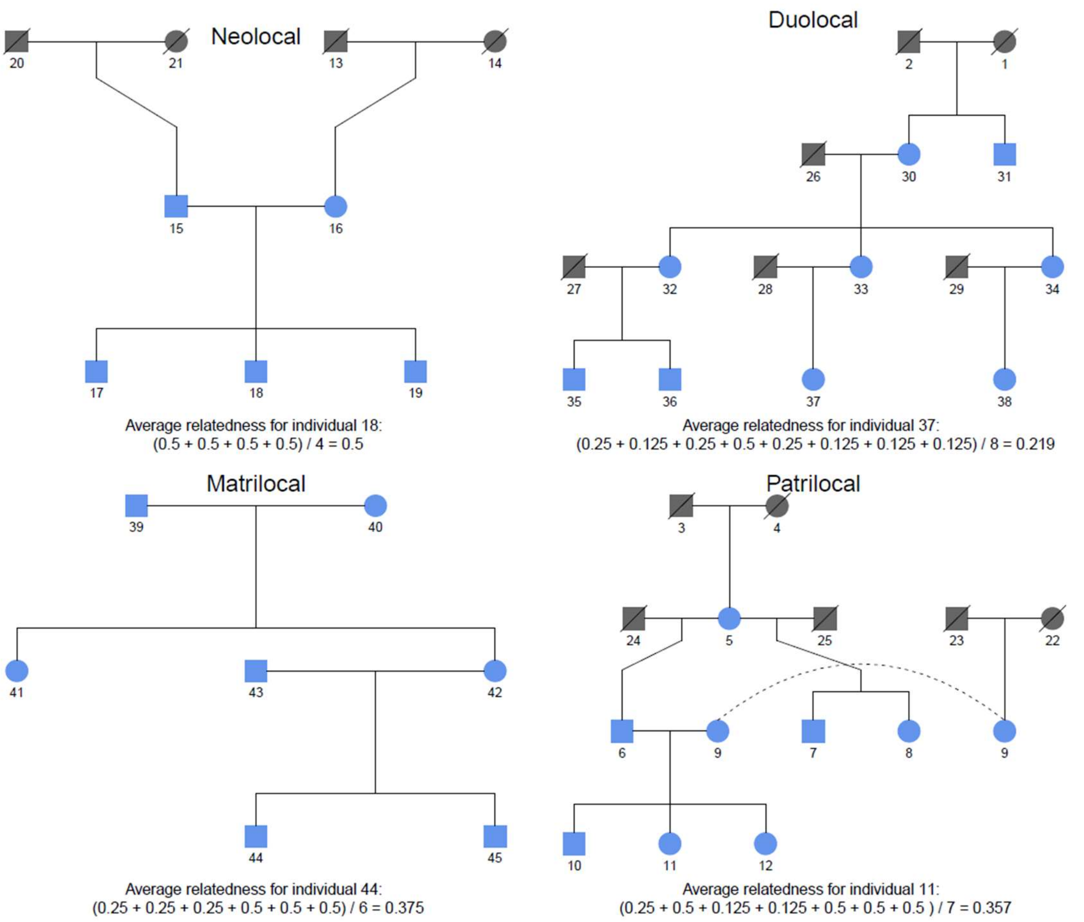

Figure 6: Examples of pedigrees illustrating each post-marital residence pattern. Circles represent females and squares represent males. Barred symbols indicate individuals present in the

genealogical dataset but not co-residing in the household (e.g., deceased members or non-resident fathers). For each individual, average relatedness is calculated by summing genealogical relatedness to all other household members and dividing by the number of co-resident individuals (excluding the focal individual)

To complement the quantitative analysis and gain insight into proximate motivations for weaning, we conducted semi-structured interviews with 44 women in Shangrila. Participants were asked to describe their reasons for stopping breastfeeding, which we subsequently classified into four categories: physical costs, social norms, opportunity costs, and other reasons (Table 2; see SI Table 3 for detailed responses).

Causal model

The comparison of hypotheses in this study is complicated by potential equifinality—that is, different causal models can produce similar patterns in the data, making them difficult to distinguish empirically. This issue arises because of the mechanism of genetic inheritance, which inherently correlates the relatedness of children and parents to other household members. Consequently, it becomes challenging to disentangle whether observed effects are driven primarily by the parent's relatedness, the child's relatedness, or both (see Supplementary Information, Section 2, for a detailed discussion of the implications for causal inference). To address these complexities and the non-mutually exclusive nature of our hypotheses, we employ a multi-method approach combining causally validated Cox regression models with comparisons between synthetic datasets (see Supplementary Information, Section 5) and empirical data on household demographics and breastfeeding durations collected in 2016–2017.

First, we use a principled causal framework to guide both model specification and interpretation. Specifically, we employ Directed Acyclic Graphs (DAGs) to clarify the assumed relationships among variables and define the appropriate adjustment set for inference. Figure 7 illustrates the variables included in our analysis. As our main goal is to estimate the effects of the mother's, father's, and child's average relatedness on breastfeeding duration (tested in Model 3), the key predictors include these three variables, along with village to account for cultural and ecological variation. We additionally control for household size, maternal birth cohort, child sex, and birth order to improve estimate precision. All variables are described in detail in Supplementary Information, Section 3.1.

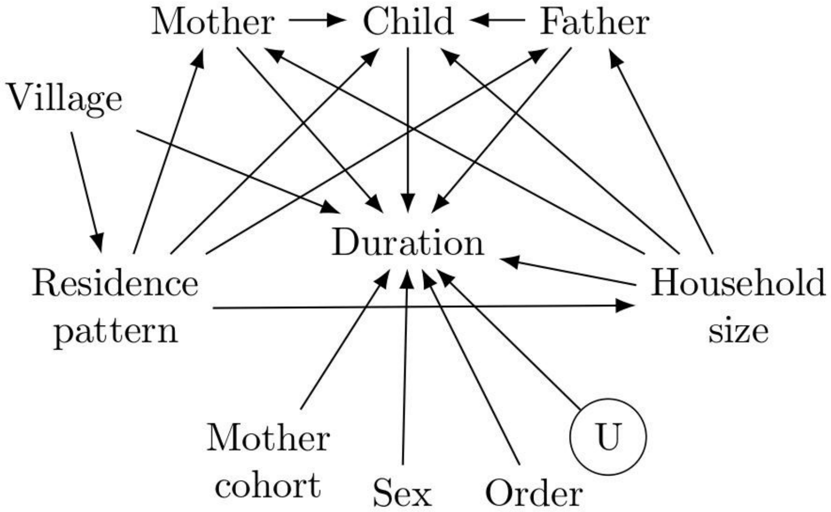

Figure 7: Directed acyclic graph (DAG) showing the relationships among variables influencing breastfeeding duration. Some relevant variables—such as physical constraints and household wealth—were not available in the dataset. The effects of these, along with other unmeasured variables (indicated by the circled U), are likely captured by the random effects for individual mothers. We do not assume that residence patterns directly affect breastfeeding duration; rather, we propose that geographical location (village), representing cultural and ecological variation, influences both residence patterns and breastfeeding duration.

Statistical analysis

We used Cox proportional-hazards regressions to test which variables were associated with the termination of breastfeeding, treating the process as a survival analysis where predictors—such as relatedness of individual relatedness and other covariates—affects the risk of breastfeeding cessation. This approach also accommodates censoring, accounting for children who were still breastfed at the time of the interview; Breastfeeding durations exceeding 24 months were censored due to both the lower reliability of maternal recall and the reduced physiological relevance of breastfeeding beyond this period for mother and child (see SI Figure 2 for complete data distribution).

Control variables included the mother’s birth cohort, child’s birth order and sex, and household size (except in Model 2, where household size lies on the causal path of residence type). Mothers’ birth cohorts were grouped in ten-year intervals (≤1980, 1980–1989, ≥1990). Because some mothers contributed more than one child to the dataset, maternal ID was included as a random effect, along with village, to control for ecological and cultural clustering. Household size was entered as an ordinal, monotonically increasing predictor. Household size varied across residence patterns (duolocal: 7.77 ± 2.92; neolocal: 5.50 ± 1.40; patrilocal: 6.83 ± 1.90; matrilocal: 6.78 ± 1.92).

Average genetic relatedness for each individual (child, mother, and father) to their co-resident household members was calculated using the Kinship2 package (version 1.9.6) based on pedigree data, following standard formulations from Hamilton (1964). Bayesian Cox models were implemented in Stan with weakly regularizing priors (details in SI section 4). Models were run using the CmdStan package (version 0.5.3) for 3,000 iterations after 1,000 warm-up iterations. Model convergence was verified by $\hat{R} \approx 1$ and large effective sample sizes. Plots were generated using the ggplot2, contsurvplot, rnaturalearth, and ggspatial packages. All analyses were performed in R (version 4.2.2). Data and reproducible code are available at: https://github.com/lalla-ilaria/breastfeeding_relatedness. Ethical clearance was obtained from University College London and Lanzhou University.

Simulations addressing risk of equifinality

Additionally, we conducted further analyses to account for the fact that children and their parents share, on average, half of their genomes. This biological reality creates a correlation between the average relatedness of children and that of their parents to other household members, introducing the potential for equifinality—the risk that different causal hypotheses could generate similar observable patterns.

