### Extended Family Influences on Fertility of Adult Children

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#### Abstract

Fertility outcomes are correlated within families both across generations (intergenerational transmission of fertility) and within siblings (peer effects). We use a rich representative dataset with up to four generations of linked family members and a causal approach based on the randomness of sex at birth and sex-mix preferences. We test whether extended family influences on adult children fertility differ by family socio-economic status. First, we classify kin networks based on the progenitors' education and income to test long-lasting sex-based preferences, possibly operating through social pressure. Second, we analyze siblings' homogamy in education and income to test whether 'fertility contagion' across peers is stronger in adult children who share socio-economic characteristics. Preliminary results support the validity of the identification strategy and the presence of sex-mix preferences in the kin network including both own children and nicces/nephews. We expect stronger results for homogamous siblings and in descendants of lower socio-economic status progenitors.

#### **Theoretical Framework**

#### Endogeneity in extended family fertility

Extended family members are part of a complex kin network. Previous research documented associations in fertility both across generations (intergenerational transmission of fertility) and within siblings (sibling peer effects). Adult children's fertility correlates with their parents' family size (Beaujouan and Solaz 2019; Murphy 2013) and the family of origin influences family size preferences, childbearing intentions, and fertility (Axinn et al. 1994; Barber 2000; Cools and Hart 2017; Dahlberg and Kolk 2018; Kotte and Ludwig 2012). Adult siblings also have a positive effect on each other's fertility, especially when they are similar along other dimensions such as age, sex, and parity (Balbo and Mills 2011; Kuziemko 2006; Lyngstad and Prskawetz 2010). While qualitative studies also confirm the importance of other family members in making fertility decisions (Bernardi 2003; Keim et al. 2013), only a few studies have used plausible causal designs based on twin and/or randomness of sex at birth, with mixed results (Buyukkececi et al 2020; Cools and Hart 2017; Hart and Cools 2019; Querin 2022).

#### Socio-economic differences

Sex-mix preferences are an ideal approach in identifying differences across socio-economic status. The few studies that have explored the reasons behind them mostly point at socio-cultural factors (Hank and Kohler 2000; Mills and Begall 2010; Nugent 2013) that are likely to differ across socio-economic strata. Historically, many populations had a son preference but, while this is still the case in some countries, in others a girl preference has emerged. Either way, when there are two children, one of each sex is always preferred (Andersson et al. 2006; Dahl and Moretti 2008; Lunderg 2005; Nath 2023). To our knowledge, the persistence of a sex-based preference has not yet been tested across socio-economic status. Our expectation is that individuals with higher socio-economic status would be displaying a less pronounced sex-based preference of offspring due to the reduced differences in economic and social prospects for their children and less gender-segregated occupations.

As we expect cultural norms to be changing slowly, older generations (in this case, grandparents) may hold stronger preferences and exercise social pressure on other family members accordingly (Bernardi and Klärner 2014; Nugent 2013). We therefore test this hypothesis by initially assigning the socioeconomic status of the kin (measured in income and education) based on the characteristics of the oldest generation.

However, the siblings peer effect literature proposes that siblings who are more similar to each other are also more likely to have stronger influences and connections to one another. Therefore, we test a second hypothesis according to which the socio-economic status (also in terms of income and education) is defined at the level of the generation of childbearing age. In particular, we are interested in the homogamy or heterogamy of socio-economic status across siblings. We expect that homogamous sibling pairs display stronger fertility peer effects.

## **Data and Methods**

## Data

The FinnFamily dataset is a nationally representative sample of up to four generation in contemporary Finland, derived from its population registry. The strengths of this dataset lay in its extent and depth of included family ties and the detailed demographic information available for each individual included in the family tree. The sampling method is as follows. First, around 60,000 index persons were randomly selected from the 1955, 1960, 1965, 1970, 1975 birth cohorts (around 10,000 individuals per year), corresponding to about 11-16% of each the birth cohort (Ghosh et al. 2017).

