When One Wife is Enough: The Determinants of Monogamy

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February, 2010

Key words: Monogamy, Polygyny, Missing data, Network autocorrelation, Galton's problem

Abstract

We construct eleven new scales to operationalize hypothesized causes of the world-wide variation in the prevalence of monogamy using data from a world-wide sample of 186 preindustrial societies. Since the diffusion of monogamy though conquest and population migration is well documented, we employ a network autocorrelation effects regression model that includes controls for horizontal and vertical transmission of female monogamy, our dependent variable. Linguistic and spatial trait transmission processes are found to be significant factors that jointly affect the world-wide variance in female monogamy. New scales for extrinsic risk and the division of labor prove to be determinants of monogamy, though no support is found for effects due to declining wealth inequality, increasing political participation, or a number of other previously proposed causes for the shift from polygyny to monogamy.

Introduction

Human pair bonds tend to be fairly stable compared to chimpanzees, our closest living relatives. It is this pair bond stability that undergirds the cultural institution of marriage, which can take on polyandrous, polygynous, or monogamous forms (Barrett et al. 2002:102). About 1 percent of ethnographically known human societies permit polyandrous marriages, while 82 percent permit polygyny; the remaining 17 percent permit only monogamy (Murdock 1967; Marlowe 2000:51). Even in societies permitting polygynous marriages, however, many marriages are monogamous: in only 23.8 percent of the societies in the Standard Cross-Cultural Sample (Murdock and White 1969; Divale 2004) are the majority of married women in polygynous marriages.[1]

Humans resemble other mammals with a moderate degree of polygyny in characteristics such as male-biased sex ratios, higher male mortality, and longer male juvenile periods (Alexander et al. 1979:434). One particularly telling piece of evidence is the degree of sexual dimorphism among humans: males are about 10 percent taller and 30 percent heavier than females, which would be typical of a species with mild polygyny (Alexander et al. 1979; Barrett et al. 2002:102). Nevertheless, there is evidence that the trend in humans has been toward monogamy. Sexual dimorphism is much less among humans than among its ancestral species (Barrett et al. 2002s:102). Recent analysis of human mitochondrial and Y-chromosome DNA indicate that the reproductively active male population was considerably smaller than the reproductively active female population until about 15,000 years ago (with an estimated range between 200 and 49,000 years ago), suggesting an early history of pronounced polygyny followed by a transition—sometime after the Upper Paleolithic revolution and most likely before the Neolithic revolution—toward increasingly monogamous pair bonds (Dupanloup et al. 2003). A further transition toward monogamy began over 2,000 years ago, as a number of societies outlawed polygyny (Alexander et al. 1979; Price 1999).

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[1] From SCCS variable 872, the percentage of married women in polygynous marriages. In only 7.6 percent of SCCS societies are the majority of married men in polygynous marriages (from variable 871).

Monogamous marriage is the human form of “social monogamy” among mammals and birds, in which a male and a female form an exclusive pair, sharing resources and living relationships, but not always an exclusive sexual relationship (Reichard 2003:4). About 5 percent of all mammal species are monogamous; among primates, the figure is 15 percent and involves bonding, which is not so common among other mammals (van Schaik and Dunbar 1990:30-31). Theoretical work in behavioral ecology has focused on how social monogamy can persist, given the fitness advantages to polygynous males, and most of that work examines how females (for whom resources are more important for fitness) distribute themselves to match the distribution of resources, and males (for whom access to fertile females is most important for fitness) distribute themselves to best find females. Monogamy is most often seen in contexts of dispersed resources, where males are unable to guard more than one female’s range (Reichard 2003). Since humans live in multi-male, multi-female groups, it is physically possible for a human male to guard more than one female, and explanations for the prevalence of human monogamy must invoke some cause other than dispersed resources.

Figure 1, based on variable 872 in the Standard Cross-Cultural Sample (SCCS), shows the distribution of monogamous marriages across SCCS societies. The boxplot on the top left shows the U-shaped frequency of monogamy across political complexity: high among non-hierarchical societies, lower among chiefdoms and pre-modern states, and high again among the largest contemporary industrial states (Marlowe 2000:51). The next two scatterplots plot the percent of marriages that are monogamous against the female contribution to subsistence (variable 826) and pathogen stress (variable 1260), respectively. The dotted line is the lowess smoother (Cleveland 1979), which shows clearly that monogamy declines as these two variables increase. The two boxplots on the right show how the frequency of monogamous marriages varies within language phyla and religions, respectively—an indication of the importance of cultural transmission, also indicated by the map. The values on the map are smoothed, using the local G* statistic (Getis and Ord 1992). High frequencies of monogamy on the map are shown by larger, darker circles; low frequencies by small, light circles.

Empirical work using cross-cultural data sets has established that monogamy is more likely in societies dependent on plow cultivation or fishing, where the climate is harsh, where pathogen stress is low, where peaceful conditions prevail, where male mortality (relative to female) is low, where the female contribution to subsistence is low, and where residence is neolocal or matrilocal (Lee 1979; White and Burton 1988; Ember et al. 2007; Quinlan 2007). With very few exceptions (e.g., Dow and Eff 2009a), cross-cultural work on marriage systems ignores the role of cultural transmission or genomic differences, and introduces sample selection bias via listwise deletion of missing data.

The following section reviews previous work explaining human monogamy. Next, we develop a simple model representing the decision by a monogamous couple and an outside female on whether to transition to polygyny. We then discuss the most important methodological problems encountered when working with cross-cultural data and define our variables. After presenting our empirical results, we conclude with a discussion of our findings.

Explaining human monogamy

Most research in human marriage systems focuses on the stability of the pair bond. Several factors contribute to stability: the need for bi-parental care; the degree of "mate guarding"; and the degree of "extrinsic risk"—pair bonds are more stable where male resources are more necessary, where males (and perhaps females) engage more vigorously in mate guarding, and where extrinsic risk is lower. Each of these conditions for stable bonds might be manifested in such a way as to lead to the prevalence of monogamy. Other explanations for monogamy are based on considerations other than fitness-optimizing behavior at the level of the individual. These include: group selection, cultural diffusion, and genomic variation.

Males provide essential resources

When males control essential resources, females select a male considering his resource endowment. The polygyny threshold model (Orians 1979; Marlowe 2000) posits that resource-shopping females should prefer to share a high resource male with other females over an exclusive relationship with a low resource male. Thus, one would expect monogamy in environments with a low variance in male resource endowment. One shortcoming of this approach is that it treats the marriage decision as if all wives enter a marriage with full knowledge of their share in the male's resources. In fact, since marriages are made sequentially, a wife will see her share fall as new wives are acquired, so that current wives and prospective wives have quite different interests—and these conflicting interests are not addressed by the model. This is a curious neglect, since inter-female aggression is one force that appears to maintain social monogamy among birds and mammals (Reichard 2003:12-13).

Empirical work in foraging societies such as the Ache and the Hadza has called into question the importance of male resources in shaping human marriage. On the one hand, the children of the best hunters are the best nourished, and the best hunters have the most surviving children, suggesting the importance of male resources. On the other hand, meat-sharing spreads a hunter's meat to all families, so that the children of the best hunter get no more meat than any other child. Their better nourishment is due to the fact that their mother works harder than other mothers—that they receive more maternal investment, not paternal investment. This paradox can be explained by arguing that being a good hunter confers status, and that the highest status males will be able to marry the hardest-working females. From this perspective, hunting is not so much paternal provisioning, but male mating competition (Hawkes et al. 2001:694-695). Nevertheless, male resources are still likely to be an important determinant of marriage choices (Marlowe 2000:51), especially since human offspring have such heavy resource costs, due to their large brains and slow maturation (Barrett et al. 2002:104).

Alexander et al. (1979) hypothesize that where male resources are important for fitness, but no male has sufficient resources to support more than one wife, one finds "ecologically imposed monogamy," as among Arctic peoples, for example.

Low (2003:161) notes that polygyny is more feasible when male resources are "generalizable" (i.e., will not be much diluted by an additional wife). One can think of "generalizable" male resources as public goods (non-rivalrous, and perhaps sometimes non-excludable), which would include such things as defense by males against hostile outsiders, male kin networks, and male social capital. Male resources which are clearly private goods (rivalrous, excludable) would include male-produced food, and time spent caring for children. In some cases, a private good, such as food, can be the subject of institutional rules giving it the character of a public good, from the perspective of a household. For example, the institution of meat-sharing gives all members of a foraging society a claim on large game brought in by hunters (Hawkes et al 1995), so that a second wife does not reduce the amount of meat received by a first wife. Similarly, when land is communally owned, an additional wife might simply increase the amount of land a household is allowed to cultivate, so that a first wife's land allotment is not diminished by the addition of a second wife.

Monogamy is therefore more likely where male resources consist of rivalrous private goods, such as food; where variation across males in resource endowments is low; where there exist few institutions treating food or productive resources as common goods; and where there is little demand for male-provided non-rivalrous public goods, such as defense.

Mate guarding

A male may control resources, which he uses to attract females, who use the resources to provision offspring. Or he may directly control females, guarding them from other males. Mate guarding is in the interest of males due to the prolonged period of human infantile dependence, which requires high parental (including paternal) investment. Because of the very large investment, there are also very large gains from impregnating females whose offspring are cared for by others. Hence human males have an incentive to devote much of their reproductive effort to both mate-guarding and cuckolding others—a de-emphasis of parental investment which may seem counter-intuitive (Hawkes et al. 1995). Mate-guarding allows males to achieve greater paternity certainty, but simulations show that even when mate-guarding is very effective, fitness-maximizing males will devote most of their efforts to mating effort, rather than care for offspring (Hawkes et al. 1995:670).

