

Maternal Inheritance and Familial Fecundity Factors in Male Homosexuality

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Abstract This study, following Camperio-Ciani, Corna, and Capiluppi [(2004), *Proceedings of the Royal Society of London, Series B, Biological Sciences*, 271, 2217–2221] aimed to examine the familial history of male homosexuality, and test the so-called “fertile female” hypothesis for this trait in a contemporary British sample. Using a comparative survey design, we found that white (comprising those of Anglo-European descent) and non-white (comprising ethnic “Blacks,” “South Asians,” “East Asians,” “Hispanics,” and “Others”) homosexual men ($n = 147$) had a significant excess of maternal but not paternal line male homosexual relatives compared to heterosexual men ($n = 155$). We also found significantly elevated fecundity of maternal aunts of white homosexual men compared to white heterosexual men, whereas non-white heterosexual men showed elevated fecundities of almost every class of relative compared to non-white homosexual men. No significant excess of older brothers was found in homosexual compared to heterosexual men, irrespective of ethnic grouping. These data were discussed in relation to possible population-related factors in evolutionary explanations for human male homosexuality.

Keywords Male homosexuality · Ethnicity · Family history · Fecundity · Liability threshold Model · Evolution

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Introduction

The evolutionary biology of male homosexuality is of increasing theoretical interest as it constitutes a key variant in the human sexual phenotype. Some forms of homosexuality may have a heritable basis with further evidence for specific genetic loci (Bailey, Dunne, & Martin, 2000; Hamer, Hu, Magnuson, Hu, & Pattatucci, 1993; Hu et al., 1995; Mustanski et al., 2005; cf. Rice, Anderson, Risch, & Ebers, 1999), and it is also a persistently appearing trait over time in spite of its reduced fitness differentials relative to male heterosexuality (Bell & Weinberg, 1978; for review, see Wilson & Rahman, 2005). Moreover, there have been two falsifications of predictions derived from widely held explanations, such as kin selection (which proposes that homosexuals act as “helpers in the nest”; Wilson, 1975, 1978), leading to a renewed interest in explicit empirical testing of evolutionary hypotheses (Bobrow & Bailey, 2001; Rahman & Hull, 2005).

Recently, one study in an Italian sample shed further light on the Darwinian paradox of male homosexuality by demonstrating that female maternal relatives of homosexual men ($n = 98$) had higher fecundity than female maternal relatives of heterosexual men ($n = 100$), a difference not found in paternal relatives, and that homosexuals had more maternal but not paternal male homosexual relatives (Camperio-Ciani, Corna, & Capiluppi, 2004). These data provide some support for threshold liability models of homosexuality whereby polygenic alleles (that is, several variants of a series of genes) responsible for the trait are predicted to confer behavioral and/or physiological advantages to heterosexual carriers. These lead to reproductive differentials between “gay enabled (carriers)” and “non-gay enabled” heterosexuals which offset the deleterious (reproductively speaking) accumulation of these

alleles leading to a “threshold liability” and resulting in exclusive homosexuality (McKnight, 1997; Miller, 2000). Specifically, Camperio-Ciani et al. suggested that polygenic X-linked allele’s beneficial to female fecundity, but detrimental (or indifferent) to male fecundity, fit the data pattern. This supports a version of threshold liability models which can be referred to as the “fertile female” hypothesis (Hamer & Copeland, 1994) whereby feminizing alleles (which produce sexual attraction towards males and, if expressed in males, results in homosexuality) increase reproductive rates in females who possess them through elevated sexual contacts or because they increase female attractiveness (e.g., by further feminizing female physical attributes). Precisely why such alleles should contribute to elevated numbers of females compared to males in the female line is unclear. The occasional expression of such alleles in males leading to homosexuality may be inconsequential to females as they may form part of an evolutionary “arms race” between male and female genes (known as sexually antagonistic competition), due to differences in gamete size and mode of transmission, which result in antagonistic mating tactics and biased sex ratios (Zeh & Zeh, 2005). In the present case, such an arms race favoring females may lead to a “behavioral sterilization” of the male line in the form of male homosexuality (Zeh & Zeh, 2005).