To address this, we generated multiple simulated datasets of breastfeeding duration under each hypothesis (H1–H3) and compared the results of Model 3—which includes predictors for the relatedness of children, mothers, and fathers—when fitted to both real and simulated data (Figure 4). We also repeated this comparison using alternative Cox models that included different combinations of relatedness predictors (e.g., only one at a time or pairwise combinations) to evaluate their ability to discriminate among hypotheses (see Supplementary Figure 6).

Model 3, which incorporates all three relatedness variables alongside the control covariates, provided an accurate performance in distinguishing among the hypothesised mechanisms and mitigating equifinality (see Supplementary Information, Section 3.3). This approach using simulations is particularly advantageous because, unlike fully parametric models, Cox regressions do not specify a complete likelihood for event times, precluding standard posterior predictive checks for model validation. Instead, we employ a simulation-based validation strategy: by generating datasets under competing hypotheses and refitting the same model to these synthetic data, we assess which of the underlying mechanisms considered here is most consistent with the observed posterior distributions.

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Supplementary information for Manuscript titled ‘Kin selection and sexual conflict drive the duration of breastfeeding’ - considerations for causal inference

The following document provides additional information for the manuscript titled ‘Kin selection and sexual conflict drive the duration of breastfeeding’. It is organized in 5 sections, as follows: Section 1 provides ethnographic details of the studied populations. Section 2 describes the data on genetic relatedness, how these were generated and the issues they represent for statistical inference. Section 3 describes in detail the variables used in the analysis and the inferential strategy, which uses a Direct Acyclic Graph to state assumed causal relationships between the variables and clearly describes how the hypotheses compared by this manuscript would affect the data. Section 4 includes additional information on the survival analysis method employed for this paper. Section 5 describes the steps taken to verify that the covariance between genetic relatedness data in our sample would not make it impossible to compare the different hypotheses presented here.

1 Study populations

This study collected data from five Tibetan populations in western China, comprising 350 female respondents and a total of 580 children. Each population exists in diverse ecological, economic, dialectal, and cultural landscapes, yet they share the same religion and governmental structure. The regions studied include two locations in the Gannan Tibetan Autonomous Prefecture of Gansu province (Zhuoni and Maqu), two in Sichuan province (Zhaba and Lugu), of which Zhaba belongs to Garzê Tibetan Autonomous Prefecture, and one (Shangrila) in the Diqing Tibetan Autonomous Prefecture of Yunnan province.

Individuals living in Zhaba and Lugu are part of matrilineal groups where female family members inherit most of the family resources, and grandmothers are the heads of the households (Wu et al., 2013). Families in these regions tend to live in large communal houses, with brothers and sisters of three generations residing together. Men visit their wives at night, but do not live with them or their offspring, a practice known as ‘walking marriage’ or ‘visiting marriage’. This post-marital residence system is referred to as ‘duolocal residence’ (Wu et al., 2013). Men invest more resources in their natal families rather than their wives’ families (He et al., 2022, Wu et al., 2013; Chen et al., 2023). There was some polygamy in the past (Shih, 2009; He et al., 2022). The people in Zhaba and Lugu primarily rely on farming as their main source of income. During the summer, they collect mushrooms, and those living near the river run guest houses during the tourist season as an additional income source (Mattison, 2010). Domestic labour, except for building work, is mostly performed by women. Men are rarely seen in the fields, except during planting and harvest times, and are more regularly involved in income-generating activities associated with the market economy (Chen, 2023).

Tibetans living in Amdo are called Amdobas. Amdobas who practice farming alongside herding are known as Rongbas, while nomadic herders who cannot rely on farming as their main subsistence are called Brogpa. In this study, Tibetans living in Maqu are referred to as Brogpa, whereas those living in Zhuoni are called Rongbas. The Rongbas from Zhuoni are agro-pastoralists and have been more influenced by Han Chinese culture compared to the Maqu Brogpas. The Brogpa in Maqu lead a more traditional pastoral lifestyle, with livestock and their dairy byproducts being the main sources of income. Some Brogpa also collect yartsa gumbu (Chinese: 冬虫夏草) in late spring and early summer, but this source of income is reducing from 2008, for the sake of grassland protection policy (Fan, 2005; Xiang and Wang, 2023). For Rongbas in Zhuoni, yaks, sheep, and pigs are important sources of family income. They also grow barley, wheat, soybeans, and potatoes to feed livestock and for family consumption (Zhou et al., 2022). The younger generations are now significantly influenced by market integration, often finding labour work in towns or cities. Polygyny, polyandry, and serial monogamy were more commonly practiced in Maqu's history than after 1980. At the time of the interview, there were only five cases of fraternal polyandry in Maqu (Du, 2017). It is rare for Brogpa in Maqu to marry individuals from other ethnic groups, whereas Rongbas in Zhuoni frequently marry Han and other ethnic minority groups. Both populations practice a patrilineal system, where men are the leaders of the family and hold absolute authority and power. However, our previous work in Maqu has shown that the absolute dominance of males is changing due to women's irreplaceable contribution to the family economy (Du and Mace, 2018).

Shangrila is in Diqing Tibetan autonomous prefecture, Yunnan province. This area is comprised of half-farming and half-pastoral land. The majority of the people living here are Tibetans, sharing a Tibetan dialect that differs from that of other regions (Wang, 2018; Leanwangdui, 2003).Traditionally, Shangri-La Tibetans had three forms of marriage: polyandry, polygyny and monogamy (Wang, 2021), but the population now is predominately monogamous (Leanwangdui, 2003). Both exogamous and endogamous marriage are common, though parents have power in deciding who their children marry, preferring marriages with natal or neighbouring village members (Wang 2021). First born children, irrespective of sex, commonly co-reside with their parents and stay at their natal family after marriage and inherit parental wealth, whereas later born will either marry into other villages or stay in the same village, albeit not in the same house as their parents. It is rare to get married outside of the township (Du et al., 2023; Zhou, 2010).

In all regions, the education level was relatively low, but the situation improved somewhat when compulsory education was implemented in China (Wu, 2013; Du, 2017). Additionally, the family structure shifted from traditional extended families to more nuclear households following the implementation of the one-child policy in the late 1980s. Under this policy, most Han Chinese were allowed to have one child, while Tibetans were permitted to have two to three children, depending on the specific ethnic minority area they lived in (Attané and Courbage, 2000). In this study, we use village as a proxy for geographical and ecological differences between these groups and for ethnicity, which is linked to cultural practices and prevalent subsistence strategies (Chen et al., 2023). In Maqu, where the population density is very low, we define a village as several families that stay in the same herding group which usually involves sharing pastureland and adhering to the same social norms regarding herding and production. In the other four areas, a village refers to natural villages (Chinese: 自然村) that are primarily based on geographical factors. Although individuals living in the same village or herding group are geographically close to each other, and they do help each other in the harvesting time (Bai et al., 2021;Thomas, 2018), household is still the central unit of daily activities, as resources do not flow between households. For Amdo Tibetans, pastureland were privatized, so the size of land each family got depends on the size of the family member (Du and Mace, 2018; Bai et al., 2021). In Lugu and Zhaba, farming and herding are mainly for family consumption, and other forms of labour income will not be shared between each households (Mattison, 2010).

Note that even though most people living in each of the five regions follow the main descendance pattern (matrilineal vs patrilineal), not all couple reside accordingly, e.g. some families can follow a matrilocal residence pattern in a patrilineal community and so on.

2 Genetic relatedness and why it can cause problems to causal inference

The present paper leverages genetic relatedness of individuals within a household as a measure of their bargaining power to define breastfeeding duration, i.e. their ability to define how long should a child be breastfed according to their (fitness) interests. We consider genetic relatedness of each focal child and that of their parents to the rest of the household.

Note that this is calculated *relative to the child's household*, so that, if the father is not co-resident with the child, their average relatedness is set to zero to represent the fact that absent fathers cannot influence decisions on breastfeeding duration. The values have been calculated from pedigree data with the R package `Kinship2`, version 1.9.6 (Sinnwell et al., 2014).

As described in the main text, we posit that the child's interest is to prolong breastfeeding as long as possible, as breastfeeding is associated with better health outcomes. Parents, on the contrary, should prefer a shorter breastfeeding duration in order to move on to produce new offspring, creating the conditions for a parent-offspring conflict. But the parents themselves have different investment in the length of the duration, which per se generates intersexual conflict. In particular, the mother is expected to prefer a longer breastfeeding duration, as females are expected to invest more in each offspring, while men should prefer shorter duration, as they have an interest in increasing the number of offspring rather than the quality. Additionally, social conditions and labour requirements at the household level influence breastfeeding duration, as breastfeeding women cannot engage in several productive activities or have limited labour outputs (reduced hours of work, reduced production per hour). We hence expect that in households where the mother has higher average relatedness to the rest of the members, these are more likely to cover for her missing labour and thus favour longer breastfeeding duration compared to households where the father has higher relatedness.