If mate-guarding were not in the fitness interests of females, then females who resisted mate-guarding would have more offspring, and the strategy would not persist. A female would benefit from mate-guarding if outside males constituted a danger to her or her offspring. Protection from violent males intent on infanticide (Schaik and Dunbar 1990), or attempting to steal food (Wrangham et al 1999), would be such a benefit. From the perspective of a female such protection would constitute a resource—and it would be a non-rivalrous public good, which would facilitate polygyny.

The difficulty of guarding more than one female may lead to the observed prevalence of monogamy, even when male care is not essential for offspring survival, a pattern seen among birds (Hawkes et al. 1995:663; Reichard 2003). Among humans, this might occur when the male/female sex ratio is high, so that married men must defend wives from a relatively large number of unmarried men (Marlowe 2000:46).

Societies where males provide little food or direct care for children are often polygynous and it is often inferred that marriages in these societies are based primarily on mate-guarding (Marlowe 2000; Quinlan and Quinlan 2007b:161), so that the marriage system is an expression of male preference, not female choice—i.e., that coercion (by males, of females) plays a role in forming marriages. Nevertheless, Marlowe (2003:285) argues that when males produce little food (as is the case with horticultural societies) females might actually prefer polygyny, since the addition of a co-wife will reduce the proportion of her production that a female must use to feed her husband. While this might be true, it nevertheless raises the question—if a husband is costly to support, why get one at all? In order to establish the pair bond, males must either coerce or provide something that females need, and if that is not food, then it must be something else—such as defense from hostile males.

Coercion may be the source of marriage decisions when females have lower fertility in polygynous marriages than they do in monogamous marriages (Marlowe 2000:54; Marlowe 2003:284). In her study of Dogon mortality, Strassman (2000) found higher mortality for children born in polygynous marriages, suggesting that there is a fitness advantage to monogamy. Among the Dogon, high male mortality rates and male-skewed migration to urban areas, combined with an average eight-year difference in ages between spouses, leads to a large number of women seeking marriage partners among a relatively small pool of men. Faced with few options, females are so constrained in their choices that one might argue that "many women are thereby forced into polygyny" (Strassman 2000:64). Nevertheless, since polygyny represents the best option, one can still think of polygyny as the outcome of female choice. The one qualification would be that since the fitness penalty is almost entirely borne by the first wife (whose children experience highest mortality), the addition of subsequent wives may be due to the first wife's coercion.

Even when females in monogamous marriages have higher fertility, fitness might be higher in the long run under polygyny if high-status males engage in polygyny and offspring acquire some of the status of their fathers—sons will therefore be more likely to be polygynous and the number of grandchildren could be very high. Such a pattern is seen among mid-19th century Mormon women, for example (Marlowe 2000:54-55).

Mate-guarding is thus likely to represent not simply the coercion of females to male reproductive interests, but the providing of a service—defense from other males—to females. This service resembles a non-rivalrous public good, and will therefore encourage polygynous marriages. Monogamy will be more likely when females have little need for defense from outside males.

Extrinsic risk

Extrinsic risk is risk that cannot easily be mitigated by parental investment—risk due to predators, pathogens, famine, and endemic violence. Low extrinsic risk environments should encourage parental investment, and one would expect to see stable pair bonds. Since male investment in offspring is higher per child under monogamy than polygyny, low extrinsic risk is often invoked as an explanation for the prevalence of monogamy (Quinlan 2007; Quinlan and Quinlan 2007a; Del Giudice 2009a; Low 2003).

Human cultural institutions—including marriage institutions—evolve to reduce extrinsic risk. Humans need not respond to predators or violence by reducing parental investment; they can respond by organizing themselves more effectively to kill predators and those who threaten them. Institutions such as food storage, irrigation, or trade can reduce the risk of famine. Of the sources of extrinsic risk, pathogens stand out as relatively impervious to efforts at mitigation.

Genetic quality is an especially important consideration in environments with high levels of pathogen stress (Low 1988, 1990, 2003). Polygynous marriages not only makes it possible for females to share high genetic quality husbands, but also facilitate female extramarital matings with males of the highest genetic quality, since males find it harder to guard multiple wives.

Group selection

A number of societies, particularly large industrial states, have “socially imposed monogamy” (SIM)—the prescription of monogamy as the sole marriage form. SIM was first discussed by Alexander et al. (1979), who suggested that it had a functional source: large states can only be stable if they successfully suppress the power of kin groups; the imposition of monogamy does exactly that, preventing the formation of lineages which might struggle for power within the state (Alexander et al. 1979:432-433). SIM weakens nepotistic ties, and therefore bases social life on reciprocity, which becomes the “binding cement of social structure”, bringing to the forefront values such as “honesty, sincerity, trust” (Alexander 1987:71). Thus, monogamy is one of the preconditions for a society in which large numbers of strangers interact peaceably.

Alexander also uses language that suggests that the imposition of monogamy directly reduces conflicts between males over access to females: “socially or legally imposed monogamy is a way of leveling the reproductive opportunities of men, thereby reducing their competitiveness and increasing their likelihood of cooperativeness” (Alexander 1987:71). One can think of this as an “elite concession” view of monogamy, since elite males are sacrificing their ability to have multiple wives in order to secure the support of the male masses. Perhaps the best-known elite concession view of monogamy is that of Betzig

(1986), who points out that large industrialized states are successful to the extent that the masses possess specialized skills and knowledge. The need of the state for masses endowed with human capital gives the masses bargaining power for income, political rights, and reproductive rights. Thus, large industrialized states impose monogamy—a restriction imposed on the elite, in the interests of the masses. The imposition of monogamy is likely to be accompanied by other concessions to the masses, such as increasingly broad-based political participation (Price 1999:49; Betzig 1986; MacDonald 1990; Kanazawa and Still 1999:30-31). The elite are motivated to make these concessions by their desire to strengthen the state when struggling for survival in war with other states (Alexander et al. 1979:432-433), so that SIM appears because of group-level selection.

Nevertheless, it is not clear that monogamy usually has stronger group selection advantages than polygyny. Polygyny ensures that each female has a husband, so that the birth rate is as high as possible, making demic expansion more likely (White and Burton 1988; Caldwell 1991:235). Additionally, one cannot point to any period in history where elites banned polygyny explicitly to curry favor with the masses (Price 1999).

Cultural transmission

The elite concession view has been criticized for ignoring the roots of SIM in the institutions of Greece, Rome, and medieval Christianity (Price 1999:19-20). MacDonald (1990) examines SIM and concludes that it is simply not adaptive. He attributes the imposition of monogamy in modern states to the chance conversion of Constantine to Christianity, and the subsequent diffusion of Christian rules of marriage throughout the Roman cultural region (Price 1999:23-24). It is clear that the spread of SIM across early medieval Europe was through the vehicle of Christianization. The cultural traits of Christianity were adopted as a package, and even though elements may not have been adaptive, they were still part of the package. Religion is a channel by which cultural transmission of monogamy takes place; all known cases of a society taking up SIM are cases of cultural transmission, not spontaneous adaptive development (Alexander et al. 1979:420; Herlihy 1995; Scheidel 2008).

Modernization is a particularly important channel of cultural transmission (Divale and Seda 2001: 128). The most successful European states conquered large areas of the Earth and reshaped local cultures in their own image. The few states that successfully avoided conquest voluntarily adopted traits of these successful states, in an effort to achieve their level of power. The traits were adopted wholesale, with little attempt to separate the traits conferring power from incidental traits in the powerful nations. SIM can thus be introduced via modernization, even when monogamy confers no advantages to the society as a whole or to the elite directing modernization.

Genomic variation

Most sociobiological research disregards the possibility that behavior across societies varies due to underlying genotypic variation. Instead, it is assumed that all humans have much the same evolved dispositions, that those dispositions include specific responses to specific environmental cues, and that variation in behavior is due to variation in the environments to which humans are responding (Tooby and Cosmides 1992). This "adaptive phenotypic plasticity" would be especially adaptive in cases where the environment changes frequently (Penke 2009).

Nevertheless, the selection of alleles favoring a particular marriage form might be expected when populations live a long time in a relatively unchanging environment (Penke 2009). For example, a harsh environment would require greater paternal provisioning (Miller 2000; MacDonald 2000), which would make monogamy more likely. Human populations in which no male has sufficient resources to support more than one wife show less pronounced sexual dimorphism than populations practicing polygyny (Alexander et al. 1979), an indication that selective pressures associated with monogamy have occurred in these harsh environments. There is some evidence that at least one gene locus (the D4 dopamine receptor) has an allele adapted for greater paternal investment. Like monogamy, the frequency of this allele follows a "U-shaped" curve relative to societal complexity: it is found at high frequencies in foraging societies and large states, but at low frequencies in chiefdoms and societies in which women perform most of the subsistence work (Harpending and Cochran 2002; Del Giudice 2009b:48).

Allele frequencies are similar in populations that are physically proximate (Barbujani et al. 1997) or speak a similar language (Cavalli Sforza et al. 1988), a pattern that may mostly reflect demic expansion during the Neolithic, as described in Bellwood (2005). Thus, any consideration of similarity in marriage practices between populations that are linguistically or physically proximate will unavoidably capture genomic similarities between those populations.

