Genetic Homophily in Adolescent Friendship Networks

Ramina Sotoudeh

Across a wide range of behaviors and social relations, individuals with similar attributes are more likely to form ties (McPherson et al., 2001). The network literature is replete with examples of behavioral homophily, whether in adolescent friendship networks (Kandel, 1978) or managerial networks (Ibarra, 1995), and a large interdisciplinary effort has gone towards developing tools for adjudicating between the fundamental mechanisms which produce it (Goodreau, Kitts, and Morris, 2009).

While phenotypic homophily is well-studied, only recently have scholars begun to study its genotypic counterpart. Though it is early days, genotypic homophily also appears to be widespread. In the literature on assortative mating, scholars have found that spouses are more alike across a wide range of genotypic risk scores, including educational attainment, depression and height than two randomly selected individuals (Conley et al. 2016; Domingue et al. 2014).

Genotypic homophily is commonly observed in friendship networks as well. Within a school context, those who are friends tend to have similar genotypes at the genotypic level as well as on an allelic level (Christakis & Fowler 2011; Domingue et al. 2018). Some of this association is due to macro-level forces such as historical migration patterns, some of it can be attributed to meso-level mechanisms such as neighborhood and school choice, while some of it still is best explained by individual-level processes, such as preferences for selecting friends who resemble the individual (Domingue et al. 2018). These studies have moved the treatment of genetic homophily in the social genetics literature away from seeing it as simply a confounding factor when estimating social genetic (sometimes referred to as metagenomic) effects (Sotoudeh, Conley & Harris, 2017; Domingue & Belsky 2017) or simply estimating heritability in the case of assortative mating towards an interesting social and biological outcome in its own right, one which is influenced by a range of complex social and biological processes.

This study builds on this very important work by using The National Longitudinal Study of Adolescent to Adult Health (Add Health) to look at the conditions under which people with similar genotypes are more or less likely to form friendships. We measure genetic homophily at the school-level for smoking, educational attainment and age at menarche polygenic scores. We then leverage cultural, institutional, and contextual variation at the school-level in order to evaluate that factors that make observing genetic homophily on these different risk scores more likely. We examine a range of mechanisms, including institutional incentive structures (i.e. penalties for smoking), social norms (i.e. the extent to which getting good grades is seen as a desirable personal trait by peers) and material availability of resources (i.e. access to cigarettes or sexual partners), which may induce or attenuate genetic homophily.

Although we would expect genetic homophily to go through behavioral homophily, looking at genetic homophily allows us to understand the non-linear thresholds at which contextual factors allow individuals to "act on" their genes or act in response to others' genes. Under this framework, the meaning that genes will have, and the actionability they will have in relational settings, will be governed by the ways in which the context shapes their expression.

The results of this study have implications for policy interventions. Specifically, the results help scholars and policy makers build better understand the institutional settings in which genetic predispositions to engage in unhealthy or risky behaviors (such as smoking and adolescent sexual behaviors) are negated and to thereby build better and more equitable social structures.

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