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Models and Better Evidence Needed to Clarify Causality: A Response to Bailey, Ellingson, and Bailey (2014)

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In a Commentary on our article (Roberts, Glymour, & Koenen, 2013), Bailey, Ellingson, and Bailey (2014) hypothesized that a set of genes influencing sexual orientation also affect neuroticism and thereby risk of divorce, risk of having a stepparent, and risk of experiencing childhood maltreatment. They invoked evidence from twin studies to propose that each link in such a causal structure is, if not actually *supported* with evidence, at least not impossible given existing evidence. We are disappointed that Bailey et al. did not take up our invitation to propose a specific data-generating structure that could produce the associations found in the National Epidemiologic Survey on Alcohol and Related Conditions (NESARC) data. Without a specific data-generating model, it is not possible to evaluate whether such a structure is plausible.

We highlight as particularly unlikely three assumptions required to demonstrate the associations found in the NESARC data under Bailey et al.'s proposed causal structure. First, the Bailey et al. hypothesis requires that a set of genetic variants exists that substantially increases likelihood of both minority sexual orientation and neuroticism. Bailey et al. cited only two studies, by the same investigators, that support this possibility (Zietsch, Verweij, Bailey, Wright, & Martin, 2011; Zietsch et al., 2012). Zietsch et al. (2011) defined participants as non-heterosexuals if they described their sexual feelings as anything other than “exclusive attraction to the opposite sex.” The majority (59%) of non-heterosexuals in this sample scored a 1 on the Kinsey Scale, describing themselves as “predominantly heterosexual, only incidentally homosexual.” The study found that people who reported exclusive heterosexuality were less likely to be neurotic than those who reported other values (although the relationship was markedly non-linear: the lowest average neuroticism of all groups was among people who reported a Kinsey score of 4). The study then reported an r of 0.25 between the inferred (via a bivariate Cholesky decomposition) genetic predictors of sexual orientation and genetic determinants of neuroticism. In their second study, Zietsch et al. (2012) found evidence of shared genetic causes of depression and non-heterosexuality. However, this study also found that depression and non-heterosexuality shared environmental causes, namely, sexual abuse in childhood and risky childhood family

environments. These findings would appear to support, rather than refute, our own conclusions.

The second highly implausible assumption required in our data simulations to obtain the associations found in the NESARC data under Bailey et al.'s hypothesis is that the relevant gene or set of genes—if they exist at all—increase likelihood of minority sexual orientation and neuroticism to the same degree. Homosexuality and neuroticism are not phenotypically similar. Even studies of outcomes that are phenotypically similar—namely, neuropsychiatric disorders—do not suggest that risk alleles have similar associations with diverse outcomes. Recent analyses by the Psychiatric Genomics Consortium of polygenic risk scores for autism spectrum disorder, attention deficit-hyperactivity disorder, bipolar disorder, major depressive disorder, and schizophrenia do not support the assumption of highly similar effect sizes across even these phenotypically similar outcomes (Cross-Disorder Group of the Psychiatric Genomics Consortium, 2013). This meta-analysis included data from more than 60,000 people and found that polygenic risk scores for one disorder, while often statistically significantly associated with other disorders, nevertheless predicted risk of other disorders to highly varying degrees (see (Cross-Disorder Group of the Psychiatric Genomics Consortium, 2013, Fig. 3). The study concluded that “accumulating evidence...suggests that *some* genetic risk factors are shared between neuropsychiatric disorders...Our results suggest a diversity of findings, with some SNPs showing diagnostic specificity and others pleiotropic effects on two or more of the five disorders” (emphasis added). Thus, far from having the same effect across disorders, some alleles had no shared effects at all.

Third, to obtain the associations present in the NESARC data using Bailey et al.'s hypothesis, it was necessary to assume that maternal neuroticism accounted for 50% of the risk of having a stepparent by age 5. It is extremely implausible that maternal neuroticism accounted for 50% of the risk of having a stepparent by age 5. As many other characteristics of both husbands and wives have been identified as predictors of divorce (e.g., income, education, occupation, religiosity, age at marriage, attitudes toward marriage, and other personality traits such as extraversion (Amato, 1996; Clarke & Berrington, 1999; Roberts, Kuncel, Shiner, Caspi, & Goldberg, 2007), the evidence does not support a hypothesis that half the risk of having a stepparent could be caused by a single maternal personality trait, whether directly or indirectly. In fact, the 1996 study of personality and divorce cited by Bailey et al. estimated that personality (all aspects, not just neuroticism) in both spouses (not just the woman) accounted for perhaps 25% of the risk of divorce (Jocklin, McGue, & Lykken, 1996).

Finally, we note that these combinations of assumptions entail the seemingly contradictory requirement that women who carried the neuroticism/homosexuality risk allele(s) nonetheless married men, not once, but twice (thus giving their children a stepparent). While minority sexual orientation in women may have increased the likelihood of divorce in the exclusively heterosexual marriages that existed during the decades in which the NESARC participants were children, it does seem unlikely that minority sexual orientation would lead to a second heterosexual marriage within a very brief time.

In short, although Bailey et al.'s alternative hypothesis has not been conclusively disproven, it rests on speculative interpretations of existing gaps in the evidence. We mentioned here three unlikely assumptions required in our data simulations of Bailey et al.'s hypothesis. Bailey et al. have declined to propose a specific data-generating structure that could account for the observed empirical evidence, and we suspect that any such structure would entail highly implausible assumptions.

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