There are additional studies bearing upon the issue of differential female fecundity rates in relation to sexual orientation. McKnight and Malcolm (2000) reported elevated maternal line fecundity as a function of greater numbers of aunts in homosexual men ($n = 60$) compared to heterosexual men ($n = 60$). However, no significant group differences were found in the number of homosexual relatives in either maternal or paternal lines. King et al. (2005) reported on a sample from the United Kingdom (UK) comprising 301 homosexual and 404 heterosexual men recruited from clinics for sexually transmitted infections. They reported mean family size to be significantly larger for homosexual men and that homosexual men had significantly more older brothers and older sisters than did heterosexual men. Finally, Widmayer and Ellis (2005) reported that the parents of homosexuals (males and females) reported having significantly fewer siblings compared to parents of heterosexuals (males and females). Thus far, three studies have found greater familial fecundity among homosexual men, two of these attributing it to a female line effect (Camperio-Ciani et al., 2004; McKnight & Malcolm, 2000), one to more or less both lines (King et al., 2005), while one further study found elevated fecundity among heterosexuals as reported by their parents (Widmayer & Ellis, 2005). It is important to note that two other studies reported elevated numbers of maternal aunts than maternal uncles (also exceeding the respective difference on the

paternal side) in some sub-samples of homosexual men (e.g., those recruited from HIV clinics compared to those recruited from Gay Pride events), although these studies were not directly concerned with familial fecundity (Bailey et al., 1999; Turner, 1995).

Differences in sample size may explain some of the inconsistencies above with the two studies reporting female line effects having smaller samples compared to the one study reporting generalized elevated fecundity in homosexuals. However, differences in recruitment strategy and geographically-determined population rates are unlikely alternative explanations as all studies effectively used forms of convenience sampling (or “snowball-type” targeted methods) and all the Western nations in which the studies took place have concurrently declining fertility rates.

The elevated numbers of maternal than paternal line male homosexual relatives in the homosexual probands also reported by Camperio-Ciani et al. (2004) supports putative X-linkage demonstrated in previous pedigree studies (Hamer et al., 1993; Hu et al., 1995). However, other studies are not supportive and point to the operation of ascertainment biases in the study samples (Rice et al., 1999). For example, homosexual men may have reported a higher frequency of homosexuality among their relatives or know more about the maternal sides of their families than their fathers’ side although why such biases should exist in one pedigree line and not the other is unclear (Bailey et al., 1999; McKnight & Malcolm, 2000). Twin studies also report that the concordance between ratings of probands’ sexual orientation and their co-twins’ self-reported orientation are lower than reported in previous studies as is the level of agreement between twin pairs in the judgement of other siblings’ sexual orientation (Kirk, Bailey, & Martin, 1999). Thus, caution needs to be exercised when considering studies examining the heritability and behavioral ecology of homosexuality which rely purely on self-report.

The present study aimed to replicate Camperio-Ciani et al. (2004) in a UK community sample. We proposed three hypotheses. Firstly, we predicted that compared to heterosexual men, homosexual men would have a significantly greater excess of maternal than paternal line male homosexual relatives. Secondly, we predicted that compared to heterosexual men, homosexual men would have significantly greater numbers of maternal than paternal line relatives. We note that King et al. (2005) also examined this second hypothesis in a UK sample but that study did not make directional predictions regarding maternal versus paternal fecundity effects and excluded non-white ethnic groups. These two predictions follow Camperio-Ciani et al.’s suggestion that genetic factors transmitted in the maternal line both increase the probability of being homosexual in males and increase female fecundity. Finally, we

also wanted to examine whether the well known fraternal birth order (FBO) effect, whereby homosexual men have a greater number of older brothers than any other class of sibling relative to heterosexual men (Blanchard, 2004), was present in our sample. This was because homosexual men may belong to larger families as a function of the FBO effect and therefore FBO becomes a confounding variable upon putative sexual orientated-related differences in the rates of homosexuality among male relatives and familial fecundity. Ultimately, further empirical data would aid in constraining the specificity of theories regarding the evolutionary maintenance of inherited factors responsible for male homosexuality (McKnight, 1997; Miller, 2000).

