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Factors Influencing the Allowance of Cousin Marriages in the Standard Cross Cultural Sample

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The purpose of this study is to examine variance in the practice and acceptance of cousin marriage in select areas of the world. This study uses Murdock's Standard Cross Cultural Sample (SCCS). The SCCS includes 186 societies ranging from contemporary hunter and gatherers to early historic states to contemporary industrial people. It is hypothesized that cousin marriages are more likely to occur in small, isolated communities, and in communities that experience high rates of pathogen prevalence. That is, the variance in the practice of cousin marriage may reflect functional responses to various local ecological and environmental pressures. The results demonstrate that geographic isolation and pathogen prevalence are both independent and significant positive predictors of whether or not a society practices cousin marriage. These findings suggest that consanguineous marriage may be an adaptive solution to the problem of mate selection, depending on the environment in which one lives. Consequently, the biological advantages may lead to and/or become an individual preference, which is then reinforced by the local culture. We contend that although social and cultural explanations are of obvious importance, they can only provide partial explanations, and much can be gained from incorporating an evolutionary perspective.

Keywords: consanguineous marriage, cousin marriage, inbreeding, standard cross-cultural sample

For most people living in North America and Western Europe, the thought of choosing a cousin as a marriage partner may feel inappropriate. Although before the 19th century, cousin marriage was permitted in the United States, this form of marriage began to be banned in the middle of the 19th century. It was believed that children from this type of marriage would suffer from genetic defects, and 'poor breeding' was viewed to hinder social progress (Ottenheimer, 1996). Therefore, many western societies created rules and cultural norms via incest taboos

that include first cousins. An incest taboo refers to the formal and informal rules against incest, which is the practice of sexual relationships between close relatives (Durkheim, 1963). First cousins might be included in a taboo because there is a .125 probability of sharing similar genes by virtue of common descent. As a result, there is a presumed increased risk of offspring inheriting recessive alleles as a result of the shared genes, which in turn may lead to, for example, higher rates of miscarriages, still births, and infant mortality among couples (Jaber, Halpern, & Shohat, 1998). Because of the presumed negative genetic effects, marriage between cousins is currently illegal in certain parts of the United States, whereas other states have laws regulating the practice (Ottenheimer, 1996). Comparable beliefs to those found in the United States concerning cousin marriages are found in Europe (Paul & Spencer, 2008).

However, in different areas of the world, such as Africa, parts of Asia, and the Indian subcontinent, marriage partners are often chosen from within the extended family. The marriage of

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individuals who are genetically related is known as consanguineous marriage (Thornhill, 1991), and commonly occurs between people who are second cousins or closer (Hamamy, Jamhawi, Al-Darawsheh, & Ajlouni, 2005). This type of marriage is practiced predominantly in Muslim and Hindu populations, among whom rates of consanguineous marriage are as high as 50% (Bittles & Neel, 1994). Not surprisingly, immigration of peoples from countries that allow cousin marriage to those that do not has generated concern about the potential social and genetic influences that it may have on, for example, public health issues and policy, and integration (Shaw, 2006). For example, a British environment minister triggered one such debate when he commented, in reference to the high rates of birth defects in the Pakistani community, "If you have a child with your cousin, the likelihood is there'll be a genetic problem" (BBC News, February 10, 2008). In a similar vein, in response to the high incidence of cousin marriage among immigrants from, in particular, Morocco and Turkey in The Netherlands, cousin marriages may soon be prohibited (de Visser, 2008).

Given its high prevalence across some cultures and absence in others, there may be an evolutionary benefit for its occurrence under specific local environmental conditions. Therefore, the goal of this article is to examine the function of consanguineous marriages by investigating some ecological conditions under which it may be adaptive.

Several explanations for the continuing practice of cousin marriages have been suggested, with the majority using sociocultural rather than biological or ecological perspectives. First, marriage among kin may lead to a decreased risk of divorce and lower rates of domestic violence. Cousins involved in a marriage may experience a positive relationship. This may lead to a better relationship between the woman and her in-laws, greater marriage stability, and a longer duration of the marriage (Barbour & Salameh, 2009). Second, cousin marriages may protect wealth from being distributed outside of the family. This practice may be extremely important in societies where inherited wealth is crucial to survival and status (Joseph, 2007). Indeed, wealth is cited as one of the reasons for the continuation of consanguineous marriages, and is quite important in some indigenous pop-

ulations, including, for example, the James Bay Cree of Canada (Flannery, 1938). Marriages between family members may also aid poorer families by reducing the burden of a child's marriage through elimination of a required dowry (Barbour & Salameh, 2009).