Modeling the maintenance of monogamy

In almost all cases, a polygynous marriage is created through the *sequential* addition of wives. Imagine a monogamous marriage, containing a male and a female (female 1), facing the decision on whether to admit another female (female 2). An uncoerced transition from the initial state of monogamy to polygyny can only occur if each of the three concerned parties approve of the transition. Each party will have preferences shaped by natural selection, and will favor or oppose adding an additional member based upon the action's effect on their fitness. Each possesses an endowment of genes and resources, which will be evaluated by the other parties. Females prefer males who seem likely to deliver a satisfactory stream of resources over a prolonged period of time and who are of good genetic quality. Males prefer females who provide high paternity certainty and who are of good genetic quality.

Each of the three parties (female 1, the male, and female 2) will have a discrete choice problem, where they will choose polygyny if the following condition is true:

$$0 < \Delta F_i + \sum_j \gamma_j \Delta F_j \qquad (1)$$

Where ΔF_i is the change in fitness party i experiences due to the entry of female 2. The second term on the right hand side considers inclusive fitness (Hamilton 1964), where γ_j is the proportion of genes party i shares by descent with some person j outside the triad, and ΔF_j is the change in fitness experienced by outside person j due to the entry of female 2. Polygyny will only be chosen—without coercion—if equation (1) is true for all three parties.

The inclusive fitness term would be large when party i has many close consanguineal kin, and where the marriage to female 2 opens access to fitness-enhancing resources to those kin. It is difficult to think of a situation where all three parties would have a large inclusive fitness term, though this could be the situation with *alliance* marriages among polygynous families in kin-based societies. Members of polygynous natal families have more close consanguineal kin than members of monogamous natal families, and a marriage linking two large households could increase resource access and the number of allies for both households.

We will examine the more restrictive case where $\sum_j \gamma_j \Delta F_j = 0$, assuming that all parties are *myopic,* acting only on their direct fitness changes ΔF_i.

Considerations of directly involved actors

The original female would prefer expanding the dyad only if her fitness increases:

$$F(\propto (R_1+R_M), G_M, G_1) \; < \; F(\omega_1 \propto_X (R_1+R_M+R_2), G_M, G_1) \tag{2}$$

The $F(R,G)$ function ($dF/dR>0$, $dF/dG>0$) represents fitness (intuitively, the number of descendents existing in subsequent generations), which has two types of arguments: a vector of resources of different types (including various material resources, time, and social capital), and a vector of genetic quality (including such things as attractiveness, health, and fertility). The term on the left hand side is the original female's fitness under monogamy, which is a function of her genetic endowment (G_1), the male's genetic endowment (G_M), and the combined resources of her and the male (R_1+R_M) scaled by an efficiency parameter ($\propto$). The term on the right hand side is her fitness when the second (unrelated) female enters the marriage; the resource term is now changed to reflect that the second female has brought additional resources (R_2), that the efficiency of resource use may well be different in this expanded domestic unit ($\propto_X$), and that the original female will now receive only a share (ω_1) of the household resources, rather than their entirety.

Since the genetic endowments are identical in the two states, the fitness differential easily reduces to a question of resource magnitude, so that female 1 will prefer whichever state provides her with most resources, choosing polygyny when:

$$\propto (R_1+R_M) < \omega_1 \propto_X (R_1+R_M+R_2) \tag{2a}$$

so that the lower limit of household resource share ω_1 acceptable to female 1 is:

$$\propto (R_1+R_M) / \propto_X (R_1+R_M+R_2) < \omega_1 \tag{2b}$$

The male's fitness equals the sum of the fitnesses of the females whose reproduction he monopolizes, weighted by paternity certainty. Thus, the male discrete choice rule would be to prefer the additional wife when

$$\pi_1 F(\propto(R_1+R_M),G_M,G_1) \; < \; \pi_2[F(\omega_1 \propto_X(R_1+R_M+R_2),G_M,G_1)+F(\omega_2 \propto_X(R_1+R_M+R_2),G_M,G_2)] \tag{3}$$

where $\omega_2 = 1 - \omega_1$ is the share of household resources, received by female 2, and G_2 is her genetic quality. The scalar π_1 is the probability that the male fathers female 1's offspring in the original dyad, and π_2 is the probability that he fathers the offspring in the proposed triad. In most cases, one would expect $\pi_1 > \pi_2$ since mate-guarding will become more difficult when adding the second female. Rearranging terms:

$$\pi_1/\pi_2 < [F(\omega_1 \propto_X(R_1+R_M+R_2),G_M,G_1)+F(\omega_2 \propto_X(R_1+R_M+R_2),G_M,G_2)]/ F(\propto(R_1+R_M),G_M,G_1) \tag{3a}$$

Paternity certainty is about 0.98 in modern (monogamous) populations (Anderson 2006), and estimates for some foraging and horticultural societies with mild polygyny are in the range 0.91 to 0.99 (Marlow 2000:56), though much lower figures can be inferred for some polygynous societies—among the Ekiti Yoruba, for example, the figure would be around 0.5.[2] Suppose that $\pi_1 = 1$ and $\pi_2 = 2/3$ (a very large drop); the left hand side would be 1.5. Even in this case of much-reduced paternity certainty, it would often increase the male's fitness to add another wife: if female 1 and 2 are of equal fecundity, the ratio on the right hand side would be about 2.

Various social institutions can increase paternity certainty: strict rules preventing the public interactions

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[2] Survey work by Caldwell et al (1991:230) showed that nearly half of the most recent sexual acts of married people were not between spouses.

of men and women; settlement patterns keeping households isolated from each other; harsh sanctions on extramarital sex; gossip that makes privacy difficult; and the presence of a male's mother to keep watch on his spouse(s). Thus it seems that males would typically find it fitness-enhancing to add another wife, so that male concern for paternity certainty is unlikely to be the force that maintains monogamy. One must rather look to the antipathy of female 1 to sharing household resources with female 2.

Female 2 will prefer to enter the marriage when her fitness is greater there than in her best alternative:

$$F(\propto_Y (R_2+R_Y), G_Y, G_2) < F(\omega_2 \propto_X (R_1+R_M+R_2), G_M, G_2) \qquad (4)$$

The term on the left hand side is her best alternative fitness: a monogamous relationship with male Y endowed with resources R_Y and genes G_Y; the efficiency parameter of this alternative marriage is $\propto_Y$. The term on the right hand side is her fitness when entering as the second wife. The fitness difference can be reduced to a question of resource magnitude, by defining δ as the resource equivalent of $G_Y - G_M$ (the difference in genetic quality of the two males).[3]

$$\propto_Y (R_2+R_Y+\delta) < \omega_2 \propto_X (R_1+R_M+R_2) \qquad (4a)$$

Substituting $1- \omega_1$ for ω_2, one obtains the upper limit of ω_1 acceptable to female 2:

$$[\propto_X(R_1+R_M+R_2) - \propto_Y(R_2+R_Y+\delta)] / \propto_X(R_1+R_M+R_2) > \omega_1 \qquad (4b)$$

Combining (4b) and (2b), and simplifying, one can characterize the conditions under which a value of ω_1 exists such that *both* females are better off with the entry of female 2 to the marriage:

$$\propto_Y (R_Y + \delta) < (\propto_X - \propto) (R_1+R_M) + (\propto_X - \propto_Y) R_2 \qquad (5)$$

Assuming that a polygynous male will have the advantage in both resources and genetic quality, polygyny will be more likely where male genetic quality is important for fitness and highly variable (most

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[3] We assume here that natural selection has provided cognitive modules enabling the female to make trade-offs between resources and genetic quality when choosing a mate, and that she is indifferent between δ and $G_Y - G_M$.

elements in δ are negative), where male resource endowments are highly variable (most elements in R_M are greater than elements in R_Y), where male resources are relatively unimportant in household production (most elements in R_M and R_Y are less than elements in R_1 and R_2), or where larger households are more efficient in converting resources into fitness than are smaller households ($\propto_X > \propto, \propto_X > \propto_Y$). Additionally, if males are scarce relative to females, then the left hand side is likely to be low, since the male available for a monogamous marriage would be of the lowest quality.

Most of these results are well-established in the theoretical literature. Nevertheless, no previous work on marriage patterns has emphasized the fitness advantage of a larger household, though this is the key result of equation (5). Uncoerced polygyny can only exist where the increased productive efficiency of adding female 2 fully compensates female 1 *and* delivers greater returns to female 2 than she would encounter in her best alternative monogamous marriage. There are a number of ways in which a larger household would increase fitness. First, an additional female allows increased within-household specialization, so that efficiency and diversification increase, improving access to food, an advantage where there is high extrinsic risk due to famine. Second, in environments with high extrinsic risk due to violence, a larger household will be more able to defend itself from others. Third, where the additional female is unrelated to the original female, the network of kin relations linking the household to the surrounding society expands, so that resources during periods of famine and allies during periods of strife are more easily obtained.

Illustrations of the fitness-enhancing nature of polygynous households are easily found in the ethnographic literature. Among the Ekiti Yoruba, for example, where women perform most of the work and where rights to land are based on the number of household members, adding a wife adds to the resource base of the household. The presence of a co-wife allows a woman to specialize in one of the traditional female tasks (farm labor, household labor, and trade), often the task that they themselves prefer. More co-wives mean more affinal kin, which widens the household's social network, providing allies in conflicts and making it possible for members to visit the villages of affines without fear of violence. As sons mature, the household becomes increasingly secure from violence. The wives benefit from the greater security of the large household, not only in terms of reduced threats from violence, but also because the greater supply of food reduces the risk of famine, and the wide social network enables them to trade in villages which would otherwise be hostile. A co-wife allows a woman to escape sexual obligations when those are unwelcome, and facilitates involvement in extra-marital affairs. Overall, the Ekiti see life as easier in polygynous households, with more hands to perform necessary duties, and more time for leisure (Caldwell et al. 1991:234-235).