Figure 1 is a schematic representation of a family structure that can be reconstructed in FinnFamily. Each index person was linked to his/her biological parents. Then, all children of those parents (including any stepchildren) were also included in the sample, providing a full sibling size for the index person. This results in the oldest generation (G0) and all their children, namely index persons, siblings, and half-siblings (G1). Any child born from individuals in G1 is also included and becomes what in the following text is referred as grandchildren (GC, G2). Any child born from G2 is also included in the sample (G3) but this generation is, for the time being, excluded from the analyses.

Following previous studies (Buyukkececi et al. 2020; Hart and Cools 2019; Lyngstad and Prskawetz 2010; Querin 2022), the sample is restricted to extended families in which G1 is composed of two full siblings. This restriction reduces external validity to kin networks with only one or more than two siblings in childbearing years and will be later relaxed. Nevertheless, it simplifies the data construction and modelling of siblings' peer effects and increases internal validity by holding constant the size of the family of origin. The analytical sample is of 12,607 kin networks (each of them including several family members) once considering those with at least two (grand)children born in G2.

## Methods

The identification strategy is based on the randomness of the assigned sex at birth. Empirically, parents with two boys or two girls (no sex-mix) are similar to parents with mixed-sex children, but they are more likely to have a third child (Andersson et al. 2006; Angrist and Evans 1998; Ben-Porath and Welch 1976). This manifestation of a sex-mix preference has been shown to hold also in extended kin, namely not only within a nuclear family but also when the (lack of) sex-mix includes the sex distribution of own children, nieces, and nephews (Querin 2022). Using a similar methodological kin network set-up, this paper

estimates whether there are more than two (grand)children born in G2 based on the sex distribution of existing G2 (grand)children. However, all the analyses can be now stratified by socio-economic status to address heterogeneous effects. Thanks to the richness of demographic information available over multiple generation the socio-economic classification of a kin network is not straightforward. We initially propose two classifications, one based on G0 and one based on G1, as described in the theoretical framework.

# **Preliminary Results**

Table 1 presents the sex distribution of (grand)children in G2 and how the births are distributed across the G1's members. The sex distribution of the first and second (grand)child is as expected close to 50% with a slight tendency towards more males than females at birth. About half of the families have reached a sex-mix with the first two (grand)children while the rest is split between only (grand)sons and only (grand)daughters. Family structures are unevenly distributed with 76% of (grand)children being born within the same nuclear family, i.e., they are full siblings, while the rest are cousins, i.e., one (grand)child is born of the index person and the other of his/her sibling.

Table 2 reports the balancing tests divided by generation and it confirms the validity of the identification strategy. The tests compare the observable characteristics of kin networks where the first two born in G2 are of the same sex (columns 1 and 2) with those in which there is a sex-mix in G2 (columns 3 and 4). The last column shows that there are no systematic significant differences (on observables, and thus plausibly also on unobservable characteristics) across these two types of kin networks. Table 2 also describes the sample for each generation. On average grandparents (G0) are two years apart and were born in the 1939-1941 range. More than 80% of the grandmothers were alive as of 2012 and more than 65% of grandfathers as well. The middle generation (G1) comprising of the sibling pair index-person and sibling has a share of brothers, sisters, and mixed-sex is not significantly unbalanced and around the expected levels. The siblings are on average 4 years apart and were born in the 1965-1970 range, which is roughly 25-30 years after the G0 generation and in the middle of the sampling years for index persons (1955-1980), as expected.

Table 3 reports the estimation of the probably of having more than two (grand)children based on the sex composition of the first two. In line with previous research, there is a significant positive effect of the lack of sex-mix on extended family fertility (column 1). The effect is in the correct ballpark as it is smaller than the 6-7 percentage points effect found in nuclear family studies. This result holds also when controlling for family structure (column 3) and its interaction with it (column 4). Column 2 confirms the importance of family structure and different probabilities of parity-specific transitions. Indeed, when the first two (grand)children come from the same nuclear family, the extended family is less likely to have three or more grandchildren. This indicates that the combined transitions to first and third births (where the first two grandchildren are siblings) are less frequent than transitions to second births (where the first two grandchildren are cousins), in line with previous demographic evidence.