The fact that there are potentially genetic costs and social benefits means that there is a threshold under which a society must decide whether these benefits outweigh the costs. To determine this threshold, Ember (1975) examined the origin and causes of the incest taboo to elucidate the circumstances under which it would include first cousins. Using data from the *Ethnographic Atlas*, he examined several theories (e.g., childhood familiarity, cooperation and inbreeding theory) and discovered that the inbreeding theory (i.e., mating with family members is avoided because of the possible genetic impact on offspring) was the best predictor of whether the incest taboo would extend beyond the immediate family. He also hypothesized that the size of the population mattered. That is, in populations where the possibility of marrying a cousin is low (i.e., large genetic isolates), it would be more likely that cousin marriage would be permitted. On the other hand, in populations where the probability of marrying a cousin is high because of the smaller population, then cousin marriage would more likely be prohibited. Using data pertaining to the number of jurisdiction levels beyond the community level, as well as community size, he found that the proportion of societies that permitted cousin marriage increased linearly in response to both variables. Indeed, 54% of the societies in the *Ethnographic Atlas* with urban aggregations allowed one or more types of cousin marriage, whereas 36% of the 357 that lacked urban aggregations would allow first cousin marriage to occur.

Although population size undoubtedly is an important consideration, as shown by Ember (1975), it does not explain why there is a definite divide in beliefs concerning the acceptability of cousin marriages between various parts of the world. We suggest that the potentially adaptive functions of consanguineous marriages have received little attention, and these might provide critical insight into the reasons underlying the cultural divide. From an evolutionary perspective, cultural differences in the acceptability of consanguineous marriages may be the

result of functional responses to differential environmental cues, such as pathogen prevalence and availability of mates.

Therefore, using a functional perspective may help to reveal additional ways that consanguineous marriage is advantageous; for example, it may explain how this choice of marriage partner may increase an individual's survival and reproductive success. Thus, two hypotheses, grounded within the framework offered by evolutionary psychology (i.e., ultimate level of explanation; Tinbergen, 1963) are proposed to explain the variation in prevalence of consanguineous marriages. First, these marriages may serve as a means to stay ahead of the evolutionary arms race with local pathogens. Second, such marriages may be the most adaptive solution under conditions where there is a lack of available mates because of geographic isolation. That is, in an evolutionary view, it would be better to mate with a cousin and risk the negative outcomes associated with inbreeding depression than to not mate at all. These two causes are expanded on in the following sections.

Cousin Marriages to Combat Local Pathogens

Because cousins are genetically related, there is a higher probability for both individuals to be carriers for harmful recessive mutations that could be expressed in their offspring (Bittles & Neel, 1994), as compared with genetically unrelated individuals. In general, any form of inbreeding tends to be avoided among most species and is associated with a loss of general biological fitness (Bittles, 2001), reduced fertility, and lower rates of individual survivability (Barbour & Salameh, 2009). Within human societies, close inbreeding (i.e., individuals who are 25% related or closer, e.g., uncles, aunts, nieces, nephews, siblings, parents) is rare. With some exceptions, mating is usually avoided and prohibited between siblings, half-siblings, parents, and children (Van Den Berghe & Mesher, 1980). Furthermore, among first-order relatives (e.g., parents and their children, or between siblings), there is typically a strong biological aversion to the notion of being involved in a sexual relationship (e.g., the Westermarck (1921) effect).

In contrast, mating with nonrelatives is generally adaptive because it promotes genetic diversity in offspring who are then able to meet diverse and unexpected environmental challenges, or to cope with harsh ecological conditions, including a high prevalence of parasites and pathogens (Hamilton, Axelrod & Tanese, 1990; Ridley, 1993; Trivers, 1985). Pathogens can be defined as “infectious microbes, such as bacteria or viruses, which are capable of causing disease. Other parasites, such as fungi and protozoans, are also considered pathogens. Because not all microbes are harmful, pathogens refer specifically to those that can cause disease or other harm” (Koo, 2014, p. 1).