Monogamy would persist when condition (5) does not hold, so that females 1 and 2 see no advantage in polygyny. This is most likely where larger households have no fitness advantages: where extra-household economic specialization is so advanced that within-household specialization is of little consequence; where the state claims a monopoly on violence and is able to enforce peace; where vast trade networks and state policies eliminate the threat of famine; and where social capital is based on ties with non-kin. Monogamy is also much more likely where males produce most of the resources used for fitness, where food-sharing across families is not pronounced, where there is private ownership of land and capital, and where there is low variation in male resource endowments.

Collective action

Beyond the three parties directly involved in the marriage decision, there are two other types of parties: other males in the breeding population, and unmarried females in the breeding population. Unmarried females would generally support the expansion of the dyad to include female 2, since it would increase female relative scarcity and improve female power in marriage negotiations.

Other males in the breeding population would, however, experience a loss in fitness, since a female gained by another male reduces their pool of potential mates. The expected fitness loss to male j of female i marrying another male k equals the probability that female i would have married male j (p_{ij}), times the fitness of female i (when mated with male j): $p_{ij} F(\propto(R_i+R_j), G_j, G_i)$

If the cost (in terms of foregone fitness) of introducing and maintaining a prohibition against female *i* marrying male *k* is *X*, and males form a coalition to introduce and maintain this prohibition, then each member *j* would have an incentive to participate in the coalition if:

$$s_j X < p_{ij} F(\propto(R_i+R_j), G_j, G_i) \tag{6}$$

where s_j is male *j*'s share of prohibition cost *X*.

Coalitions to reduce the power of dominant males are characteristic not only of humans, but of our nearest relatives such as chimpanzees (Boehm 1999). Nevertheless, two reasons suggest that coalitions enforcing monogamy are unlikely to form. First, there is a free rider problem: all males would be able to enjoy the public good (increased availability of females) whether contributing to the coalition or not; hence all males would have an incentive to stay aloof, and the coalition would attract no members. Only in small groups, where free riders can be easily identified and punished, would coalitions emerge (Olson 1971). Second, the only beneficiaries of a ban on polygyny would be unmarried males, who would presumably be among the least influential members of a society. Coalitions would be much more likely to emerge to restrict the number of wives to a low number (three, for example), since the pool of potential beneficiaries would be much larger (men with fewer than three wives). Thus one might expect collective action reducing the number of wives of dominant males, but only in small-scale societies and never a complete ban on polygyny.

Nevertheless, one can still argue that elites in state-level societies might be able to overcome the difficulties of collective action to impose SIM. The elite governing a state typically constitute a small group, able to identify the free riders in their ranks and thus able to engage in collective action; they can then use the state's instruments of social control to implement SIM.

Methodological Problems with Comparative Survey Data

Since we employ variables selected from the Standard Cross-Cultural Sample (SCCS) data set (Murdock and White 1969; Divale 2004), we begin with a brief overview of methodological problems that comparative survey researchers face when using cross-cultural or cross-national data but that have been ignored in previous empirical studies of marriage systems. These are: 1) the non-independence of sample units due to horizontal and vertical diffusion; 2) specification of an appropriate multivariate statistical model to incorporate these interdependencies; 3) multiple imputation of missing data; and 4) combining indicator variables into scales.

Horizontal and Vertical Cultural Trait Transmission: Galton's Problem

The underlying structure of interdependencies among cross-cultural or cross-national sample units due to cultural trait transmission is widely referred to as Galton's Problem. Any process that is hypothesized to result in connections among N sample units can be represented as an N by N connectivity matrix. By far the most common connectivity matrix is based on some function of geographic distance. The underlying premise in this case is that close physical proximity promotes more frequent interaction between individuals or communities, which in turn makes adoption of cultural traits by diffusion and borrowing among neighbors more likely. A similar premise underlies the use of language relations to construct autocorrelation weight matrices: societies that are more closely related linguistically are more likely to have inherited similar trait complexes from a common ancestor. Other processes of cultural trait transmission are also straightforward to capture: for example, the world-wide spread of monogamy through the extensive horizontal transmission of Christianity by conquest (Macdonald 1995; Herlihy 1995) can be represented by a connectivity matrix based on similarity of religion.

The three autocorrelation weights matrices used in the current study were constructed as follows.

Geographical Distance: The distance matrix is based on spherical distances using the SCCS global coordinates for each society (v833_1 and v833_2.) However, this yields a matrix where every society is related to every other society around the world, irrespective of whether or not each pair of societies have or previously had any interactions, however indirect. Following one of the rules of thumb proposed by Griffith (1996) for constructing autocorrelation weights matrices, that overspecification (including too many neighbors) decreases statistical power, we used only the distances to the closest 25 neighbors for each society, and set all other distances to zero. The reciprocal of each positive distance was squared to give the final weights. The diagonal elements of this distance weight matrix, and both of the matrices described next, were set equal to zero.

Language: We employ the matrix produced by Eff (2008); each cell gives the proximity of the row society to the column society, based on language phylogeny. The diagonal is set to zero, and each row is row-standardized.

Religion: This matrix was based on a nine category World Religion variable coded for the SCCS. Table 1 shows the proximity score between each of the nine categories; these scores are then substituted into a matrix where each row and column represents a society. Each cell is exponentiated to get the matrix weights $w_{ij} = exp^{score(ij)}$. The diagonal is then set to zero, and each row is row-standardized.

Obviously, there are alternative metrics that could be used to construct each of the autocorrelation weight matrices described here. It seems reasonable to suppose, however, the alternative metrics would yield fairly similar weight matrices, and so those described above should provide insight into the levels of autocorrelation in the SCCS data set that might be expected with respect to the dependent variable of interest here. Such networks should generate observable implications if the relevant network structure is at least partially observable. For example, if networks based on geographical distances are important, then our female monogamy variable distribution will be related to physical distance. Likewise, if the non-physical network dimensions, such as religious similarity, are important they should also be systematically related to the distribution of our monogamy variable. How these dependency matrices are included in our regression model is outlined next.

Modeling horizontal and vertical diffusion: The network autocorrelation effects regression model

Recently, Dow (2007) proposed that Galton’s problem be formulated as a network autocorrelation effects regression model, where the autocorrelated dependent variable is included as an endogenous predictor variable. The autocorrelation effects model thus implies that cultural trait diffusion can be conceptualized as a potential missing variable problem. That is, if the omitted autocorrelation effects variable is correlated with both the dependent variable and one or more of the independent variables, biased coefficient and variance estimates will result if the appropriate effects variable is not included in the model.

It is straightforward to extend the usual regression model to include an additional variable that incorporates the effects of trait transmission on the distribution of percentage of married females in monogamous marriages, the dependent variable (*y*) in our proposed model:

$$y = \alpha + \lambda \mathbf{W}y + \mathbf{X}\beta + \varepsilon \qquad (7)$$

where ε is a vector of normally distributed error terms with zero mean, **X** is the set of k exogenous variables, β is a $k \times 1$ vector of regression coefficients, α is an intercept, and λ is the scalar network autocorrelation effect coefficient. The first independent variable on the right of the equals sign is the product of a square $n \times n$ connectivity matrix **W**, where the i^{th} row contains the weights w_{ij} that connect society *i* to each other society *j*, and the $n \times 1$ vector of scores on the dependent *y* variable. The weights w_{ij} of a **W** matrix are customarily row normalized to sum to unity, i.e. $\sum_{\mathrm{i}} w_{ij} = 1$, so the resulting values of **W***y* are simply a weighted average of the *y* variable scores for the societies to which the focal society is connected via the process(es) represented by **W**. For example, with a spatial diffusion process the $\sum_{\mathrm{j}} w_{ij} y_j$ value for the i^{th} society is a weighted average of the scores on the *y* variable of all of the other *j* societies, where closer societies are weighted more heavily than distant societies. It is also customary to code $w_{ii} = 0$ for all *i*, that is, self-proximities are ignored.

Estimation of the network autocorrelation effects regression model in equation 1 is not straightforward, however. The **W***y* variable is endogenous by definition, that is, it is correlated with the error term ε, since in equation 1 *y* is expressed as a function of ε. Ordinary least squares regression requires that all of the independent variables be uncorrelated with the errors, ε, since if not all of the estimated regression coefficients will be biased. Two-stage least squares (2SLS) estimation procedures are commonly used to deal with endogenous predictor variables. The first step in the 2SLS estimation of equation 1 is to generate an estimate of **W***y* that is independent of the ε term. This can be done by regressing **W***y* on one or more "instrumental" variables, which are independent variables that predict **W***y* but are uncorrelated with ε. Dow (2007) suggests **WX** as a suitable set of instrumental variables, which means that the following equation is estimated at stage 1 using OLS :

$$\hat{y}_{\mathrm{w}} = \hat{a} + \mathbf{WX}\hat{c} \tag{8}$$

The vector of predicted scores is then entered into equation 1 and the following stage 2 equation is estimated, again using OLS regression:

$$y = \alpha + \lambda\,\hat{y}_w + \mathbf{X}\beta + \varepsilon \tag{9}$$

The estimates from this second stage model permit valid inferences about the effect of trait diffusion net of the functional associations (assessed by the λ estimate and its associated significance level), and the functional associations net of diffusion (the β coefficients and their significance levels.)