Method

Participants

A total of 155 heterosexual men and 147 homosexual men participated in the study. Both groups were recruited from the student population of the University of East London and from the Soho district of London, a recognized gay area of the city also frequented by heterosexuals. We ensured that heterosexual men were recruited from the same sources as homosexual men to help proportionate any ascertainment biases across the groups.

Participants' sexual orientation was assessed using one 7-point Kinsey scale of sexual feelings (fantasies and attractions) ranging from 0 ("exclusively heterosexual") to 6 ("exclusively homosexual") (Kinsey, Pomeroy, & Martin, 1948) and one categorical item about self-identification as either "homosexual/gay," "heterosexual/straight," or "bisexual." Only participants who checked "homosexual/gay" or "heterosexual/straight" on the self-identification item and responded as 0 or 1 and 5 or 6 on the Kinsey item were included (i.e., were classified as "heterosexual" and "homosexual"). Demographic information was obtained regarding age, number of years spent in full-time education since the age of 5, and ethnicity classified as "White" (White European including Spanish/Anglo-American/Australian/New Zealand/White South African), "Black" (African/Afro-Caribbean), "South Asian" (Indian/Pakistani/Bangladeshi/Sri Lankan), "East Asian" (Chinese/Japanese/Korean/Burmese/Vietnamese/Thai), "Hispanic" (South American/Mexican), or "Other" (e.g., Turkish). Participants were also classified by parental socioeconomic status (SES) into the nine categories according to the standard occupational classification of the Office for National Statistics (2000): (1) managerial, (2) professional occupations, (3) associate professional/technical occupations, (4) administrative/secretarial occupations, (5) skilled trade occupations, (6) personal service occupations, (7) sales/cus-

tomers service occupations, (8) process, plant and machine operatives, and (9) elementary occupations.

Measures and procedure

The central variables of interest were biodemographic. All participants were asked to list the exact numbers of relatives and their sexual orientations rather than to make estimates (see below). This would aid in reducing group-dependent estimation biases.

Participants completed the questionnaire developed by Camperio-Ciani et al. (2004). The questionnaire was translated from Italian into English and back-translated to ensure accuracy of translation by a qualified translator masked to the study aims. The questionnaire contained items regarding the numbers of each class of male and female relatives (older and younger siblings, first cousins, parents, aunts, and uncles) and their sexual orientation (probands to check "yes" or "no" whether they were "completely certain" or "certain to a high degree" that the mentioned relative was homosexual in feelings and/or behavior). Additional items included in the English version of the questionnaire were number of children (sons and daughter separately) the proband had and their sexual orientation, the numbers of nephews and nieces (the proband's siblings children) and their sexual orientation, and the demographic and sexual orientation items detailed earlier. The item regarding sexual orientation of grandparents employed in the Italian version of the questionnaire was excluded from the current version as constraints imposed by the ethical committee approving this study meant this information could not be collected (it was felt that asking about the sexual orientation of elderly and possibly deceased relatives may cause distress to participants). All participants provided informed consent and all procedures were approved by the University of East London Ethical (Research) Committee.

Results

Participant characteristics

There was no significant age difference between heterosexual and homosexual men, $t(300) < 1$. The mean age of heterosexual men was 33.79 years ($SD = 12.49$) and the mean age of homosexual men was 33.52 years ($SD = 9.21$). There was no significant group difference in years spent in full-time education since the age of 5 years, $t(297) = -1.93$. The mean number of years spent in education by heterosexual men was 14.77 ($SD = 3.12$) and 15.51 ($SD = 3.43$) by homosexual men. For the analysis of