As mentioned, this approach hinges on using on the average relatedness level of children and parents to the household as a predictor of breastfeeding duration, which creates problems for causal inference, as the genetic relatedness of parents and offspring is tightly correlated by mechanisms of genetic inheritance. Because offspring inherit half of the chromosomes from each parent, children are always 0.5 related to each of their parents. The relation between the average relatedness to the whole household of children and that of the parents, however, depends on the structure of the household itself. In a case limit where the household is composed by only a child and their unrelated parents, the relatedness of the parents to the rest of the household is $\frac{0.5+0}{2} = 0.25$, as each parent shares half of their genome with their child and none with the partner. The child shares half of their genome with each parent, making the child's average relatedness $\frac{0.5+0.5}{2} = 0.5$ equivalent the sum of their parents' average relatedness $0.25 + 0.25 = 0.5$. But parents can also be related to each other, and as the number of the member of a household increases, the average genetic relatedness of a child to the rest of the household approximates the sum of the relatedness of the parents divided by two $\frac{relatednessMother+relatednessFather}{2} = relatednessChild$ (for example in the limit case where there is an infinite number of siblings of the focal child, each related 0.5 to both the parents and the focal child, i.e. where everyone is approximately 0.5 related to each other, given that the fact that the parents are not related to each other would be swamped by the infinite number of siblings all 0.5 related to both parents and focal child, or $\frac{0.5+0.5}{2} = 0.5$)[1]. This is important because it imposes a serious collinearity problem to the children's and parents' relatedness (and it guides our simulation exercise, see below).

Differences in household composition and in relatedness between the parents (who can be cousins, for example) generate variation in the ratio of parents' and children's relatedness. The area of western China where data was collected offers just such variation, as there coexist multiple ethnic groups who differ in preferred residence patterns. Moreover, not all households within an ethnic group follow the mainstream residence type. This creates a reasonable amount of variation between and within ethnic groups in choice of residence (i.e. duolocal, matrilocal, neolocal or patrilocal). The resulting variability in how related are individuals within a household (see figure 1, main text) can be leveraged for the statistical analysis. SI Table 1 reports average relatedness between Mothers, Fathers and Children and the rest of their households by residence type (at the household level).

Table 1: Average relatedness of mothers, fathers and children to other household members.

	Duolocal (N=128)	Matrilocal (N=131)	Neolocal (N=132)	Patrilocal (N=189)	Total (N=580)
Mother					
Mean (SD)	0.41 (0.08)	0.38 (0.05)	0.32 (0.08)	0.19 (0.07)	0.31 (0.11)
Range	0.17 - 0.50	0.20 - 0.50	0.14 - 0.50	0.05 - 0.38	0.05 - 0.50
Child					
Mean (SD)	0.31 (0.08)	0.36 (0.08)	0.45 (0.07)	0.36 (0.08)	0.37 (0.09)

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[1] Note that these represent limit cases used to illustrate the range of mathematical relations between parents' and child's relatedness values

	Duolocal (N=128)	Matrilocal (N=131)	Neolocal (N=132)	Patrilocal (N=189)	Total (N=580)
Range	0.16 - 0.50	0.10 - 0.50	0.23 - 0.50	0.10 - 0.50	0.10 - 0.50
Father					
Mean (SD)	0.00 (0.00)	0.19 (0.11)	0.31 (0.11)	0.38 (0.06)	0.24 (0.17)
Range	0.00 - 0.00	0.00 - 0.43	0.00 - 0.48	0.08 - 0.50	0.00 - 0.50

However, the significant correlation between parents' and children's relatedness can generate problems for causal inference and requires careful consideration. We thus develop a workflow that aims on the one hand to define a causal inference strategy for causal effects of relatedness on breastfeeding duration. On the other hand, we attempt to address in a principled way how predictions driven by competing hypotheses manifest themselves in the data, controlling for the risk of equifinality, as generated by covariation in the genetic relatedness data. We begin by using Direct Acyclic Graphs (DAGs) as a tool to illustrate causal connections between the relevant variables (see next section). This helps in one hand to construct statistical models that are able to produce the correct inference to understand the effect of the relevant variables (i.e. define causal queries and choose the appropriate control sets), but also as a lead to build simulations. The use of simulations is helpful in this case to guide our intuition on what the statistical models can tell us about the *real* effects of genetic relatedness. Because of the correlation in genetic relatedness, we could observe the phenomenon of equifinality: different causal models can produce the same distribution in the data and thus be practically non-distinguishable in the real data (e.g. the model could estimate the same values for parameter relative to the effect of mother's relatedness if the causal effect came from *her* relatedness or from that of her child). Simulating data according to realistic relatedness patterns and following different causal models allows us to observe in a controlled (simulated) setting *what* the statistical models can tell us (i.e. which hypotheses are virtually indistinguishable in the real data), but also guide us in the interpretation of the results of the analyses on the real data.

2.1 Estimating multicollinearity

While collinearity between relatedness of family members *must* arise from the combination of residence strategies and genetic inheritance, standard measures of multicollinearity do not reveal an excessively problematic pattern. Variance Inflation Factor values for a linear regression including child, mother and father as predictors are 2.32 , 2.64 and 3.32 respectively. While these values indicate that some collinearity is present (obviously) they are well within the threshold of 5 usually considered problematic. A calculation of correlations (correlation matrix) returns values below the warning level of 0.7 (mother-child: 0.14, father-child: 0.42, mother-father: -0.63). This means that, while we still believe that it is important to address the necessary correlation between the average relatedness of parents and children, the coefficients returned by the statistical models we used should be reliable, at least in the direction of the correlation, if not as precise.

Additional concern could be raised by the observation that mothers' and fathers' relatedness appears to be negatively correlated (-0.63 in the correlation matrix). This arises because of the clustering within matrilocal and patrilocal households, where mothers and fathers are respectively more related to the rest of the household. Once controlling for residence pattern, no correlation appears within patrilocal or duolocal households, a positive correlation emerges within matrilocal households and a negative correlation still appears within neolocal households (see figure SI1). This depends on relocation strategies, as most likely the relatives beyond the nuclear family do not join a household independently. Or, once someone from the matriline or patriline moves in, it is more likely the other people from that side of the family join the household (e.g. John's sister moves in with her three kids, but then Mary's sister cannot also move because of lack of space). Indeed, the majority of focal children in neolocal households lives in medium or large households (87%), and in 29 of these families, other individuals that are not part of the nuclear family (reproductive couple and their children) live under the same roof. These are most commonly grandparents (~70% of the non-nuclear family members of the household), following a widespread pattern in which widowed or otherwise lonely older individuals move in with their children. These are obviously related to either the mother or the father of the focal child, and it is very unlikely that grandparents from both sides join the same households, thus creating a negative relatedness pattern. Similarly, unpartnered siblings of the reproductive couple can join the household, sometimes bringing together their offspring (12% of non-nuclear family members of the household are aunts and uncles and 2% are cousins). Finally, half siblings of the focal child and great-grandparents can also join a neolocal household.

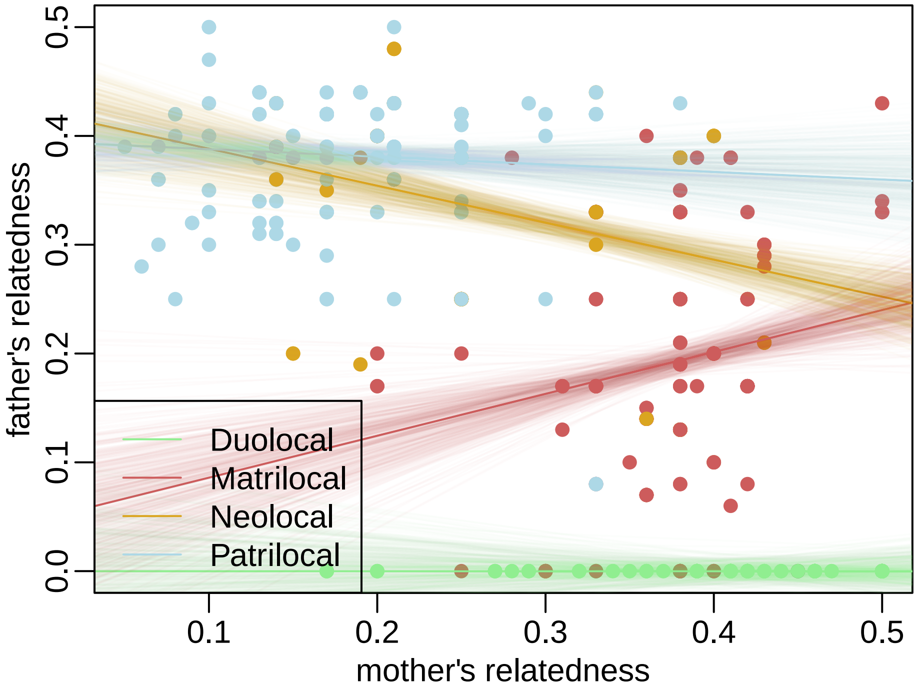

Figure 1: Correlation between mothers' and fathers' relatedness by residence strategy. Green represents Duolocal; Red represents Matrilocal; Yellow represents Neolocal; Blue represents Patrilocal.

Ultimately, while the correlation between the average relatedness of family members is is a feature of the data and unavoidable within this dataset, we believe that the data will yield the relevant information, given that the level of multicollinearity is estimated to be relatively low and should not distort the results.

3 Variables used and inference strategy

We first describe all the variables considered in the analysis and ways by which they influence the outcome, before describing the causal inference strategy we used.