It is straightforward to extend the 2SLS approach to handle multiple **W** weight matrices simultaneously (Dow 2007). Often, however, network matrices representing commonly posited diffusion processes are highly correlated with each other, thus the use of multiple weight matrices may result in problems of multicollinearity and disentangling their separate contributions may be difficult. Dow and Eff (2009a) suggest one approach to handling this problem: combine multiple proximity matrices into a single **W** matrix as follows: $\mathbf{W}_{\mathrm{DLR}} = \pi_D * \mathbf{W}_{\mathrm{Distance}} + \pi_L * \mathbf{W}_{\mathrm{Language}} + \pi_R * \mathbf{W}_{\mathrm{Religion}}$, where $\pi_D + \pi_L + \pi_R = 1$ and $0 \leq \pi_D, \pi_L, \pi_R \leq 1$, that is, each weight lies in the [0,1] interval, inclusive. In the example reported below, the three combination weights were varied in increments of .05 to yield 231 combined matrices, and the $\mathbf{W}_{\mathrm{DLR}}$ combination matrix that maximized the R^2 for the second stage regression equation was selected as the "best" matrix. The individual weights currently have no known distribution, and therefore no associated significance levels can be estimated. However, the magnitude and significance of the λ for each individual matrix together with the weights of the combined matrix offer an indication of their joint contributions.

Missing Data and Multiple Imputation

The problem of missing data has been addressed in only one previous cross-cultural study of marital institutions (Dow and Eff 2009a). Missing data renders all other previous cross-cultural and cross-national survey research on marital institutions problematic for two reasons. First, statistical power may be significantly reduced if all cases with missing data are deleted from the analysis. When there is missing data on each variable in a study the reduction in sample size can be considerable. For example, in her study of correlates of monogamy, Osmond (1965) dropped 45 percent of the cases from the total world-wide sample of 862 societies in the Ethnographic Atlas (Murdock 1967) because of missing data. Similarly, all of Kanazawa and Still’s (1999) regressions results are based on subsamples of between 31 and 102 from their sample of 127 modern nation states because of missing data, that is, from 20 percent to 76 percent of cases were dropped from each reported regression analysis due to missing data.

The second, and more important, problem raised by missing data in previous studies is that the usual default option (listwise deletion of all cases with missing data prior to statistical analysis) can lead to biased parameter estimates, inflated Type I errors, and distorted confidence intervals (Sinharay et al 2001). This happens when the subsample of cases that remains is no longer representative of the original sample of cases. For example, if missing data on male mortality in warfare occurs more often in societies that have low levels of warfare, and cases with missing male mortality data are discarded prior to analysis, then the means and variances of the male mortality and possibly other correlated variables will be biased in the remaining subsample. Any analysis based on biased estimates of means, variances, and correlations will result in bias in higher level statistics, such as regression coefficients, confidence intervals and tests of significance.

Over the past two decades or so statisticians have developed multiple imputation (MI) methods for dealing with missing data that generate consistent and efficient estimates (Rubin 1987; Schaefer 1997). The fundamental idea of MI is to generate multiple estimates of each item of missing data so that the uncertainty due to imputation can be taken into account. MI is a principled method that consists of three basic steps: 1) Create *m* (*m*>1) complete data sets by filling in each missing value *m* times using *m* independent draws from an appropriate imputation model; 2) analyze the *m* complete data sets as true complete data sets using any standard statistical model; 3) combine the results from the *m* analyses in a simple way to obtain the repeated imputation inferences.

The results presented below are based on *m*=60 fully imputed data sets using the SCCS variables of interest as the initial input, plus a set of auxiliary variables from the SCCS that have no missing data, as described in Eff and Dow (2009). The network effects regression equation was then estimated on each of the 60 imputed data sets, which yielded sets of 60 estimates of the regression parameters and their standard deviations. Other statistics, such as R^2 measures of fit, were also computed. These estimates were then combined to yield the final estimate of each of the regression parameters and their variances, using the rules described in Rubin (1987: 76-77.) Detailed discussion of these rules and empirical examples are given in Dow and Eff (2009a; 2009b) and Eff and Dow (2009).

Some statisticians have suggested that only the cases that have observed values on the dependent variable be used to calculate the point estimates using the *m* imputed data sets. Von Hippel (2007) shows that using cases with imputed values for the dependent variable introduces error into the final variance estimates that can be avoided if these cases are deleted. The estimates reported in the tables shown below are based only on observed dependent variable cases.

The above statistics are routinely computed by all of the easily available software packages that perform MI analyses. We employ the multiple imputation by chained equations (MICE) approach available in the R package of statistical routines to impute missing data (Van Buuren et al 2007.)

Exogenous variables and scale construction

Cross-cultural researchers often combine several variables into a composite index or scale. Scales created by summing component variables (e.g., Murdock and Provost 1971; Low 1988; Divale and Seda 2000), or by factor analysis (Divale and Seda 1999) are all examples of composite indices, in which the values of component variables are combined into a single scale. A composite index, in its most general form, is the weighted sum of the component variables:

$$\theta_i = \sum_r y_{ri} \mu_r \tag{10}$$

where the value of the index for society i (θ_i) is the sum of the component variable values (y_{ri}) for p components, each component value weighted by weight μ_r. The component variables are almost always scaled similarly, typically by standardizing or converting to ranks. A wide variety of methods exist for specifying the weights μ_r, and in most cases there is no *a priori* reason to choose one weighting scheme over another. The choice of weights can therefore often be criticized as arbitrary. We use the linear programming method of Eff (2009) in order to reduce the effect of weight choice in ranking societies. The method is based upon tiered data envelopment analysis (Barr et al. 2000) and separates societies into groups, such that the between-group differences in index rank are based solely on data values (y_r), not on weights.

Data

Table 2 shows the variables we employ in our empirical model. Most are drawn from the SCCS, and most are combined into indices or "scales." Each variable has missing values imputed, using the auxiliary data set described in Eff and Dow (2009) as well as closely related SCCS variables. We create 60 imputed data sets—a much larger number than the 5 to 10 typical of studies using MI, but since our data set is relatively small (186 observations), the increase to 60 costs little in terms of computing time.

We produce 11 scales, employing Eff's (2009) linear programming method, to operationalize the key concepts in our theoretical discussion. Three are measures of extrinsic risk: *violstr*, which combines eight variables related to endemic within-society violence; *path*, which combines seven variables measuring the severity of risk from pathogens; and *famstr*, which combines 12 variables related to famine. Higher values of these should all reduce the incidence of monogamy. The 14-variable scale *benenv* can be taken as an inverse measure of extrinsic risk, in that it measures the degree to which the environment is beneficent; it is intended as a test of Alexander's "ecologically imposed monogamy" hypothesis—that in harsh environments, monogamy prevails because no man can afford to maintain more than one wife.

The scale *fpecon* combines six variables to measure the economic importance of females, while *resinq* uses eight variables to produce a measure of resource inequality. Higher values of either of these should make monogamy less likely. The scale *socont* combines five variables to measure the degree to which extramarital affairs face sanctions; high values should indicate that paternity certainty is higher, making polygyny more feasible for males.

Two variables (not scales) measure the relative scarcity of females: *v714* is the male:female sex ratio, and *mmort* is male mortality in warfare. As *v714* increases or *mmort* decreases, monogamy should be more likely.

Several scales attempt to measure the conditions associating collective action with SIM. Combining seven variables, the scale *polpart* measures the degree to which there is broad political participation, which should coexist with SIM, if the mechanism is one of elite concession. Measuring the degree of economic specialization, *techdol* combines nine variables. A society with a fine-grained division of labor should be more likely to have enforced SIM. The scale *socscale* combines four variables to give a sense of the size of the society, allowing a test of Alexander's hypothesis that large-scale societies diminish the importance of lineages by prohibiting polygyny.

Cultural transmission is partly measured by the scale *modern* which combines six variables for modernization. We rely, however, on the network lag term for our main measure of cultural transmission, along channels of religion, historical descent (linguistic phylogeny), and geographic diffusion; implicitly, genomic effects will be captured by this term.

Our dependent variable is *–ln(1+v872)* where *v872* is the percentage of married women in polygynous marriages.[4] This will vary directly with the frequency of monogamous marriages in the society.

Results

Table 3 reports results for four 2SLS network autocorrelation effects regressions. At the top are standardized coefficients and stars reporting significance levels for the unrestricted model.[5] The first three columns of coefficients give the results for regression models that include a single endogenous autocorrelated dependent variable for each of the religion, language, and distance weights matrices, plus all 11 scales and two individual variables. The fourth column shows the results from a regression that includes a "best" composite weights matrix that is a weighted sum of these three weights matrices, where the final weights give the maximum possible regression R-squared, as described above.

The first row of standardized coefficients in Table 3 show that the female monogamy diffusion variables are highly significant for the language (0.294) and distance (0.296) weights matrices, but insignificant for the religion weight matrix (0.130); when all three matrices were combined into a composite network (0.321), the composite weights were: religion = 0, language = 0.5, and distance = 0.5.

Taken together, these results clearly show that cultural trait transmission operates through channels of descent (language) and geographic diffusion (distance). Religion does not present an independent channel, and there is only weak evidence for the influence of modernization. It is noteworthy that the two channels that transmit monogamy are those most likely to transmit genes, in addition to culture.

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[4] Adding one shifts the range of v872 from 0-97 to 1-98, so that logs can be taken; the log transformation reduces the effect of the variable's skewed distribution on estimation and inference; taking the negative allows us to interpret the coefficients as affecting the proportion of marriages that are monogamous.

[5] Using the heteroskedasticity-consistent standard errors, based on the appropriate residuals for two-stage least squares.