ethnicity, there were too few cases (<5) in some cells to permit meaningful χ^2 analysis and therefore the data were collapsed into “white” and “non-white” categories. There were more non-white participants among heterosexuals than among homosexuals, $\chi^2(1) = 17.44$, $p < .01$. The frequencies for heterosexual men were 102 whites and 53 non-whites (21 Blacks, 20 South Asians, 1 East Asian, 0 Hispanic, and 11 Others) while for homosexual men there were 127 whites and 20 non-whites (2 Blacks, 6 South Asians, 3 East Asians, 4 Hispanics, and 5 Others). Parental SES variables “personal service occupations” and “sales and customer service occupations” were collapsed due to one cell having <5 cases and the analysis revealed no significant group differences, $\chi^2(7) = 11.53$, ns . For the entire sample, total family size (sum of each proband’s uncles, aunts, first cousins, siblings, nephews and nieces, and own children) was significantly higher among non-whites ($M = 41.42$, $SD = 33.00$) than whites ($M = 17.46$, $SD = 14.31$), $t(300) = -8.72$, $p < .01$. There was no significant difference (using one-way ANOVA) as a function of parental SES, $F(7, 278) < 1$. Subsequent analyses were separated by ethnic group.

Homosexuality in Relatives

We summed the number of relatives who were reported to be homosexual for paternal line male relatives (paternal uncles, male cousins through paternal uncles and aunts), paternal line female relatives (paternal aunts, female cousins through paternal uncles and aunts), maternal line male relatives (maternal uncles, male cousins through maternal uncles and aunts), and maternal line female relatives (maternal aunts, female cousins through maternal uncles and aunts).

Non-parametric Mann–Whitney U tests were used because the data were non-normally distributed and could not be corrected following the application of square root and logarithmic transformations. The analysis showed that both white and non-white homosexual men had a significant excess of homosexual maternal line male relatives compared to white and non-white heterosexual men ($U = 3277.50$, $p = .02$, and $U = 198.00$, $p = .01$, respectively; see Tables 1 and 2). Comparisons for the other classes of homosexual relatives were not significant (all $ps > .05$). Note that the mean rate of homosexuality in all groups of relatives was higher for homosexual men, except for paternal line female relatives and maternal line female relatives in non-white homosexual men, bearing in mind the small N ’s here for the non-white probands (Tables 1 and 2). There were no significant differences between white and non-white heterosexual and homosexual men in the numbers of reported homosexual children, siblings, nephews or nieces (all $ps > .05$).

Familial fecundity

Following Camperio-Ciani et al.’s (2004) pedigree analysis, we calculated fecundity rates for the following relative classes (Tables 3 and 4): mothers (the number of siblings and the number of siblings’ children, i.e., nephews and nieces); maternal aunts (maternal male and female cousins through aunts); maternal uncles (maternal male and female cousins through uncles); maternal grandparents (cumulative fecundity of mothers, maternal aunts and maternal uncles); paternal aunts (paternal male and female cousins through aunts); paternal uncles (paternal male and female cousins through uncles); and paternal grandparents (cumulative fecundity of fathers, paternal aunts and

Table 1 Means, SDs, and frequencies for maternal and paternal line homosexual relatives of white probands

Variable	Heterosexual				Homosexual				Cohen’s d^e
	M	SD	Homosexual/ total	% homosexual	M	SD	Homosexual/ total	% homosexual	
Homosexual paternal line male relatives ^a	0.12	0.47	6/72	3.7	0.28	0.76	17/92	10.4	.25
Homosexual paternal line female relatives ^b	0.09	0.53	3/61	2.1	0.17	0.44	13/85	8.9	.16
Homosexual maternal line male relatives ^c	0.08	0.39	4/74	2.3	0.19	0.46	17/100	9.8	.25
Homosexual maternal line female relatives ^d	0.01	0.11	1/70	0.6	0.06	0.25	6/87	3.8	.25