3.1 Description of variables

- Age at stop breastfeeding: this is our outcome variable. It is the age at which the child was not breastfed anymore. SI figure 2 shows the duration of breastfeeding in our sample. The majority of mothers wean within the first 12 months (66%) and only 13% takes longer than two years (although we can see a large variation by residence type, as only 11% of mothers in neolocal households breastfeed after this time). Note that values corresponding to yearly marks are much more frequent than expected at random. This can reflect a real phenomenon, i.e. children are more likely weaned at round years, because of cultural reasons, for example. But it is more likely that people tend to answer to uncertain, time-related questions with round numbers (a phenomenon known as age-heaping when the question is 'how old are you'). At least in part to deal with these issues, the data used for this analysis has been censored at 2 years (i.e. number of months up to 24 during which each child was breastfed, not exclusively). Moreover, some of the data is censored because of time of observation: a mother of a fifteen months old child reports she is still breastfeeding, but we have no information on how long that will last. Note that the variable used in the analysis is the similar column named 'time', which contains the same information unless the data is censored at 24 months, in which case it contains the number 24 (this passes the correct censored values to the model). Moreover, the variable 'status' indicates whether the data has been censored or not.

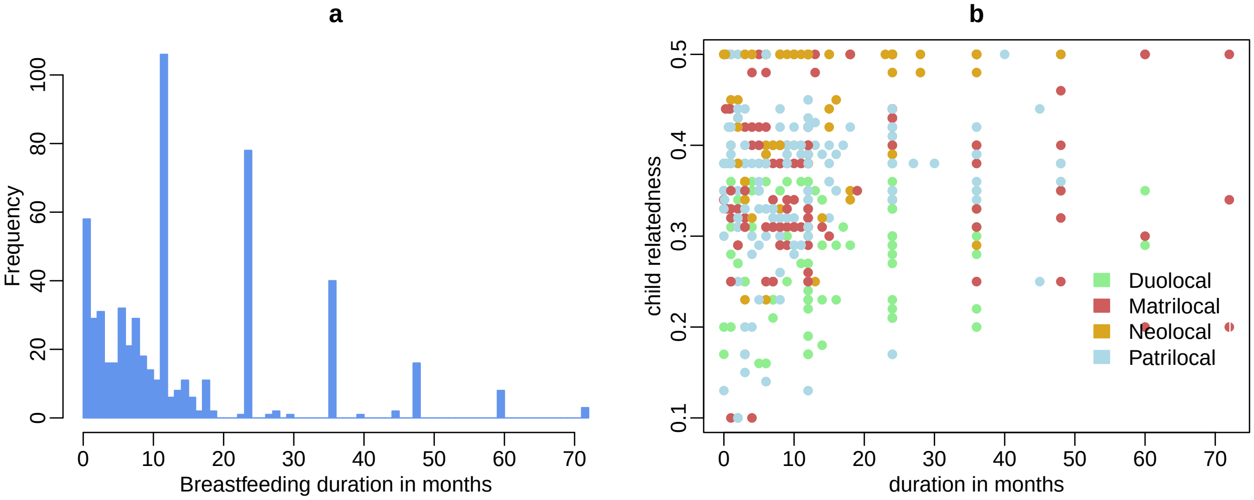

Figure 2: a - Histogram showing the duration of breastfeeding in our sample. Note the heaping at values corresponding to yearly marks. b - Duration of breastfeeding by child relatedness, color coded by residence pattern.

- Child relatedness: one of the main predictors, estimated genetic relatedness of the focal child to the rest of their household given the reported family relations (parents are on average 0.5 related to their children, grandparents 0.25 and so on; the relatedness for the parents is similarly calculated, see notation in the main text). We expect longer duration of breastfeeding the higher the average genetic relatedness to the household, under the assumption that in a more related household the interests of the child (longer duration of breastfeeding) count more.
- Mother relatedness: see child relatedness for the calculation of this measure. The mother optimal breastfeeding duration is influenced by her cost in producing milk, her interest in her child's well-being and the opportunity cost of not doing something else
- Father relatedness: see child relatedness for the calculation of this measure. Fathers' interests are likely associated with a shorter duration of breastfeeding, as he is expected prefer having another baby sooner than the mother's preference (breastfeeding inhibits the luteal cycle thus rendering women temporarily infertile).
- Village: Data was collected across the Zhaba, Lugu, Zhuoni, Maqu, and Shangrila regions, each comprising numerous distinct villages. Village is used as a proxy for geographical/ecological differences between these groups and for ethnicity, which is linked to cultural practices and prevalent subsistence strategies that can influence breastfeeding duration. The prevalence of residence patterns varies in each region, see SI Table 2, for example Duolocality is prevalent in Zhaba (53.4% of households), present in Lugu (16.5%) and completely absent in Zhuoni, Maqu and Shangrila, the last of which is prevalently matrilocal (47%), while the remaining two are largely patrilocal.
- Residence pattern: one between duolocal (each parent remains within their natal household, relatedness of the mother is highest, lowest for the father), matrilocal (the couple lives with the wife's family, relatedness is high for the child and mother, low for the father), neolocal (the couple lives in a new household, relatedness is lower and similar for mother and father, high for the child) or patrilocal (the couple lives with the husband's family, father and child have high relatedness, lowest for the mother). We assume that any cultural effect linked to residence pattern is clustered at the level of village (ethnicity), rather than residence pattern.

- Household size: The people you live with can greatly influence the amount of assistance you receive; in some cases, it also determines the number of potential competitors you may face. Therefore, the size of the household is crucial for breastfeeding practices, as it is associated with the level of direct support (such as bottle-feeding infants) or indirect support (such as relieving the mother of household chores so she can focus on breastfeeding) that the mother can receive during her breastfeeding journey. Household size ranges from 2 to 22, with a median 7.
- Birth order: Siblings compete for family resources, a competition that begins from birth. For instance, if a mother breastfeeds one child for an extended period, it may delay her ability to have another baby. The intensity of this competition varies between full and half-siblings, as noted by Trivers in 1974. Parents might exhibit a preference for the older offspring, a phenomenon known as primogeniture, which has been documented in one of the populations from the same database (Du et al. 2023). However, parents may also show a preference for the youngest child, particularly in contexts where child policies reduce the likelihood of having more children. In this paper we present this variable as either 1st born or >=2nd born. This is because we only included births after 2010 (to improve accurate recalling of breastfeeding information), by which point the area was interested by a fully implemented child policy (a maximum of 3 children per woman in this area). As a result, our data include only 4 births of a 3rd child, which were thus classified together with 2nd borns.
- Child sex: Parents may exhibit gender-biased parental investment, with preferences that vary according to ecological and social norms. In one of our studied populations, we have previously demonstrated that mothers tend to breastfeed daughters longer than sons (Du & Mace 2018). However, the patterns of gender-biased investment across five different populations remain unclear. To address this, we controlled for the gender of the offspring in our analysis, categorizing them into two groups: daughters/females and sons/males.
- Mother cohort: the middle and latter half of the 20th century saw a gradual decline of breastfeeding, which was replaced by formula feeding in many high-income contexts (Tomori et al., 2016). We controlled for mother birth time at 10 years cohort, which could capture how globalization influences the norm and the practices of feeding. In addition, several political factors might also influence the feeding practices, for example, child policy that was implemented in the early 1980s, and the compulsory education policy that was implemented at 1990s. We thus categorized mother birth into 10 years cohort: <=1980, 1980-1989 to >=1990
- Physical constraints: physical problems are one of the important reasons for terminating breastfeeding (Verronen, 1982; Page et al 2021), i.e. sore and cracked nipples, painful breasts and poor latching et al (Li et al., 2008) are commonly reported as important problems and act as a barrier to continued breastfeeding. Individual data on physical constraints was unfortunately not available for this analysis. In the DAG, this information falls within the unknowns labeled as U.
- Household wealth: higher household wealth is expected to be associated with longer breastfeeding if mothers' labour is needed in poorer households, or shorter if alternative food sources are a limiting factor for weaning. Detailed data on household wealth was unfortunately not available for this analysis. Similarly, ithis information falls within the unknowns labeled as U in the DAG.

Table 2: Descriptive statistics by ethnic group.