We used a Wald test to test for the propriety of dropping insignificant independent variables (though retaining the trait transmission variable in all cases); the resulting restricted models are reported in the second section of Table 3. The bottom part of Table 3 reports p-values from various diagnostic tests for these restricted models. The model containing the religion trait transmission term is poorly specified, failing five of the tests, and the religion trait transmission coefficient is itself insignificant. All models have heteroskedastic errors, which required the use of heteroskedastic-consistent standard errors for the coefficients in Tables 3 and 4. Five independent variables are significant in at least one of the four restricted models. Three of these have some relation to extrinsic risk: *violstr* (violence stress), *path* (pathogen stress), and *benenv* (beneficial natural environment). The fourth is a scale measuring female economic importance (*fpecon*); and the last is the scale for the society-level division of labor (*techdol*).

Our preferred model uses the composite weight matrix, which is shown in more detail in Table 4. The first four columns report the coefficients and their associated inference statistics. The variance inflation factors (VIF) reported in the fifth column demonstrate that there is no issue with multicollinearity among the independent variables. The final column provides a decomposition of the R-squared for the composite model, partitioned among the independent variables using the procedure proposed by Chevan and Sutherland (1991) of averaging over all possible orders of entering the variables. This provides a succinct way of comparing the explanatory contributions of cultural trait transmission (0.118), the division of labor (0.031), and extrinsic risk (0.054+0.076+0.009=0.139). Overall, extrinsic risk is the strongest determinant of monogamy; pathogen risk exerting the strongest effect, followed by risk due to endemic violence, and then (much more weakly) risk due to harsh environment.

Discussion

Our model assumes that the decision to practice monogamy or polygyny is freely made by agents who are acting on preferences that have been shaped by natural selection. Nevertheless, polygyny may arise because of coercion, by some males, of females; examples would include the marriage of women captured in war, and the selling of girls into concubinage. In such cases, females are not exercising free choice, and our model would not apply. In many other cases, females do not choose their own marriage partner, and must follow the dictates of their parents or male kin. While coercion arguably exists in these cases, inclusive fitness would guide kin to make decisions that would favor the female's fitness, with results similar to the model given above (Scheidel 2008:8).

Equation (5) provides five testable hypotheses. The first of these is that monogamy would be more prevalent where male genetic quality is less variable and/or less important for fitness. Male genetic quality is particularly critical in environments with high pathogen stress, allowing us to test this hypothesis with the independent variable *path*, which proves to be the most influential independent variable, excepting only cultural transmission.

The second hypothesis is that monogamy would be more prevalent where male resource endowments are less variable. We test this with the independent variable *resinq*—a general measure of resource inequality—and the estimated coefficients are not only insignificant, but of the wrong sign in our unrestricted models. The third hypothesis is related: those societies where male resources are important in household production will have a higher proportion of monogamous marriages. Our independent variable *fpecon* provides a test of this, and provides weak evidence that this is indeed the case, though failing to be significant in our preferred composite model. Taken together, these results suggest that male resources are not an important determinant of the choice between monogamy and polygyny.

Our fourth hypothesis is that where females are scarce relative to males, then monogamy is more likely, since the best male available for a monogamous marriage will be of better quality. We tested this with two independent variables: *mmort* and *v714,* both of which were insignificant in the unrestricted models, and of the wrong sign. There is no evidence that relative female scarcity is a determinant of monogamy.

Our fifth hypothesis is that large polygynous households will be more efficient in converting resources into fitness than small monogamous households. We reasoned that this would be the case since members of a large household could specialize in tasks for which they were best suited, because resources become more secure when obtained from a larger and more diverse productive base, and because the addition of new wives would create affinal ties with new outsiders—expanding trade and alliance networks. We test this with three independent variables—*violstr*, *famstr*, and *techdol*—though recognizing that the independent variable *benenv* might capture the same variation as *famstr*.

Of these, the most influential is *violstr*, showing that monogamy is more prevalent in societies with lower levels of endemic violence. This indicates an important advantage of a polygynous household is shielding members from endemic violence—an advantage that would be moot in a society where the state effectively enforced peace. In their study of the spread of monogamy in West and Middle Africa, Caldwell et al (1991:253) state that the shift from polygyny to monogamy that accompanied the spread of colonial administration came about in part because "….native courts and the police would guarantee personal safety and liberty, and suppress physical force and punishments within the community…"

The second most influential variable in this group is *techdol*, whose positive sign shows that monogamy is more likely in societies with a fine-grained division of labor. This provides supports for Betzig's (1986) hypothesis that a highly developed division of labor, at the level of the society, will lead to monogamy. We would argue, however, that an interpretation consistent with our model is more likely to explain this result than is Betzig's "elite concession" hypothesis. Our view is that larger households can gain productive advantages though specialization of their members, but those advantages really only matter when there is little or no between-household specialization. Thus, societies with a well-articulated division of labor will provide little incentive for women to choose polygyny.

One unexpected result was that *famstr* (famine stress), though of the expected negative sign, failed to be significant. Instead, *benenv* (beneficial natural environment) was significant, though of the wrong sign: the variable had been intended as a test of Alexander et al's (1979) ecologically imposed monogamy hypothesis, and should have had a negative sign (showing that harsher environments have more monogamous marriages). Since one can interpret *benenv* as an (inverse) measure of famine risk, this result can be explained, but it leaves the implication that the ecologically imposed monogamy hypothesis, though intuitively plausible, is not true. This would be consistent with the suggestion of Low (2003:165-166) that the weak association between monogamy and the harshness of the environment may be due to the ability of humans to overcome many environmental limitations.

We argued that equation (3a) is unlikely to be a binding constraint: males would in most circumstances find it fitness-enhancing to add another wife, since paternity certainty is not likely to decline by much. In environments with few social controls bolstering paternity certainty, however, monogamy would be more likely, since males would have greater difficulty in guarding additional wives. We test this with the variable *socont,* which is insignificant and of the wrong sign, confirming that paternity certainty does not drive the choice for monogamy.

We also argued that collective action is unlikely to account for SIM. Our results provide no support for Alexander et al's (1979) hypothesis that elites of larger scale societies impose monogamy in order to squelch the power of kin groups: the variable *socscale* is insignificant in all regressions, though of the correct sign. The insignificance of the variable *polpart* likewise dispels the notion that societies with broad political participation are more likely to have SIM.

The single most important determinant of monogamy, however, is cultural trait transmission. Societies practicing monogamy may adopt the trait from neighboring groups, or it may be part of a heritage acquired from ancestral cultures. There may be a genomic basis for a propensity for monogamy, and our trait transmission variable may reflect genomic effects. The spread of monogamy through the conquest and colonization of large swathes of the world by the Christian nations of Europe is historically well-documented (Scheidel 2008; Herlihy 1998; Macdonald 1990.) Nonetheless, the potential effects of this extensive horizontal and vertical diffusion of monogamy on statistical tests using world-wide samples of preindustrial societies or nation states have been completely ignored in previous empirical work. Our network effects regression results provide the first statistical evidence that the joint effects of horizontal diffusion, as indicated by religious and spatial relationships, and vertical diffusion, as indicated by language relationships, have been important factors in bringing about the observed pattern of female monogamy in the preindustrial world.

Conclusion

Our empirical results provide support for two different views of the prevalence of monogamy in human societies. The first is that monogamy is not imposed by an elite seeking to increase the stability and survivability of the society, but rather appears as an adaptation chosen by individuals, striving to increase their own fitness. The key decision makers choosing monogamy are women, since male fitness can in most circumstances be enhanced by polygyny. Women will see no advantage in polygyny when: 1) there exists such a fine-grained extra-household division of labor that increasing within-household specialization brings no advantages; and 2) a large household brings no advantages in shielding members from endemic violence. Both of these conditions will be met in societies with a high degree of role specialization and functions for policing and justice administration, which explains the observed prevalence of monogamy in large industrialized states.

The natural environment also frames the female choice for monogamy. Most importantly, in an environment of low risk of pathogen infection, women are less motivated to mate with men of the highest genetic quality, and are therefore less inclined to share men in polygynous marriages. In addition, areas with a beneficent climate will have a higher incidence of monogamy, presumably because there is less need for the protection from famine provided by relatively diverse production of a polygynous household.

The second view supported by our results is that monogamy has spread through borrowing and descent, so that societies that practice monogamy do so because ancestral and neighboring societies do so—not because the practice is necessarily adaptive. The channels of transmission are language phylogeny (common descent) and geographic (diffusion from neighbors)—but *not* from religion. Interestingly, the two active channels are those that transmit genes, in addition to culture, leaving open the possibility that inter-societal differences in marriage practices may be partially conditioned by genotypic differences.