^a $U = 2979.50$, $p > .05$

^b $U = 2296.00$, $p > .05$

^c $U = 3277.50$, $p < .05$

^d $U = 2878.50$, $p > .10$

^e Cohen’s d was calculated as $(M_1 - M_2) / ((SD_1 + SD_2) / 2)$

Table 2 Means, SDs, and frequencies for maternal and paternal line homosexual relatives of non-white probands

Variable	Heterosexual				Homosexual				Cohen's d^e
	M	SD	Homosexual/ total	% homosexual	M	SD	Homosexual/ total	% homosexual	
Homosexual paternal line male relatives ^a	0.04	0.20	2/45	3.2	0.17	0.39	3/17	4.8	.41
Homosexual paternal line female relatives ^b	0.09	0.36	3/44	5.2	0.00	0.00	0/14	0.7	.35
Homosexual maternal line male relatives ^c	0.07	0.34	2/41	3.7	0.46	0.87	4/13	7.4	.59
Homosexual maternal line female relatives ^d	0.04	0.21	2/42	3.7	0.16	0.57	1/12	1.9	.27

^a $U = 332.00, p > .05$

^b $U = 287.00, p > .10$

^c $U = 198.00, p < .05$

^d $U = 242.00, p > .10$

^e Cohen's d was calculated as $(M_1 - M_2) / ((SD_1 + SD_2) / 2)$

Table 3 Reported maternal and paternal line fecundities of white probands' relatives

Relative Class	Heterosexuals			Homosexuals			U	p	Cohen's d^a
	N	M	SD	N	M	SD			
Mothers	453	4.44	8.09	476	3.74	3.62	6391.50	<i>ns</i>	.11
Maternal aunts	185	3.18	2.65	335	4.92	3.59	1316.00	<.01	.55
Maternal uncles	182	3.50	4.88	253	3.51	3.25	1824.00	<i>ns</i>	.00
Maternal grandparents	820	8.03	11.78	1064	8.37	7.07	5986.00	<i>ns</i>	.03
Paternal aunts	162	3.52	3.22	333	4.82	4.39	1314.00	<i>ns</i>	.33
Paternal uncles	202	3.74	2.91	326	4.59	4.25	1677.50	<i>ns</i>	.23
Paternal grandparents	817	8.00	9.22	1135	8.93	8.43	5923.00	<i>ns</i>	.10

^a Cohen's d was calculated as $(M_1 - M_2) / ((SD_1 + SD_2) / 2)$

paternal uncles). Sibling sex composition (numbers of male and female older and younger siblings) and total family size were also examined.

Mann–Whitney U tests were used because the data were non-normally distributed and could not be corrected following the application of square root and logarithmic

transformations. Table 3 shows that, for whites, the maternal aunts of homosexual men had significantly higher fecundity than the maternal aunts of heterosexual men. Comparisons for other relative classes, total family size, and sibling sex composition variables were not significant. In contrast, Table 4 shows that, for non-whites, the moth-

Table 4 Reported maternal and paternal line fecundities of non-white probands' relatives

Relative Class	Heterosexuals			Homosexuals			U	p	Cohen's d^a
	N	M	SD	N	M	SD			
Mothers	731	13.79	16.64	88	4.40	4.75	295.50	<.01	.76
Maternal aunts	308	8.55	7.78	71	7.10	4.77	173.00	<i>ns</i>	.22
Maternal uncles	343	8.57	7.83	43	4.30	3.97	134.50	<i>ns</i>	.68
Maternal grandparents	1382	26.07	19.76	202	10.10	8.46	245.00	<.01	1.05
Paternal aunts	303	7.97	7.97	40	3.63	3.44	118.50	.02	.70
Paternal uncles	395	10.39	8.62	69	4.92	3.56	163.00	.03	.82
Paternal grandparents	1429	26.96	23.75	197	9.85	6.08	241.00	<.01	.98

^a Cohen's d was calculated as $(M_1 - M_2) / ((SD_1 + SD_2) / 2)$

ers, maternal grandparents, paternal aunts, paternal uncles, and paternal grandparents of heterosexual men had significantly higher fecundities than those of homosexual men (the comparisons for the remaining relative classes were non-significant). Non-white heterosexual men also had significantly greater total family size, and greater numbers of younger brothers and younger sisters than did homosexual men (Tables 5 and 6).