	LuGu (N=103)	MaQu (N=121)	ShangriLa (N=83)	ZhaBa (N=208)	ZhuoNi (N=65)	Total (N=580)
Residence						
Duolocal	17 (16.5%)	0 (0.0%)	0 (0.0%)	111 (53.4%)	0 (0.0%)	128 (22.1%)
Matrilocal	15 (14.6%)	27 (22.3%)	39 (47.0%)	37 (17.8%)	13 (20.0%)	131 (22.6%)
Neolocal	37 (35.9%)	35 (28.9%)	14 (16.9%)	35 (16.8%)	11 (16.9%)	132 (22.8%)

	LuGu (N=103)	MaQu (N=121)	ShangriLa (N=83)	ZhaBa (N=208)	ZhuoNi (N=65)	Total (N=580)
Patrilocal	34 (33.0%)	59 (48.8%)	30 (36.1%)	25 (12.0%)	41 (63.1%)	189 (32.6%)
Cohort						
<1980	11 (10.7%)	3 (2.5%)	1 (1.2%)	14 (6.7%)	5 (7.7%)	34 (5.9%)
>=1990	56 (54.4%)	60 (49.6%)	55 (66.3%)	140 (67.3%)	28 (43.1%)	339 (58.4%)
1980-1989	36 (35.0%)	58 (47.9%)	27 (32.5%)	54 (26.0%)	32 (49.2%)	207 (35.7%)
Birth order						
1st	38 (36.9%)	51 (42.1%)	57 (68.7%)	112 (53.8%)	20 (30.8%)	278 (47.9%)
2nd	65 (63.1%)	70 (57.9%)	26 (31.3%)	96 (46.2%)	45 (69.2%)	302 (52.1%)
Gender						
daughter	55 (53.4%)	55 (45.5%)	39 (47.0%)	106 (51.0%)	29 (44.6%)	284 (49.0%)
son	48 (46.6%)	66 (54.5%)	44 (53.0%)	102 (49.0%)	36 (55.4%)	296 (51.0%)
Household						
Big	27 (26.2%)	31 (25.6%)	30 (36.1%)	74 (35.6%)	20 (30.8%)	182 (31.4%)
Medium	66 (64.1%)	50 (41.3%)	50 (60.2%)	115 (55.3%)	44 (67.7%)	325 (56.0%)
Small	10 (9.7%)	40 (33.1%)	3 (3.6%)	19 (9.1%)	1 (1.5%)	73 (12.6%)
Duration						
Mean (SD)	14.6 (9.9)	19.0 (19.3)	8.0 (3.2)	16.5 (13.0)	7.3 (6.4)	14.4 (13.3)
Range	0.0 - 48.0	0.0 - 72.0	1.0 - 14.0	0.0 - 72.0	1.0 - 36.0	0.0 - 72.0
Mother						
Mean (SD)	0.3 (0.1)	0.3 (0.1)	0.3 (0.1)	0.4 (0.1)	0.2 (0.1)	0.3 (0.1)
Range	0.1 - 0.5	0.1 - 0.5	0.0 - 0.4	0.1 - 0.5	0.1 - 0.4	0.0 - 0.5
Child						
Mean (SD)	0.4 (0.1)	0.4 (0.1)	0.3 (0.1)	0.4 (0.1)	0.3 (0.1)	0.4 (0.1)
Range	0.2 - 0.5	0.1 - 0.5	0.1 - 0.5	0.1 - 0.5	0.1 - 0.5	0.1 - 0.5
Father						
Mean (SD)	0.3 (0.2)	0.3 (0.1)	0.3 (0.1)	0.1 (0.2)	0.3 (0.1)	0.2 (0.2)
Range	0.0 - 0.4	0.0 - 0.4	0.0 - 0.4	0.0 - 0.5	0.1 - 0.5	0.0 - 0.5

3.2 A digression on causes for weaning

The current section reports information on the causes women adduce for stopping breastfeeding, introducing further details over table 4 in the main text. Across the populations, the majority of causes are relative to social norms or opportunity costs (27% and 36% respectively). But once we split by residence pattern, opportunity cost becomes a much more prominent cause in patrilocal households (57%, see table 4 in main text).

Table 3: Reported reasons for weaning, categorized into physical costs, social norms, opportunity costs and other reasons.

category	Reasons for weaning	count	total (%)
Physical costs	Mastitis	1	7 (16 %)
	Constantly ill	2	
	Sterilization surgery	1	
	Not enough breast milk	3	
Social norm	I heard that the breast milk has become clear , lacking fat	1	12 (27 %)
	Family members say that the breast milk is no longer nutritious	3	
	The child keeps crying because the milk is not good	1	
	Several of my friends weaned their children at this time	3	
	If the feeding time is too long, it's not easy to wean	1	
	Most people around me wean at this time	3	
Opportunity cost	It's too time-consuming, I can't do long-distance work	6	16 (36 %)
	Frequent breastfeeding can lead to breast engorgement , affecting farm work	2	
	Can't go out to work	5	
	Went to help with work at my sister's house for a while	1	
	Went off to work	2	
Other	The child sleeps with the grandmother, so he / she doesn't eat my breastmilk	1	9 (20 %)
	The child refuses to eat	5	
	Stopped breastfeeding after getting pregnant with the second child	2	
	I don't want to breastfeed	1	

3.3 Direct Acyclic Graph and causal inference strategy

Our causal inference strategy relies on estimating the relative effects of children's and parents' relatedness on breastfeeding duration. We considered a set of covariates that could influence the results, as described in the previous section. According to our proposed causal structure, shown in Figure 6 in the main text, a minimum set of controls for correctly estimating the direct effects of individuals' relatedness include only village, household size and mother's cohort in addition to our estimands (model 3). To estimate the total effect of residence strategy (model 2), we do not control for household size. In both models, we also control for sex of child, birth order of child, cohort of mothers and random effects for mothers' IDs, which help the estimate. The linear regression for the cox model 3 used to report the results of the effect of individual's relatedness on breastfeeding duration includes as predictors: child relatedness, mother relatedness, father relatedness, sex of child, household size, child birth order, cohort of mother, village and mothers' IDs as random effects (see section 4).

In order to estimate the total effect of residence pattern on breastfeeding duration, model 2, which summarizes the separate effects of the various relatedness structures, the minimum adjustment set (i.e. which control variables need to be considered to obtain a reliable causal inference) includes only village, to which we add sex of child, birth order of child, cohort and random IDs for mothers, to increase the precision of the estimate. The linear regression for the cox model used to report the results of the effect of residence pattern on breastfeeding duration includes as predictors: residence pattern, sex of child, child birth order, birth cohort of mother, village and mothers' IDs as random effects. Note that while household size is an appropriate control variable for the control model and for a model aiming to estimate the effect of mother, father and child relatedness on breastfeeding duration, it should not be included in a model that aims to estimate the total effect of postmarital residence strategy. It is indeed on the downstream path between postmarital residence strategy and breastfeeding duration.

The following section will help elucidate why these models are appropriate for testing the predictions for the hypotheses considered and provide additional material for inference.

3.4 Hypotheses and causal models

While we believe that the statistical models presented above report the correct estimates for our predictors, the causal interpretation of these estimates require careful consideration. Because of the genetic mechanism correlating children's and parent's relatedness to the rest of the family, we aimed at improving our ability to parse out between different predictions associated to the hypotheses. We recur to the use of simulations to address the problem of equifinality and better understand how different cox models are able to pick up on the differences between data associated to generative causal models.

We start by reviewing the main hypotheses, the causal models associated with these hypotheses, i.e. the expected directions of the effects of the variable, and the reasons why it can be difficult to compare them, before moving on to simulation, testing and interpretation.

Parent-offspring conflict: We expect the child's relatedness to have a positive effect on the duration of breastfeeding, while parents' relatedness would have a negative effect.

Sexual conflict: We expect mothers' relatedness to have a positive effect on the duration of breastfeeding, while father's would have a negative effect

This would result in longer breastfeeding expected in households where the child has higher than average relatedness and shorter where the father has higher relatedness. However, intermediate duration is consistent with both hypotheses, as we can see when we simulate them.

4 Survival analysis

We use tools from survival analysis to address the duration of breastfeeding in our sample. In particular, we employ semiparametric cox models, with a set of linear predictors defined depending on the inferential goal of the analysis, for which we define informative priors.

4.1 Cox Likelihood

The Cox proportional hazards model is used to estimate the effect of covariates on the hazard rate of an event, accounting for censored data. The likelihood is based on comparing the relative risks of individuals who are still at risk at the time of an observed event.

For each individual i with an observed event, the likelihood is given by the following partial likelihood:

$$L(\theta) = \prod_{i \in R(t)} \frac{\exp(\theta_i)}{\sum_{j \in R(t)} \exp(\theta_j)}$$

Where: - $R(t)$ is the risk set at time t_i, consisting of individuals who are still at risk at time t_i (i.e., have not experienced an event before t_i). - $\exp(\theta_i)$ is the risk for individual i, where θ_i is the linear predictor. - The denominator sums the risks of all individuals in the risk set at time t_i, ensuring that the likelihood reflects the relative hazards among those at risk.

In the model, the log of the sum of risks for individuals at risk is subtracted from the individual's own risk, capturing the proportional relationship between individuals' risks at each event time.

This formulation allows for the estimation of regression coefficients for covariates, accounting for censored data while modeling the hazard (expressed as log hazard coefficients) for each individual relative to others at risk.

4.2 Linear models

The linear predictor θ_i for each individual i is defined differently for each model employed.