Parasites and pathogens have produced strong selection pressures on humans who have continuously needed to evolve new ways to fight against them. As noted by Lieberman (2007), because pathogens can reproduce and evolve extremely quickly, the better equipped a host is to deal with these threats, the less likely it is that the consequence will be fatal. As a result of pathogen evolution, there is a selection pressure for increased genetic diversity within humans because infections can spread more quickly through genetically homogenous hosts. With respect to mating, then, individuals who avoid reproducing with close kin therefore avoid an inbreeding depression and maximize the probability of having offspring who will remain healthy and become reproductively successful. Pathogens are one of the main reasons why sexual reproduction and inbreeding avoidance mechanisms evolved, such that a greater pathogen load in the environment should favor greater genetic mixing, not less. It is important to note that the evidence for the genetic risks faced by offspring from cousin marriage may be exaggerated and potentially exacerbated by socioeconomic circumstances (Bennett et al., 2002).

Despite all the presumed negative consequences of inbreeding, previous research by Hoben et al. (2010) demonstrated that areas with higher rates of historical pathogen prevalence had higher rates of cousin marriage, as based on current worldwide rates of cousin marriage and historical pathogen prevalence. In addition, there is evidence that inbreeding may, under certain conditions, actually *enhance* rather than suppress individual genetic fitness. For example, Philippe's (1974) study of a

French Canadian isolate showed that women in consanguineous marriages had lower intrauterine mortality, which in turn resulted in greater overall fertility (see also Bittles, Grant, Sullivan, & Hussain, 2002). This finding, however, may in fact be attributable to the younger age at which many consanguineously married women tend to have their first live birth (Jaber, Halpern, & Shohat, 1998). Furthermore, it has been speculated that, among consanguineous couples, prenatal losses and involuntary sterility is lower as a result of greater mother–fetus compatibility. The increased fertility of consanguineous couples may be a compensatory mechanism for increased postnatal deaths (Bittles, 2001; Schull & Neel, 1972; Tuncbilek & Koc, 1994). More recent research by Özener and Graham (2014) examined the influence of inbreeding and parental education on growth and fluctuating asymmetry in newborns in Turkey. Weight, height, head circumference, and chest circumference were measured in the newborns, in addition to four bilateral traits, which included ear width, ear length, and second and fourth digit lengths. Results of their study revealed that once education was taken into account as a covariate in their analysis, none of the size measurements and the fluctuating asymmetry were found to be significantly different between the inbred and outbred newborns. The authors of this study concluded that, in their sample, inbreeding depression did not cause an increase in fluctuating asymmetry in the newborns, or a decrease in body size.

It must be noted, though, that the majority of research leads to the conclusion that fertility among consanguineous couples is reduced. It has been demonstrated that spontaneous abortions are less likely to occur in fetuses that are conceived from individuals who are histoincompatible (that is, fetuses that have different paternally and maternally derived antigens); couples who share histocompatibility antigens (HLA) often experience reduced fertility (Ober, Elias, Kostyu, & Hauck, 1992). The lower fertility in these couples may also be a consequence of the expression of harmful genes that negatively affect early development and that may lead to periconceptual losses (Ober, Hyslop, & Hauck, 1999).

Nevertheless, although it has been argued that inbreeding may prove to be harmful for immune functioning because of increased ho-

mozygosity (see Kempenaers, 2007 for review), the actual evidence for any heterozygotic advantage is mixed. For example, inbreeding would better enable individuals to have offspring who retain the genes that are necessary to combat local pathogens. Thus, mating with a cousin may prove to be beneficial in areas that are characteristically prone to endemic pathogens via enhanced immunological resistance (Denic, Nagelkerke, & Agarwal, 2008; Denic & Nicholls, 2007; Fincher & Thornhill, 2008a, 2008b; Shields, 1982).