These preliminary results show the solidity of the identification strategy and the increased fertility effect in the main sample. Subsequent results to be presented at the conference include: (i) siblings vs. cousins effects (ii) heterogeneous effects by G0 socio-economic status (iii) heterogeneous effects by G1 socioeconomic status and homogamy (iv) additional robustness tests by gender, family structure, and relaxation of the sibling-pair design.

## **Figure and Tables**





Notes: This is an illustrative example of the kin structures that can be reconstructed in the sample. Generations are, from top to bottom row: G0 - progenitors; G1 - index person and siblings; G2 - all children born from G1; G3 - all children born from G2.

	Mean	SD	Ν
First GC is a boy	0.52	0.500	15,586
Second GC is a boy	0.51	0.500	12,625
Grandsons: Two oldest GC are male	0.27	0.443	12,607
Granddaughters: Two oldest GC are female	0.24	0.426	12,607
Two oldest GC are same sex	0.51	0.500	12,607
Two oldest GC are siblings	0.76	0.424	12,607
Number of GC	2.86	1.901	18,707

Table 1 Descriptive statistics for three-generational kin networks with two siblings in the middle generation: sex distribution of grandchildren and their distribution across nuclear families, Finland

Notes: GC refers to grandchildren. The three data columns show means, standard deviations (SD), and sample size (N), respectively.

	First two GC are the same sex		First two GC are different sexes		
	Mean	SD	Mean	SD	t-stat
Oldest Generation (G0)					
Grandmother's birth year	1941.4	9.640	1941.2	9.688	-0.734
Grandfather's birth year	1939.5	9.893	1939.2	9.813	-1.196
Grandmother is alive	0.820	0.384	0.824	0.381	0.557
Grandfather is alive	0.671	0.470	0.655	0.476	-1.964*
Grandmother's year of death	2000.1	9.741	2000.6	9.359	1.122
Grandfather's year of death	1998.1	10.54	1998.1	10.58	0.044
Grandparents' age difference	2.173	3.738	2.272	3.701	1.466
Middle generation (G1)					
Brothers	0.246	0.430	0.242	0.428	-0.491
Sisters	0.229	0.420	0.223	0.417	-0.707
Mixed-sex	0.526	0.499	0.535	0.499	1.015
Older sibling's birth year	1965.8	8.294	1965.7	8.235	-0.667
Younger sibling's birth year	1970.1	8.171	1970.0	8.230	-0.767
Sibling age difference	4.252	2.841	4.238	2.865	-0.273
Youngest generation (G2)					
First GC is male	0.528	0.499	0.506	0.500	-2.496*
Two oldest GC are siblings	0.766	0.424	0.764	0.425	-0.276
Ν	6,376		6,231		12,607

**Table 2** Balancing tests comparing observable characteristics of kin networks with at least two grandchildren: first two grandchildren of the same sex vs first two grandchildren of different sexes, Finland

N 6,376 6,231 12,607 Notes: GC refers to grandchildren. First and third columns show means and proportions; second and fourth columns show standard deviations; and last column shows t-statistics.

	Dependent variable: Family has three or more grandchildren				
	(1)	(2)	(3)	(4)	
Two oldest GC are same sex	0.020** (0.008)		0.021** (0.008)	0.033** (0.017)	
Two oldest GC have same parent		-0.154*** (0.010)	-0.154*** (0.010)	-0.146*** (0.014)	
Interaction: same parentXsame sex				-0.016 (0.019)	
Constant	0.688***	0.816***	0.806***	0.800***	
	(0.006)	(0.008)	(0.009)	(0.012)	
Observations	12,607	12,607	12,607	12,607	
R-squared	0.000	0.020	0.021	0.021	

Table 3 Effect of no sex mix in pool of grandchildren on family fertility, Finland

Notes: GC stands for grandchildren. Standard errors in parentheses. The sample size is reported as number of kin networks rather than individuals within those extended families.

Standard errors in parentheses. \*\*\* p<0.01, \*\* p<0.05, \* p<0.1

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