Model 1:

$$\theta_i = \omega + \gamma_{\text{sex}[i]} + \kappa_{\text{ord}[i]} + \epsilon \cdot \sum_{y=1}^{\text{hsz}[i]} \delta_y + \zeta_{\text{coh}[i]} + \eta_{\text{vil}[i]} + \iota_{\text{mid}[i]}$$

Model 2:

$$\theta_i = \omega + \alpha_{\text{res}[i]} + \gamma_{\text{sex}[i]} + \kappa_{\text{ord}[i]} + \zeta_{\text{coh}[i]} + \eta_{\text{vil}[i]} + \iota_{\text{mid}[i]}$$

Model 3:

$$\theta_i = \omega + \sum_{k=1}^{K} \beta_k \cdot \text{rel}_{ik} + \gamma_{\text{sex}[i]} + \kappa_{\text{ord}[i]} + \epsilon \cdot \sum_{y=1}^{\text{hsz}[i]} \delta_y + \zeta_{\text{coh}[i]} + \eta_{\text{vil}[i]} + \iota_{\text{mid}[i]}$$

Where:

- ω is the intercept term.
- α is the effect associated with each residence strategy.
- β_k are the coefficients for each of the individuals' relatedness rel_{ik}, the relatedness of individual k between child, father and mother.
- $\gamma_{\text{sex}[i]}$ represents the effect of sex (a binary variable: male or female).
- $\kappa_{\text{ord}[i]}$ represents the effect of birth order (also a binary variable).
- ϵ is the coefficient for household size, which is modeled as a monotonically increasing categorical variable.
- δ_y modulates the household size-specific effects, which are parameterized by a Dirichlet prior and reflect the varying effects of household size. This adds a small increase of the total effect ϵ per each additional household members up to the household size y, allowing for non-linear variation of the outcome with household size (variables with monotonically increasing effects can be modelled by two parameters, δ,which represents the unit specific effect, and δ_y, or the sum of effects up to y units, the number of household co-residents for individual i).
- $\zeta_{\text{coh}[i]}$ represents the effect of mother cohort as a random effect.
- $\eta_{\text{vil}[i]}$ captures the village-level multilevel random effect.
- $\iota_{\text{mid}[i]}$ represents the mother-level random effect.
- K is 3, or the total number of relatedness parameters β_k, i.e. mother's father's and child's parameter.

4.3 Priors

The model assigns the following priors to its parameters:

$$\begin{aligned} \omega &\sim \mathcal{N}(0, 2) \\ \alpha, \beta, \gamma, \kappa, \epsilon, \zeta &\sim \mathcal{N}(0, 1) \\ \eta &\sim \mathcal{N}(0, \sigma_\eta) \\ \sigma_\eta &\sim \text{Exponential}(1) \\ \iota &\sim \mathcal{N}(0, 0.5) \\ \delta &\sim \text{Dirichlet}(2) \end{aligned} \tag{1}$$

These are simple informative priors designed to restrict the spatial search of the MCMC chain. Note that the intercept ω is assigned a different prior in the case of Model 3 in order to stabilize the model and does not hold inferential value. Values for η are pooled across villages by the standard deviation σ_η.

4.4 Full results from cox models

Here we report estimated log Hazard coefficients for the three main cox linear regression models.

Table 4: Results from Bayesian Cox regression models predicting factors associated with likelihood of weaning, censored at two years old. Log Hazard Coefficients (LHC, positive values mean higher hazard, associated with shorter breastfeeding duration), and 89% Percentile Intervals (PI). Model 1: the Control model (accounting for child sex, child birth order, mother's birth cohort, and household size). Model 2: residence pattern effect, with control model, except household size, plus post-marital residence. Model 3: includes, Control model plus child, mother and father's average relatedness to other household members. The Hazard Ratio (HR) is indicated; a value greater than 1 suggests a higher likelihood of breastfeeding termination, while a value less than 1 indicates a lower likelihood.

	Model 1 - LHC (89%PI)	Model 2 - LHC (89%PI)	Model 3 - LHC (89%PI)
Household size	1.2 (0.45 , 1.99)		0.7 (-0.22 , 1.58)
Daughter	-0.03 (-1.15 , 1.12)	-0.02 (-1.13 , 1.16)	-0.04 (-1.15 , 1.14)
Son	0.02 (-1.08 , 1.18)	0.05 (-1.06 , 1.23)	0.02 (-1.1 , 1.19)
1st child	0.05 (-1.09 , 1.17)	0.09 (-1.08 , 1.2)	0.09 (-1.04 , 1.24)
2nd child	-0.1 (-1.23 , 1.01)	-0.04 (-1.2 , 1.07)	-0.04 (-1.2 , 1.11)
Mother cohort <1980	0.05 (-0.92 , 0.99)	-0.04 (-1.01 , 0.88)	0.02 (-0.93 , 1.01)
Mother cohort 1980-89	0.01 (-0.97 , 0.98)	-0.03 (-1.02 , 0.89)	0.02 (-0.93 , 1.01)
Mother cohort >=1989	-0.03 (-1.01 , 0.98)	-0.01 (-1.05 , 0.93)	0.02 (-0.93 , 1.01)
Duolocal		-0.37 (-1.18 , 0.43)	
Matrilocal		0.03 (-0.8 , 0.84)	
Neolocal		-0.09 (-0.91 , 0.71)	
Patrilocal		0.47 (-0.36 , 1.31)	
Child relatedness			-1.34 (-2.4 , -0.27)
Mother relatedness			-0.84 (-1.84 , 0.18)
Father relatedness			0.63 (-0.18 , 1.41)

5 Approach

Because of the high degree of multicollinearity in the relatedness variables, we employ a simulation-based strategy: by simulating data from parameter sets consistent with the competing hypotheses considered here, we can assess whether the model can distinguish among them when applied to the synthetic datasets. By comparing simulated and observed posterior distributions, we examine whether the data-generating mechanisms implied by different hypotheses could be observationally indistinguishable, helping us assess risks of equifinality.

This approach resembles an approximate Bayesian computation, or likelihood-free inference (Beaumont, 2010), and complements the more traditional statistical analysis, allowing to address an additional inferential difficulty. Moreover, because the Cox proportional hazards model is semiparametric and does not specify the baseline hazard function, standard posterior predictive checks are not straightforwardly applicable (Gelman et al., 2020). This limits the model's internal capacity for self-validation through simulated outcomes based on posterior predictions. The approach based on simulated data allows to address this limitation, functioning as an external adequacy test of the model's ability to differentiate among plausible causal structures, given the data and its constraints.

5.1 Simulate relatedness

We simulate N = 500 children and assign them to one of the four possible residence types (Duolocal, Matrilocal, Neolocal and Patrilocal). We then generate for each child the relatedness of the mother, father and child itself. The relatedness of the parents is sampled from normal distributions that match the real data for the four residence types (means of 0.4, 0.36, 0.3 and 0.22 for the mothers and 0.06, 0.22, 0.30 and 0.38 for fathers respectively, with a standard deviation around 0.1). For children, instead, we generate a relatedness level by summing the parents' relatedness and dividing by two and add a random value sampled from a Gaussian distribution with mean 0.1 and SD 0.05, which simulates variation in household structure within the residence pattern and brings the generated distribution closer to the observed distribution for children's relatedness by household (see SI Figure 3).

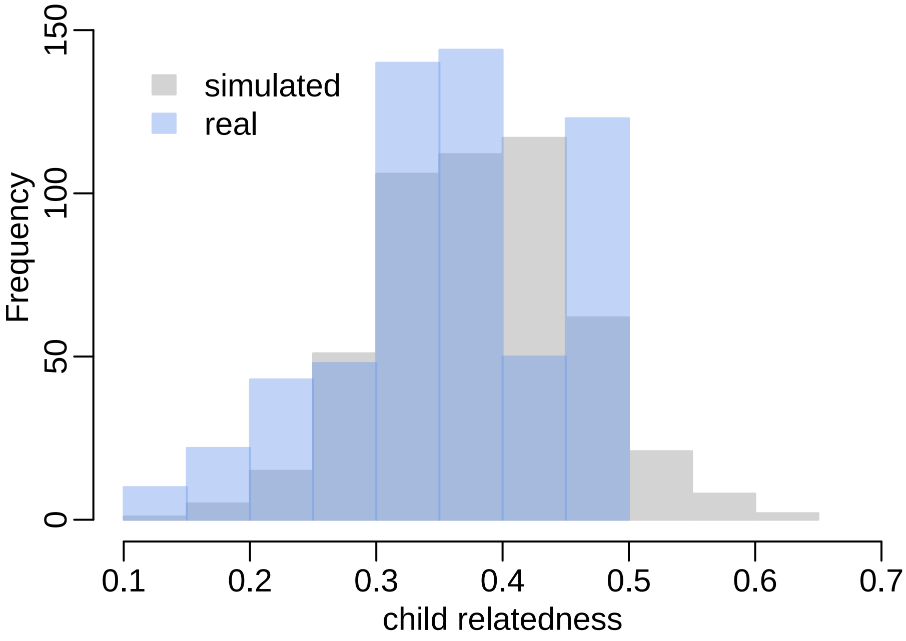

Figure 3: Real distribution of relatedness (grey) and simulated relatedness (blue).

Note that, because our simulation adheres to the generative process that produces the data in the real world, it inherently generates also a certain degree of multicollinearity observed in the real data. This happens even though we do not actively construct any correlation between mothers' and fathers' relatedness, because of the interdependencies of family members and residence strategy. Indeed, even though we simulated mother and father's relatedness independently, only from the distributions of these measures in the real data, the negative relationship emerges as a feature of these distributions. Calculating the correlation coefficients for children and parents' relatedness for both real and simulated data returns relatively similar results within the simulations and real data.