Research has also shown that the frequency and degree of consanguinity is correlated with the geographic distribution and intensity of *Plasmodium falciparum*, one of the parasites that causes malaria in humans (Denic & Nicholls, 2007). At present, the most common monogenic disorder in humans is α +-thalassemia; the high prevalence might be attributable to the fact it decreases the probability of death from *P. falciparum* (Allen, O'Donnell, Alexander, Alpers, Peto, Clegg, & Weatherall, 1997; Carter & Mendis, 2002). Caballero and Hill (1992) demonstrated that inbreeding actually accelerates the selection of many recessive alleles, including α +-thalassemia, in areas of the world where malaria is endemic. Among humans, the α +-thalassemia allele provides protection against malaria and those individuals who are homozygotic are less likely to develop deadly forms of malaria (Allen et al., 1997; for further review see Denic et al., 2008). Similarly, individuals who are homozygotic for a defect on *CKR-5* appear to be immune to sexual transmission of HIV-1 (Liu et al., 1996). This homozygotic advantage has also been found in nonhuman species. For example, among water buffalo (*Bubalus bubalis*), brucellosis, which is a pathogen that causes spontaneous abortions, has devastating effects on herds. One study revealed a significant association between animals who were homozygotic for the allele *Nramp1 B* and resistance to this infection (Borriello et al., 2006). Likewise, in a species of fish, the rostrum dace (*Leuciscus leuciscus*), and those fish who were either highly homozygous or highly heterozygous at the multilocus level, were found to have fewer ectoparasites than fish of intermediate heterozygosity (Blanchet, Rey, Berthier, Lek, & Loot, 2009).

The homozygotic advantage may therefore provide an explanation for the cultural differ-

ences in the acceptance of consanguineous marriage. That is, such marriages may function to combat pathogens, and thus, these behaviors will likely be exhibited in areas with high pathogen prevalence (Fincher, Thornhill, Murray, & Schaller, 2008). Therefore, the first hypothesis is that societies located in areas of the world with higher pathogen prevalence will be more likely to permit consanguineous marriage than those located in areas with lower prevalence. This hypothesis has been tested in previous research by Hoben et al. (2010), but not by using current rates of both variables.

Cousin Marriages as a Result of a Lack of Mates

As Ember (1975) suggested, geographic isolation is a factor that may affect the occurrence of consanguineous marriages. Depending on the geographic (or social) location, groups may vary considerably in the likelihood of coming into contact with potential mates, and as a result, at any given time the number of available nonrelated individuals of a suitable mating age will vary. On average, kinship between subpopulations decreases with geographic distance, and thus, geographic isolation is a major factor in genetic isolation (Rahman et al., 2003). Most isolated populations have significantly less genetic diversity than the world population as a whole, as is documented via analyses of both chromosomal and mitochondrial DNA (Peltonen, Palotie, & Lange, 2000). All population isolates begin with a few founding individuals and can experience population bottleneck and genetic drift (Peltonen et al., 2000). If the isolated population does not expand rapidly in size, these effects can be counteracted through immigration. However, because these populations are isolated and immigration is limited, quick growth is unlikely and potentially leaves individuals with no alternatives except to mate with a potential relative. For example, the Northeast Algonquian Indians of North America practiced cousin marriage because they are geographically isolated from other tribes and have a small population (Strong, 1929). Therefore, our second hypothesis is that geographically isolated societies will be more likely to allow cousin marriage, independent of pathogen prevalence rate. Lastly, it is critical to note that for the purposes of this study, cousin marriage is de-

finied as marriage between first cousins, as this type of information was readily available in the Ethnographic Atlas.

Method

Data were obtained from Murdock and White's (1969) Standard Cross Cultural Sample (SCCS), which was created from the Ethnographic Atlas. One well-documented culture from each of the sampled provinces was chosen to create a cross-cultural sample. The SCCS includes 186 societies ranging from contemporary hunter and gatherers to early historic states to contemporary industrial people. The SCCS was obtained online from World Cultures electronic open access journal in February 2009, with creation of the data file by William Divale in 2007. Different individuals coded each of the variables used in the analyses. Variables 64 (community size), 79 (polygyny), and 80 (family size) were coded by Murdock and Wilson (1972). Murdock (1967) also coded societies that allowed first cousin marriage in the Ethnographic Atlas. Low (1990) coded total pathogen stress for each society. Hartmut (1998) coded number of rich and poor individuals in each of the societies and social stratification. Lastly, Cashdan (2001) coded variable 1875, the number of societies with 150-mile radius (Divale, 2007).