Discussion

The current data showed elevated numbers of homosexuals in the maternal line of homosexual compared to heterosexual men, irrespective of ethnicity, supportive of the hypothesis that maternally inherited factors may be involved in human male homosexuality. The data also suggest that female line fecundity factors may favor male homosexuality insofar as one class of females (maternal aunts) in the maternal lines of homosexual men were significantly more fecund than those in the maternal lines of heterosexual men. However, this finding was observed in white men only. In contrast, five out of the seven main classes of relatives of non-white heterosexual men were significantly more fecund than those of non-white homosexual men. However, note the small sample sizes for the non-white group.

The present study was somewhat consistent with past studies in suggesting elevated rates of homosexuality among maternal line relatives of homosexual probands, which supports the notion that X-linked genetic factors influence male sexual orientation (Camperio-Ciani et al., 2004; Hamer et al., 1993; Hu et al., 1995). However, this study was also inconsistent with others showing no such effects (Bailey et al., 1999; McKnight & Malcolm, 2000) but which have reported elevated rates of homosexuality in the siblings of homosexual men, a pattern not demonstrated here. The current study had a total sample size higher than other studies, although falling short of one reporting null findings in three carefully selected samples used to limit ascertainment bias (Bailey et al., 1999). The rate of reported homosexuality in relatives was marginally higher here than those reported in previous studies, and also consistently higher for certain classes of relatives among the homosexual men. This raises the possibility that the estimates of familial homosexuality are biased in some way depending on proband sexual orientation even though the questionnaire and instructions were designed to tap certain or near certain estimates.

Heterosexual probands may underreport homosexuality due to their limited knowledge of homosexuality among their relatives while homosexuals may over report because of sensitivity to certain behavioral indicators of homosexuality in relatives (e.g., gender nonconformity) or because

Table 5 Sibling sex composition and total family size of white probands

Relative class	Heterosexuals			Homosexuals			<i>U</i>	<i>p</i>	Cohen's <i>d</i> ^a
	<i>N</i>	<i>M</i>	<i>SD</i>	<i>N</i>	<i>M</i>	<i>SD</i>			
Older brothers	54	0.52	0.87	71	0.55	0.82	6208.00	<i>ns</i>	.03
Older sisters	57	0.55	1.11	62	0.49	0.79	6361.50	<i>ns</i>	.06
Younger brothers	59	0.57	0.83	53	0.42	0.77	5562.00	<i>ns</i>	.18
Younger sisters	43	0.42	0.69	51	0.40	0.61	6312.00	<i>ns</i>	.03
Total family size	1665	16.32	15.80	2334	18.37	12.97	5701.00	<i>ns</i>	.14

^a Cohen's *d* was calculated as $(M_1 - M_2) / ((SD_1 + SD_2) / 2)$

Table 6 Sibling sex composition and total family size of non-white probands

Relative Class	Heterosexuals			Homosexuals			<i>U</i>	<i>p</i>	Cohen's <i>d</i> ^a
	<i>N</i>	<i>M</i>	<i>SD</i>	<i>N</i>	<i>M</i>	<i>SD</i>			
Older brothers	43	0.81	1.05	12	0.60	0.82	484.00	<i>ns</i>	.22
Older sisters	45	0.84	1.13	9	0.45	0.60	456.50	<i>ns</i>	.43
Younger brothers	62	1.16	1.41	4	0.20	0.41	278.00	<.01	.92
Younger sisters	75	1.41	1.59	15	0.75	1.48	343.00	<.05	.42
Total family size	2596	48.98	35.21	428	21.40	12.38	257.50	<.01	1.04

^a Cohen's *d* was calculated as $(M_1 - M_2) / ((SD_1 + SD_2) / 2)$

the homosexual men recruited were more self-accepting and open about their sexuality. Generally, reporting on the sexuality of distant relatives is likely to be less accurate. Thus, future work must include methods for ensuring the validity of family history data (such as matching proband's responses with a percentage of those reported by their actual relatives). However, it is unclear why any reporting biases should result in an excess reporting of maternal than paternal line male relatives as demonstrated here and in previous work (Camperio-Ciani et al., 2004; Hamer et al., 1993; Hu et al., 1995).