5.2 Generate simulated breastfeeding duration according to different causal models

We then generate duration of breastfeeding from these genetic relatedness (simulated) data we sample from a Poisson distribution which rate λ depends on a linear function of child and parent's relatedness (indicated in the equation below as C, M and D respectively). The parameters for the predictors χ, ψ and ϕ are selected depending on the two main alternative hypotheses and possible other scenarios, including a combination of

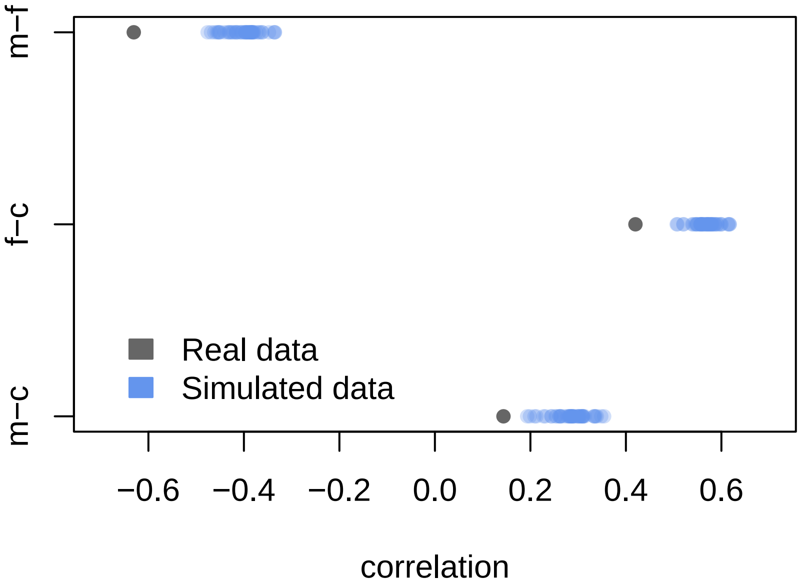

Figure 4: Multicollinearity in the real data (grey) and simulated (blue) calculated as a correlation matrix.

the two hypotheses (see SI table 5, which recapitulates table 1 in the main text plus an additional hypothesis considered here to add a case study).

$$Duration \sim \text{Poisson}(\lambda)$$

$$\lambda = \alpha + \chi C + \psi M + \phi D$$

Table 5: Hypotheses associated to causal models.

	Hypothesis	Child	Mother	Father
H1	Parents-offspring conflict	+	-	-
H2	Gender conflict	0	+	-
H3	Both	++	+	-
H4	No effect of parents	+	0	0

Note that the columns 'Child', 'Mother' and 'Father' indicate the expected direction of the effect for genetic relatedness as a predictor in the different hypotheses. According to the Parent offspring conflict hypothesis, the more a child is related to their household the longer they are breastfed, while it is the contrary for the parents, and so on. SI Figure 5 shows simulated duration of breastfeeding according to the parameters associated with the causal models above. The points are colored depending on residence strategy.

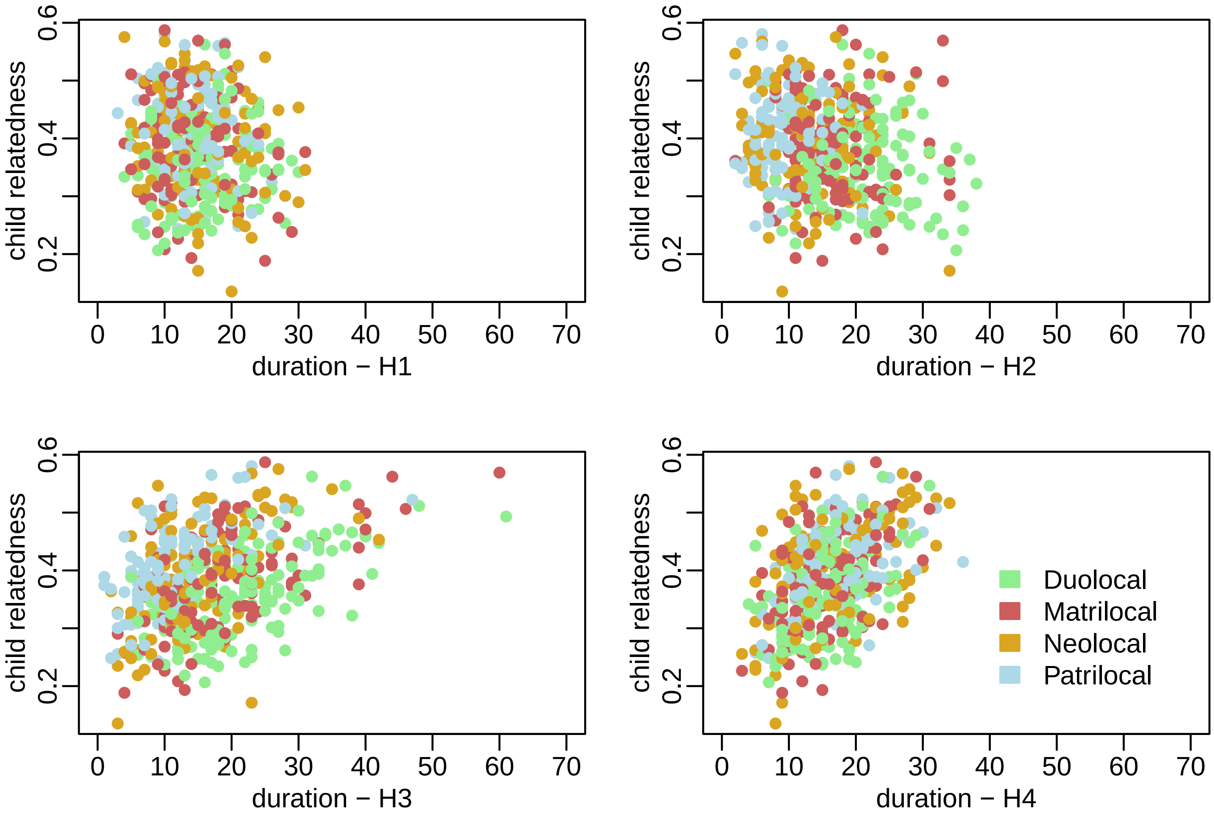

Figure 5: Simulated breastfeeding duration for four different hypotheses (causal models), color coded by residence pattern. Green stands for Duolocal, Red stands for Matrilocal, Yellow stands for Neolocal and Blue stands for Patrilocal.

5.3 What can we learn about the causal model from simulations?

The first objective is to use our simulations based on different causal models to qualitatively evaluate which of the dataset generated by each causal model produces parameter estimates from the cox model that are the most similar to those generated by the real data. The second objective is to find a set of generative parameters for our simulation that generates data producing the most similar results (once the cox regressions are fit on them), and then compare this ‘most-likely parameters set’ to our causal models.

5.3.1 Simulate data from causal models and compare results of simulated and real data

We start by running six combinations of cox regression models on the real data (see SI table 6 to see which sets of predictors and covariates were included; the last two correspond to models 3 and 2 in the main text respectively). From these models we obtain multiple estimates for the effect of parental and child's relatedness on the duration of breastfeeding (note that these effects are estimates for log hazard coefficients from the cox model, so that negative numbers mean a reduction of risk, and a positive effect on breastfeeding duration). We then run the same six cox model (including only the main predictors, as we did not simulate the covariates) on data simulated according to our causal models. This allows us, as a first step, to observe the ability of the cox models to qualitatively recover the effects of the main predictors and make inferences.

Table 6: hypotheses associated to causal models (note that the column 'Panel' indicates the panel in SI Figure 6, below, that reports the results relative to each regression).

model	main predictors	covariates	panel
child	child relatedness	sex + birth order + family size + age + birth cohort + village	a
mother	mother relatedness	same as above	b
father	father relatedness	same as above	c
parents	mother relatedness + father relatedness	same as above	d
everyone	child relatedness + mother relatedness + father relatedness (model 3)	same as above	e
residence pattern	household type (post marital residence)	sex + birth order + age + birth cohort + village	f

The large grey dots in SI figure 6 refer to the results from the datasets shown in SI figure 5, while the smear of smaller dots is given by 50 datasets simulated with different parameters. These represent parameter estimates of cox regression models for each causal model (listed as H1 to H4) estimated by the different cox regressions. Panel a) shows data relative to a model where we include only the child's relatedness as a predictor. Let's look at each hypothesis one at a time. In the first row we observe the estimated effect of the child's relatedness calculated on data simulated according to H1. Note that the simulation included *postitive* effect of the child's relatedness on breastfeeding duration, so we would expect a negative effect, i.e. the more the child is related to the rest of the family, the longer will breastfeeding be. But if we include only the child's relatedness as a predictor, the negative effect of the parents' relatedness overcomes that of the child's relatedness, and the parameter estimated will be positive: a counterintuitive result, but unavoidable given the connection between the parents' and child's relatedness. Data simulated according to H2, where the child's relatedness has no direct effect, also produce an estimation that the child's relatedness will negatively affect breastfeeding duration. Once we move to H3 and H4, on the contrary, the child's relatedness has a positive effect. Remember that in both cases the data was simulated with a consistent positive effect of the child's relatedness, only including some effect for parents in H3 (positive for mother, negative for father) and no parental effect in H4. In panel b, are shown the results from a model that estimates only the effect of maternal relatedness, and again, let's look at the grey dots. The model applied on data generated according to H1 correctly estimates a negative effect of maternal relatedness on breastfeeding duration, or a positive estimated parameter from the cox model. Similarly, H2 and H3 pick up on the positive effect of mother's relatedness, however they provide different effect sizes, even though the Poisson simulation used the same parameter. This is because in H3 there is also a positive effect of the child's relatedness, which correlates to maternal relatedness and hence is picked up by the model. Data generated according to H4 still produce a positive effect of maternal relatedness, even though there was none in the simulation: this is because maternal relatedness is connected to the child's relatedness, which in turn has positive effect on breastfeeding duration. By this point it should be clear that simply interpreting the regression coefficients for these models will be unlikely to provide a reliable inference on the causal model generating the real data because of equifinality. Only the model including the three relatedness measures is able to recover the original relations between the factors (positive effect of the child's and mother's, negative of father's relatedness).