Type of Cousin Preferred/Allowed

Within each society that practices cousin marriage, there are rules determining which type of cousin is appropriate for consideration. Cousins are distinguished in two ways, the first of which is to note whether they are "parallel" or "cross." Parallel cousins are children of a parent's same sex sibling, while cross-cousins are children of the parent's opposite sex sibling. The second issue is if the cousin is from the father's side (i.e., patrilineal) or the mother's side (i.e., matrilineal).

Furthermore, within the SCCS, cousin marriages are classified such that there is a distinction of whether or not cousin marriage was preferred (identified as variable 226) or allowed (variable 227). Then for both of these variables, each society is coded using one of the following categories: all four types of cousins, three of four cousins, two of four, one of four, no first

cousins and unknown for second, no first or second cousins, and last, no preferential or prescriptive unions.

For the purpose of statistical analysis, societies were categorized as either allowing or not allowing some form of cousin marriage. This dichotomy was used because many historical changes have occurred in at least a few societies, which has influenced the preference for this type of marriage. For example, among the Inuit of Northern Canada, cross-cousin marriage was traditionally preferred, however with the introduction of Christianity and the prohibition of this practice by the missionaries, the number of cross cousin marriages decreased. Despite the prohibition, many Inuit people continued its practice late into the 20th century (Mailhot, 1999). Furthermore, because the preferred type of cousin (i.e., patrilineal or matrilineal) seems to be predominately a matter of cultural choice, groups were collapsed into two categories, first cousin marriage present and first cousin marriage absent. The first cousin marriage present category ($n = 83$) included all four types of cousins, three of four cousins, two of four cousins, and one of four cousins. The first cousin marriage absent category ($n = 91$) included no first cousins, no first and unknown for second, and no first or second cousins. Of the 186 societies in the SCCS, 12 did not have data on cousin marriage. It should be noted that total numbers of societies vary in the analyses depending on available data.

Pathogen Prevalence

In this particular dataset, pathogen prevalence (indicated as variable 1260 in the SCCS) is the sum of seven diseases, which includes leishmanias, trypanosomes, malaria, schistosomes, filariae, spirochetes, and leprosy. Severity for each is measured on a 3-point scale (1 = *absent or not recorded*, 2 = *present with no indication of severity*, 3 = *present and serious, widespread*). Overall severity is then the sum of the severity for the seven diseases.

Geographic Isolation

Within the SCCS, lack of geographic isolation is measured as the number of other groups within a 100-, 150-, 200-, 250-, 300-, 350-, 400-, 450-, and 500-mile radius. It is acknowledged that this is a simplistic measure, as geo-

graphic distance is only one way to measure possible contact between communities, and that two communities in close proximity may not have any contact at all. However, despite this limitation, geographic distance is a useful indicator for the *potential* of contact. For the sake of simplicity within the present analysis, the lack of geographic isolation was measured as the number of other groups within 150-mile radius (variable 1875). Please note that the decision to use 150 miles was based on a statistical difference. An independent sample t test was conducted, and significant results were found, for the number of other groups within 150-mile radius and higher, between societies that allow cousin marriage and societies that do not.

Results

Pathogen Prevalence and Geographic Isolation

To determine whether there was a difference between the two groups (i.e., cousin marriage present vs. absent) for level of pathogen stress, an independent sample t test was performed. There was a significant difference in total pathogen stress as measured by disease severity between the first cousin marriage present group ($M = 13.16$, $SD = 3.45$) and the first cousin marriage absent group ($M = 11.97$, $SD = 4.08$), $t(174) = -2.067$, $p = .04$. Societies with higher pathogen stress were more likely to allow first cousin marriage.

With respect to the number of groups within a 150-mile radius, there was a significant difference between the first cousin marriage present group ($M = 4.23$, $SD = 4.79$) and the first cousin marriage absent group ($M = 6.53$, $SD = 8.01$), $t(170) = 2.23$, $p = .03$. Thus, societies that allowed first cousin marriages had significantly fewer communities within 150-mile radius than those societies that did not allow first cousin marriage.