The observed differences in fecundity patterns in white men were broadly consistent with three studies also showing elevated female line fecundity in the relatives of homosexual men (Camperio-Ciani et al., 2004; McKnight & Malcolm, 2000; Turner, 1995). Nonetheless, the findings for whites were inconsistent with one other British study reporting greater general familial fecundity in white homosexual compared to heterosexual men (King et al., 2005) and with Camperio-Ciani et al. (2004) in that the effect was specific to fecundities for one class of relative, namely, maternal aunts. While our sample was larger and more carefully ascertained than the three studies demonstrating female line effects, it was smaller in comparison to King et al. (2005) and this may explain some of the inconsistency with that study.

Another source of inconsistency with previous work as gleaned from our data was ethnicity. If we take the pattern of findings to suggest that genetic factors transmitted in the maternal line increase both the probability of being homosexual in males and increase fecundity through the female line, our data may also suggest that this occurs in white males only. This limits the relevance of evolutionary accounts of male homosexuality to specific ethnic populations and suggests that threshold liability models must factor in ethnic group variables (and not simply exclude non-white samples from the analysis). While speculative, it is possible that maternally-linked inherited factors may increase the probability of homosexuality in males irrespective of their ethnic group (consistent with the current data) but that these factors may not extend to promoting female fecundity in non-white populations. This mitigating influence is by no means assumed to be genetic and could be due to differentials in the behavioral ecology of the populations in question (e.g., marriage patterns, parental influences over reproduction, differences in offspring viability, and familial contributions to child care as a function of family size; Coleman, 1994), which may explain the observation that non-white heterosexual men showed elevated familial fecundity compared to non-white homosexual men. In the UK, some of the groups categorized under non-whites here (i.e., Black, South Asian, and East Asian), and who were part of the “first generation” of immigrants

to the UK following the end of World War II, tend to marry earlier, reproduce earlier, and have marginally larger numbers of offspring than their white counterparts (Coleman & Salt, 1992). Whether this pattern appears in subsequent UK-born generations of the groups in question is yet to be determined. At this stage, we have no way of knowing exactly how such “ecological” differences map onto to sexual orientation-related variation in familial composition. The findings were also consistent with one further study reporting elevated fecundity in heterosexuals compared to homosexuals (as reported by their parents) from North America although the ethnic composition of that study was not described (Widmayer & Ellis, 2005).

While the present study had some advantages over previous work in terms of sample size and the examination of ethnicity, several limitations are worthy of note. It is possible that reporting biases between men of different sexual orientations and ethnic groupings explain why non-white heterosexuals reported more relatives, although it is unclear why this should be. Equally, there is no a priori reason why non-white homosexual men should report fewer relatives overall and yet more maternal line male homosexual relatives. Given low numbers of non-whites in both groups of men, the findings must be interpreted with caution until further work in larger samples is done. We were also unable to replicate the well-established FBO effect of male homosexuality (Blanchard, 2004). This suggests that the sample was mildly anomalous with regard to sibling sex composition although this appears true for both heterosexual and homosexual men. While this may be a limitation, the potential confound of homosexuals coming from slightly larger families than heterosexuals due to a FBO effect would not operate here.

In conclusion, if maternally inherited factors are involved in male homosexuality and aid in promoting female fecundity, then they appear to depend on ethnicity. The data indicate that specific familial-related reproductive differentials were associated with male homosexuality, which may offset the deleterious fitness effects of having a family member with the trait, at least in white ethnic groups. We suggest that population-level investigations are now needed in order to examine the contribution of ethnicity more fully and to triangulate the data obtained from the smaller comparative studies conducted thus far.

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