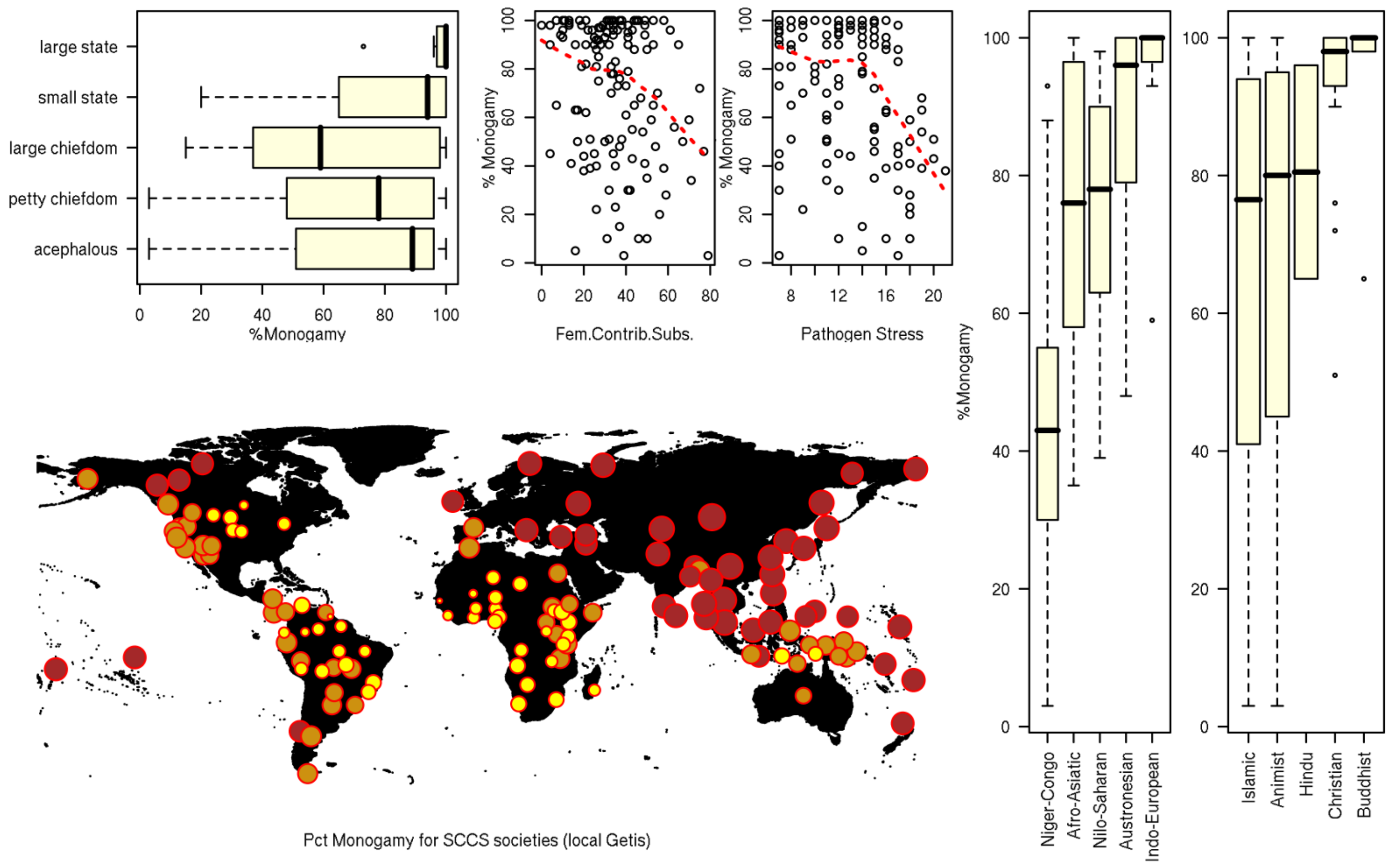

Figure 1. Percentage of married females in monogamous marriages. The map shows the 143 SCCS societies with non-missing values: larger and darker dots represent higher percent monogamous marriages; values are spatially smoothed (Getis and Ord 1992). The boxplot at the upper left shows the U-shaped distribution of monogamy across political complexity. The scatterplots show the relationships between monogamy and female contribution to subsistence and pathogen stress, respectively; the dotted line is the lowess smoother (Cleveland 1979). The boxplots at the right show the range of monogamous marriages across language phyla and religions, respectively.

Table 1: Raw proximities for religions

	Indigenous religion	Deep Islamization	Deep Christianization	Superficial Islamization	Superficial Christianization	Hebrews	Mahayana Buddhism	Hinayana Buddhism	Vajrayana Buddhism	Hinduism
Indigenous religion	1	1	1	1	1	1	1	1	1	1
Deep Islamization	1	4	2	3	2	2	1	1	1	1
Deep Christianization	1	2	4	2	3	2	1	1	1	1
Superficial Islamization	1	3	2	4	2	2	1	1	1	1
Superficial Christianization	1	2	3	2	4	2	1	1	1	1
Hebrews	1	2	2	2	2	4	1	1	1	1
Mahayana Buddhism	1	1	1	1	1	1	4	3	3	2
Hinayana Buddhism	1	1	1	1	1	1	3	4	3	2
Vajrayana Buddhism	1	1	1	1	1	1	3	3	4	2
Hinduism	1	1	1	1	1	1	2	2	2	4

Notes: The above scores are used to create weights $w_{ij}=exp(score_{ab})$ where society *i* has religion *a* and society *j* has religion *b*.

Table 2: Descriptive statistics

variable	Description	N	min	max	mean	stdev
Modernization						
modern	Modernization (LP scale)	186	1	12	7.44	2.430
v1841	Sum of Educational Changes	135	0	6	2	1.120
v1842	Sum of Family Changes	135	0	6	2.23	1.500
v1843	Sum of Governmental	135	0	5	2.25	1.180
v1844	Sum of Religious Changes	135	0	4	2.23	1.060
v1845	Sum of Technological Changes	135	0	6	1.59	1.150
v1848	Sum of Transportation Changes	135	0	3	0.62	0.730
Violence stress						
violstr	Violence stress (LP scale)	186	1	12	7.7	2.190
v1665	Homicide	121	1	9	3.92	2.840
v1666	Assault	113	1	9	4.64	3.060
v1667	Theft	112	1	9	4.33	3.070
v1668	Individual aggression – trespass	54	1	9	3.63	2.960
v1669	Suicide	87	1	9	3.08	2.520
v1675	Social homicide	67	1	9	4.14	2.890
v1676	Social assault	46	1	7	3.66	2.350
v1677	Social theft	38	1	7	2.78	2.480
Pathogen stress						
path	Pathogen stress (LP scale)	186	1	14	6.68	3.650
v1253	Leishmanias	186	1	3	1.55	0.780
v1254	Trypanosomes	186	1	3	1.35	0.620
v1255	Malaria	186	1	3	2.3	0.900
v1256	Schistosomes	186	1	3	1.53	0.830
v1257	Filariae	186	1	3	2.04	1.000
v1258	Spirochetes	186	1	3	1.94	0.870
v1259	Leprosy	186	1	3	1.86	0.770
Famine stress						
famstr	Famine stress (LP scale)	186	1	12	7.86	2.290
v1262	Occurrence of short-term starvation	169	1	3	1.97	0.460
v1263	Occurrence of seasonal starvation	168	1	5	3.12	1.360
v1265	Occurrence of famine	170	1	4	3.3	1.060
v1267	Severity of famine	110	1	4	2.89	1.150
v1268	Persistence of famine	105	1	3	2.08	0.870
v1269	Recurrence of famine	129	1	3	1.8	0.580
v1683	Threat of famine	119	1	6	2.57	1.560
v1684	Threat of weather or pest disasters	114	1	4	2.46	1.150
v1685	Chronic resource problems	144	1	5	2.16	1.270
v1719	Periodical variation of food scarcity	91	1	8	3.39	2.570
v1720	Land shortage (Ta)	82	1	2	1.36	0.480
v678	Food stress or hunger	138	1	4	1.89	0.770
Female economic importance						
fpecon	Female economic importance (LP scale)	186	1	26	13.28	5.790
v585	Propor. contribution of women to overall subsistence	92	1	8	4.7	1.400
v591	Ownership or control of the use of dwellings	72	1	4	2.43	1.110
v658	Females produce goods for nondomestic distribution	152	1	2	1.83	0.380
v659	Demand for female produce beyond household	135	1	2	1.72	0.450
v660	Female economic control of products of own labor	139	1	2	1.71	0.450
v826	Average female contribution to subsistence	183	0	79	32.92	16.520
Beneficial natural environment						
benenv	Beneficial natural environment (LP scale)	186	1	17	12.31	3.760
bio11	Mean temperature of coldest quarter (a)	186	-363.3	276	132	141
bio12	Annual precipitation (a)	186	0.4	5,135	1,415	973