To determine whether pathogen prevalence and geographic isolation were independent predictors of whether first cousin marriage is allowed, a binary logistic regression was used to analyze the data. The first cousin marriage present group was coded as 1 and the first cousin marriage absent group was coded as 0. Total pathogen score, geographic isolation and the interaction term were all entered together in

Step 1. The first prediction, that independent of the other factor, areas with high pathogen prevalence will be more likely to permit cousin marriage, was supported, $\beta = 0.10$, $p = .02$. That is, as the total pathogen stress decreased, the likelihood of allowing cousin marriage decreased. Again independent of the other factor, the second prediction, that geographically isolated areas are more likely to permit cousin marriage, was supported, $\beta = -0.08$, $p = .02$. As the number of societies within 150 miles decreased, the probability of allowing cousin marriages increased. The possibility of an interaction between the two factors was also tested. Both variables were centered and entered into the model in the logistic regression analysis. The interaction term was found to be nonsignificant, $\beta = -0.01$, $p = .46$.

Additional Analyses

To explore the possibility of confounding variables, we conducted chi-square analyses using various variables and the presence or absence of first-cousin marriage.

These variables include: family size (variable 80), $\chi^2(4, n = 174) = 1.74$, $p = .54$, number of poor individuals (variable 1723), $\chi^2(3, n = 52) = 4.56$, $p = .21$, number of rich individuals (variable 1721), $\chi^2(3, n = 85) = 2.81$, $p = .42$, social stratification (variable 1751), $\chi^2(3, n = 94) = 1.64$, $p = .65$, polygyny (variable 79), $\chi^2(3, n = 174) = 2.80$, $p = .42$, and community size (variable 63), $\chi^2(3, n = 173) = 7.63$, $p = .37$. Thus, there were no significant differences between the first cousin marriage present versus absent societies on any of these variables.

In addition, because the basis of the proposed hypotheses was Ember's (1975) extension of the incest taboo to first cousins, an attempt was made to replicate his analyses from the *Ethnographic Atlas* that pertained to the inbreeding hypothesis. As previously mentioned, Ember examined the origin and cause of the incest taboo and the circumstances under which the taboo would extend to other family members outside of the immediate family. In addition to the inbreeding hypothesis, that is that mating with family members is avoided due to potential negative consequences on offspring, Ember also hypothesized that population size would also influence whether cousin marriage would be permitted. Ember examined jurisdiction levels

beyond community level and community size and found that the proportion of societies that permitted cousin marriage linearly increases in response to both of the variables. In an attempt to replicate Ember's results in the SCCS, a chi-square analysis was also performed on jurisdiction level and the presence or absence of first cousin marriage, which was nonsignificant, $\chi^2(3, n = 172) = 4.19$, $p = .38$.

Discussion

The findings support both hypotheses; pathogen prevalence and geographic isolation were independent predictors of whether or not consanguineous marriages (i.e., marriages between first cousins) were permitted. Support was found for the prediction that societies that were highly exposed to the selection pressure of severe pathogen endemics would be more likely to permit cousin marriage. Mating with a cousin could potentially increase the likelihood that the genes that are necessary to fight local pathogens are expressed in subsequent offspring (e.g., malaria).

The second prediction was that societies that were relatively more geographically isolated would allow cousin marriages. Because individuals living in remote areas would have a relatively small pool of people to select a mate from, they would be more likely to mate with someone who is genetically related, including cousins. Age is likely a factor that makes this situation even more problematic. Although a society might be composed of multiple families and contain nongenetically related individuals, at any given time there is presumably only a small number of individuals who are of a suitable age. Consequently, if the pool of available potential mates is very small and includes a relative, it might be worth the potential risks to select that individual rather than to not have a mate at all. As predicted, as the number of societies within a 150-mile radius decreased, there was an increase in the likelihood that the society would practice consanguineous marriages.