Moreover, we compare the results of all these six cox regressions on the real data to results obtained with data generated according to different causal models. We qualitatively compare the cox parameters estimated from the real data, shown by a light blue dot in panels a-c, and by lighter colors in panels d-f, to the estimates based on data simulated according to each causal model (H1-H4), shown in grey in panels a-c, in darker colors in panels d-f (note that the smear of points shows parameter estimates for 50 different simulations for which were used different sets of parameters, generated by sampling from a Gaussian distribution with mean 2 and SD 1 and multiplying according to the causal model, e.g. $\beta = 4, \gamma = 2, \delta = -2$, for H3). We then qualitatively look at which of the casual models produces data that, once analyzed with the different cox models, *looks the most like* the real data *across* the different statistical cox models. This allows us to address equifinality issues beyond the correct estimates for the parameters.

The model including only the child's relatedness, in panel a), shows a positive effect of the child's relatedness (the cox parameter estimated is negative) for the real data and for H3 and H4, which suggests that H1 and H2 do not match the real data. The model that estimates only the effect of maternal relatedness, in panel b), shows a negative effect of maternal relatedness only in H1, while the real data, and H2-H4 are consistent with a positive effect of maternal relatedness on breastfeeding duration. Panel c) shows the results of a model including only the father's relatedness as a predictor. The real data, as well as hypotheses H1-H3 predict a negative effect of paternal relatedness (H4 was generated with no effect of paternal relatedness, but because the child's relatedness has a positive effect, if we include only the father's relatedness, this will appear to have a positive effect because it is correlated to the child's relatedness). If we include a predictor for each of the parent's relatedness, in panel d), we can look at the effect of each parent once we *control for the effect of the other parent's relatedness*. We can see that with the data generated according to H1, which posits a negative effect of both parents, the effect of their relatedness is markedly negative, while in the real data mother's effect is positive and father's effect is only slightly negative. H2 posits a marked negative effect of fathers (positive estimated parameter in the cox regression), and positive of mothers, which is what we observe in the real data, albeit with a smaller effect size. H3 generates a markedly positive effect of the mother's relatedness and close to zero effect for the father's relatedness, which is qualitatively similar to the results from the real data in this model. H4 produces a positive effect for both parents' relatedness (even though in the generative simulation we included no effect of parents, again, this is caused by the positive effect of the child's relatedness, which is picked up by both parents). As indicated by the analysis of the DAG represented in Figure 7 in the main text, the model including predictors for all members of the family is the one better able to disentangle the relative effects of each of their relatedness: it correctly picks up on the positive effect of the child's relatedness, in contrast to the negative effect of that of the parents in H1; it correctly estimates the effect of the child's relatedness close to zero, that of mother's relatedness to be positive, and father's relatedness to be negative, as generated by H2; it picks up on the positive effect of both child and mother's relatedness, with the former having a more positive effect, while fathers have a negative effect, for H3; and similarly positively correlates the child's relatedness to breastfeeding duration for data generated according to H4, while the parent's relatedness is close to zero. Comparing the results from the real data to those of the different models, H3 seems to generate data more closely fitting the real results.

Summing up, while multiple causal models *could* have generated results similar to those from the real data in some of the cox regression sets (i.e. equifinality), when all the models are observed together, and focusing on the linear model presented in panel e), model 3 from the main text, which includes predictors for all family members, H3 seems to be the causal model more closely matching the results obtained from the real data.

5.3.2 Estimate the parameter set most closely matching the real data

A second contribution to inference comes from a search in the parameter space for a combination of parameters that more closely match the results from the real data. To do so, we simulate 100 datasets from a random set of parameters where the intercept, the parameter for the child's and parents' relatedness are sampled from a Gaussian distribution with mean 0 and SD 3. We calculate the mean difference between the coefficients estimated from the real data and the coefficients estimated from each dataset for the different cox models (described in SI table 6), and select the set of parameters with the best match to the real data. We repeat the process 250 times, and calculate the mean value of these parameters, as well as the 5th and 94th percentiles. These are reported in table 1 in the main text. This approach resembles an Approximate Bayesian Computation method where the ABC rejection algorithm is based on the Log Hazard Coefficients resulted from the Cox models.

As we can see, the parameters generating data whose results in a cox model are the most similar to the real data indicate a similarly positive effect for child and maternal relatedness, and a mostly negative effect for paternal relatedness, which is coherent with the predictions of H3.

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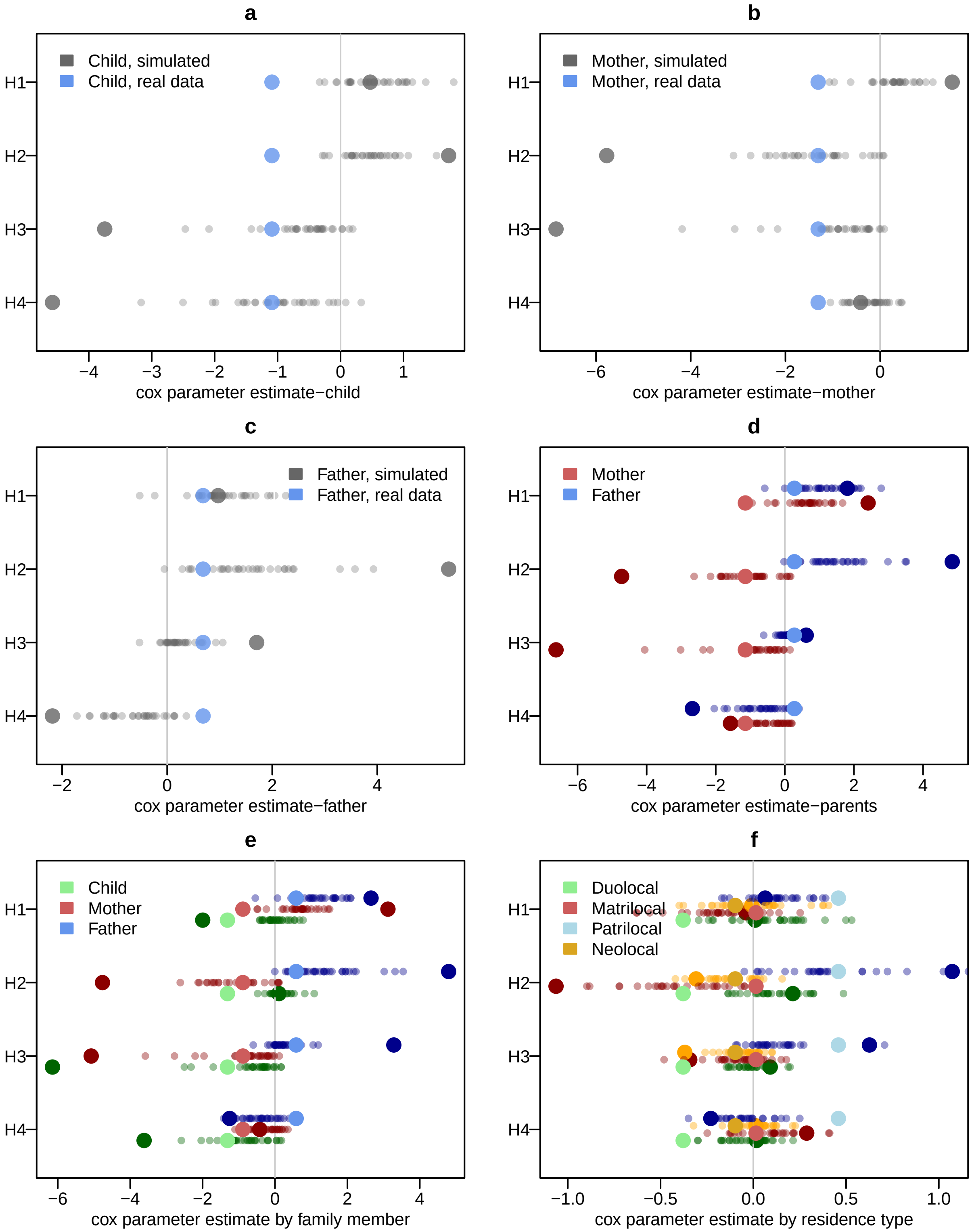

Figure 6: Multiple plots showing parameters estimated by cox models run on the real data (light blue in a-c, light colors in d-f), in comparison to similar models run on simulated data (each row in each model represents an hypothesis, larger grey/darker color dot is relative to one specific set of data, smear is from replication with 50 different parameter sets).

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