variable	Description	N	min	max	mean	stdev
bio13	Precipitation of wettest month (a)	186	0.2	724	225	137
bio16	Precipitation of wettest quarter (a)	186	0.3	1,904	599	369
bio3	Isothermality (a)	186	15.1	92	56	21
bio4	Temperature seasonality (a) (inv)	186	104.9	19,118	3,982	3,911
bio6	Min temperature of coldest month (a)	186	-415.2	251	71	145
bio7	Temperature annual range (a) (inv)	186	56.7	620	228	118
NPP	Net primary production (c)	186	10,419	1,083,803	389,099	280,470
v857	Access to rich ecological resources	186	1	6	3.55	1.260
v921	Agr. potential 1: sum of slope soils climate scales	186	4	23	16.73	3.460
v924	Suitability of soils for agriculture	186	0	8	4.15	1.560
v926	Climate suitability for agriculture	186	0	8	6.26	2.320
v928	Agr. potential 2: lowest of slope soils climate scales	186	0	8	3.76	1.630
Resource inequality						
resinq	Resource inequality (LP scale)	186	1	17	8.26	4.540
v158	Social stratification	186	1	5	2.45	1.460
v1721	Number of rich people (Tb)	98	1	4	2.46	0.930
v1723	Number of poor (Tb)	88	1	4	2.25	1.070
v1724	Number of dispossessed (Tb)	88	1	4	1.77	1.040
v270	Class stratification	186	1	5	2.41	1.500
v274	Type of slavery	180	1	4	1.99	1.260
v709	Social stratification in larger community	92	1	4	2.38	1.120
v710	Social stratification in local community	91	1	4	2.07	1.040
Political participation						
polpart	Political participation (LP scale)	186	1	19	11	3.620
v1134	Degree of despotism (inv)	104	1	2	1.15	0.360
v1744	Low level particpn in high level decision making (Td; inv)	95	0	3	1.53	1.060
v761	Checks on leaders power	86	1	4	2.83	0.860
v763	Leaders exercise of authority	87	1	3	2.16	0.820
v764	Decision making bodies	88	1	5	2.9	1.480
v765	Political participation: community decision making	88	1	4	2.44	1.140
v766	Polit participation: extent of adult involvement (inv)	84	1	4	2.49	0.960
Division of labor						
techdol	Division of labor (LP scale)	186	1	15	6.32	4.000
v153	Technological specialization	186	1	5	3.09	1.410
v254	Metalworking (dummy=1 for craft specialization) (Tc)	183	0	1	0.43	0.500
v255	Weaving (dummy=1 for craft specialization) (Tc)	174	0	1	0.11	0.310
v256	Leather (dummy=1 for craft specialization) (Tc)	139	0	1	0.13	0.340
v257	Pottery (dummy=1 for craft specialization) (Tc)	170	0	1	0.15	0.360
v258	Boat building (dummy=1 for craft specialization) (Tc)	160	0	1	0.07	0.260
v259	House construction (dummy=1 for craft specialization) (Tc)	150	0	1	0.09	0.280
v777	Enforcement specialists (inv)	89	1	3	2.1	0.870
v90	Police	180	1	5	2.1	1.710
Societal scale						
socscale	Societal scale (LP scale)	186	1	23	11.46	5.57
v63	Community size	185	1	8	3.46	1.7
v64	Population density	184	1	7	3.76	1.97
v756	Political Role Differentiation (inv)	90	1	7	3.85	2.12
v83	Levels of sovereignty	184	1	4	1.99	1.22
Social control enforcing marriage						
socont	Social control enforcing marriage (LP scale)	186	1	22	10.86	4.480
v1137	Lack of virginity as justification for divorce	160	0	4	0.14	0.750
v1250	Consequence for adolescent girls premarital pregnancy	50	1	7	3.35	1.690
v961	Restrictions on premarital sex	61	1	7	3.83	2.090
v962	Punishment for premarital sex	51	1	6	2.81	1.770

variable	**Description**	**N**	**min**	**max**	**mean**	**stdev**
v964	Punishment for extramarital sex	54	1	8	4.66	2.050
Variables not combined into scales						
mmort	Male mortality (b)	80	0	6	2.56	2.520
v714	Sex ratio	90	1	3	2.13	0.560
v871	Pct. of married men with more than one wife (inv)	145	0	90	16.23	19.710
v872	Pct. of married women polygynously married (inv)	143	0	97	25.64	27.660

Notes: Variables of the form v# are given the name of their SCCS number. Component variables for each LP scale are shown together with the scale descriptive statistics. Transformations: (Ta) if (x>1) then x=2; (Tb) if (x=2) then x=3; (Tc) if (x=3 or x=4) then x=1, x=0 otherwise; (Td) if (x>0) then x=x-4; (inv) indicates that the variable is multiplied by negative one prior to creating LP scale. Sources: (a) GIS data from Hijmans, et al (2005); (b) data kindly shared by authors of Ember et al (2007); (c) GIS data from Imhoff et al (2004); all other variables are found in the SCCS (http://eclectic.anthrosciences.org/~drwhite/courses/index.html).

Table 3: Comparison of four network autocorrelation effects regression models. The dependent variable is natural log of percentage of married females in monogamous marriages.

Variable	Description	Religion	Language	Distance	Composite
Unrestricted model standardized coefficients					
Wy	Network lag term	0.130	0.294 ***	0.296 ***	0.312 ***
modern	Modernization	0.113	0.130 *	0.134	0.134 *
violstr	Violence stress	-0.276 **	-0.260 **	-0.288 ***	-0.283 ***
path	Pathogen stress	-0.406 ***	-0.354 ***	-0.294 ***	-0.301 ***
famstr	Famine stress	-0.080	-0.074	-0.051	-0.055
fpecon	Female economic importance	-0.133	-0.146 *	-0.116	-0.123
v714	Sex Ratio	-0.136	-0.094	-0.108	-0.099
mmort	Male mortality	0.036	0.039	0.041	0.043
benenv	Beneficial natural environment	0.165	0.176	0.124	0.139
resinq	Resource inequality	0.075	0.018	0.060	0.041
polpart	Political participation	0.084	0.081	0.091	0.088
techdol	Division of labor	0.214	0.184	0.229 *	0.222 *
socont	Social control enforcing monogamy	0.050	0.055	0.032	0.039
socscale	Societal scale	0.064	0.060	0.044	0.042
Restricted model standardized coefficients					
Wy	Network lag term	0.144	0.305 ***	0.342 ***	0.336 ***
path	Pathogen stress	-0.472 ***	-0.405 ***	-0.270 ***	-0.352 ***
violstr	Violence stress	-0.263 **	-0.252 **	-0.297 ***	-0.296 ***
techdol	Division of labor	0.278 ***	0.218 **	0.272 ***	0.266 ***
benenv	Beneficial natural environment	0.209 **	0.209 **		0.158 *
fpecon	Female economic importance	-0.142 *	-0.146 *		
Restricted model p-values on diagnostics					
Hausman	H0: *Wy* exogenous	0.097 *	0.909	0.119	0.479
Hausman	H0: *path* exogenous	0.611	0.240	0.381	0.303
Hausman	H0: *stress* exogenous	0.576	0.807	0.957	0.910
Hausman	H0: *techdol* exogenous	0.252	0.887	0.960	0.960
Hausman	H0: *benenv* exogenous	0.553	0.462		0.740
Hausman	H0:*fpecon* exogenous	0.753	0.767		
Ramsey RESET	H0: model correct functional form	0.088 *	0.396	0.353	0.389
NCV	H0: residuals homoskedastic	0.019 **	0.045 **	0.014 **	0.016 **
Wald-restrictions	H0: dropped variables have coef=0	0.269	0.286	0.131	0.197
Shapiro-Wilk	H0: residuals normally distributed	0.131	0.169	0.096 *	0.154
LMerr: religion	H0: spatial error model inappropriate	0.268	0.554	0.600	0.600
LMlag: religion	H0: spatial lag model inappropiate	0.283	0.633	0.674	0.672
LMerr: distance	H0: spatial error model inappropriate	0.008 ***	0.608	0.508	0.552
LMlag: distance	H0: spatial lag model inappropiate	0.005 ***	0.707	0.718	0.571
LMerr: language	H0: spatial error model inappropriate	0.122	0.402	0.551	0.561
LMlag: language	H0: spatial lag model inappropiate	0.028 **	0.297	0.855	0.683
R^2		0.228	0.282	0.269	0.288
N		143	143	143	143

Notes: Dependent variable is –ln(1+v872). "***" p-value ≤0.01, "**" p-value ≤0.05, "*" p-value ≤0.10 (coefficient p-values from heteroskedasticity-consistent standard errors). All estimations from multiply imputed data (*m*=60); only observations non-missing for the dependent variable are used in the *m* regressions. Composite matrix weights: distance=0.5, language=0.5, religion=0.

Table 4: Estimates from optimally weighted composite matrix model for percentage of females in monogamous marriage.

Variable	Description	coef	Fstat	df	p-value		std. coef	VIF	R^{2p}
(Intercept)		1.658	2.762	1,905	0.097	*			
Wy	Network lag term	1.205	16.811	4,038	0.000	***	0.336	1.137	0.118
violstr	Violence stress	-0.197	9.998	675	0.002	***	-0.296	1.071	0.054
path	Pathogen stress	-0.150	14.472	6,382	0.000	***	-0.352	1.565	0.076
benenv	Beneficial natural environment	0.066	3.094	24,670	0.079	*	0.158	1.290	0.009
techdol	Division of labor	0.109	9.194	1,222	0.002	***	0.266	1.173	0.031

Adequacy tests

Test	**Null hypothesis**	**Fstat**	**df**	**p-value**	
Hausman	H0: *Wy* exogenous	0.502	1,191	0.479	
Hausman	H0: *violstr* exogenous	0.013	1,044	0.910	
Hausman	H0: *path* exogenous	1.060	7,074	0.303	
Hausman	H0: *benenv* exogenous	0.110	6,843	0.740	
Hausman	H0: *techdol* exogenous	0.002	3,175	0.960	
Ramsey RESET	H0: model correct functional form	0.742	809	0.389	
NCV	H0: residuals homoskedastic	5.767	2,301	0.016	**
Wald-restrictions	H0: dropped variables have coef=0	1.669	442	0.197	
SWnorm	H0: residuals normally distributed	2.034	1,093	0.154	
LMerr: religion	H0: spatial error model with Wt(religion) inappropriate	0.275	3,312	0.600	
LMlag: religion	H0: spatial lag model with Wt(religion) inappropriate	0.179	4,789	0.672	
LMerr: distance	H0: spatial error model with Wt(distance) inappropriate	0.353	4,892	0.552	
LMlag: distance	H0: spatial lag model with Wt(distance) inappropriate	0.321	6,184	0.571	
LMerr: language	H0: spatial error model with Wt(language) inappropriate	0.338	6,606	0.561	
LMlag: language	H0: spatial lag model with Wt(language) inappropriate	0.166	12,524	0.683	

Notes: Dependent variable= -ln(1+v872). Estimates from multiple imputation (*m*=60). "***" p-value ≤0.01, "**" p-value ≤0.05, "*" p-value ≤0.10. R^2=0.288. N=143. Composite matrix weights: distance=0.5, language=0.5, religion=0. R^{2p} is the R^2 partitioned to each independent variable (Chevan and Sutherland 1991). Standard errors are heteroskedasticity-consistent (Greene 2008:163).

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