Together, these findings suggest that consanguineous marriage may be an adaptive solution to the problem of mate selection, depending on the environment in which one lives. For example, in environments that are plagued with pathogens, are geographically isolated, and are

limited with respect to population size, it may be advantageous to mate with cousins. The biological advantages, which are emphasized in the current study, may lead to and/or become an individual preference. This preference then may be reinforced by the local culture. However, in environments in which the same biological benefits of mating with a cousin are not present, there appears to be a preference for mating with individuals who are not genetically related. Culture, whether overseen by religion or government, reinforces this preference by distinguishing between those who are suitable as a mating partner, and those who are not. In a similar vein, one issue that remains to be mentioned is the relationship between mating and marriage. For purposes of this study the terms have been used interchangeably, but this is a limitation that warrants further investigation. It could be the case that who one marries and who one prefers as a mating partner are not the same individual.

The influence that environmental factors such as pathogen prevalence have on behavior is not limited to just one's choice of marriage partner. Pathogen prevalence has also been shown to have an effect on other cross-cultural differences. For example, in regions with historically high levels of pathogen prevalence, individuals tend to be less extraverted, to be less open to novel experiences, and to have more restricted approaches to mating (Schaller & Murray, 2008). It has also been found that people living in these regions are more likely to support collectivist values that highlight within-group interdependence, extended-family nepotism, xenophobia, xenophobia, and philopatry (Fincher & Thornhill, 2008a, 2008b; Fincher et al., 2008). Interestingly, these characteristics are typically associated with countries that practice cousin marriage and may actually aid in facilitating this type of marriage. To gain a better understanding of the advantages and disadvantages of marriage between cousins, future research should take a combined approach examining social, cultural, and adaptive explanations.

There are other noteworthy limitations with this type of data set. The reliability of the informants and accuracy of those collecting the data may be questionable, and there is a potential for a sampling bias. Additionally, assessing causation from mean values for traits at a group level may also be problematic because it tends to ignore within group variation (Marlowe,

2003). However, despite these concerns, the results are significant and based on a priori hypotheses, and they are maintained in spite of potentially confounding variables, including family size, community size, number of economically poor individuals, number of rich individuals, social stratification, and polygyny.

A further alternative explanation that was not addressed in the analyses is the notion of kin alliances and their impact on the allowance of cousin marriages. The alliance theory is derived from incest taboo, in that it is the universal exclusion of incest that requires humans to seek mates outside their own kinship groups. In other words, the incest taboo forces exogamy. Therefore, in any particular society there are certain kin members who are forbidden to marry with each other. According to the alliance theory put forth by Strauss (1970), there are two different models of marriage exchange. In one, the women of a group is offered to another group and individuals who are suitable for marriage would be explicitly defined by social institutions. In the other, the group of potential mates for a women is unspecified and always open, with the exception of particular kin members, such as immediate family members, aunts, uncles. Cousin marriage could potentially fall into either of these categories; for example, among some Muslim societies, marriage between patrilineal kin are preferred and arranged by parents. On the other hand, in some Western societies there are no specific laws, with the exception of the United States, which prohibit marriage between cousins, and individuals are free to choose who they marry yet the incest taboo, including relatives such as siblings, is still upheld. Marriages in some countries were and continue to be regarded as a union between kin groups, not solely a union between two individuals, and which over time has created specific social structures. A regular, reciprocal exchange of women between specific groups presumably created a debtor/creditor relationship and in order to maintain a balance, a repayment to the next generation would be made in the form of wives. Although this is a noteworthy hypothesis to explore, the SCCS lacks data that would lend itself to test the kin alliance theory.

Furthermore, because the data available in the SCCS on pathogen prevalence and cousin marriage are from differing time periods, it is probable to assume that present day pathogen

loads are correlated with ancestral pathogen prevalence, however given the type of data it is difficult to conclusively determine that the tradition of cousin marriages is the direct result of pathogen loads. Alternatively, kin alliances offer a very strong evolutionary incentive for the allowance of cousin marriages. Furthermore, within the SCCS data set the fact that societies distinguished between the different types of cousins, that is, matrilineal cross, patrilineal parallel lends itself to the notion that it is not simply inbreeding, but ties between kin are also involved.

The results of the current study provide insight into why there is variability in the acceptability of consanguineous marriages. Although they are of obvious importance, social and cultural explanations can only provide partial explanations, and much can be gained from understanding the adaptive function of behaviors that potentially have negative impacts on the fitness or the survivability of offspring. Understanding behaviors from an adaptive perspective may aid in reducing negative stereotypes and stigma, such as that which is seen for consanguineous marriages.

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