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Genes, Roommates, and Residence Halls: A Multidimensional Study of the Role of Peer Drinking on College Students' Alcohol Use

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Abstract

Background: Peer drinking is one of the most robust predictors of college students' alcohol use and can moderate students' genetic risk for alcohol use. Peer effect research generally suffers from two problems: selection into peer groups and relying more on perceptions of peer alcohol use than peers' self-report. The goal of the present study was to overcome those limitations by capitalizing on a genetically-informed sample of randomly assigned college roommates to examine multiple dimensions of peer influence and the interplay between peer effects and genetic predisposition on alcohol use, in the form of polygenic scores.

Methods: We used a subsample (n = 755) of participants from a university-wide, longitudinal study at a large, diverse, urban university. Participants reported their own alcohol use during fall and spring and their perceptions of college peers' alcohol use in spring. We matched individuals into their rooms and residence halls to create a composite score of peer-reported alcohol use for each of those levels. We examined multiple dimensions of peer influence and whether peer influence moderated genetic predisposition to predict college students' alcohol use using multilevel models to account for clustering at the room and residence hall level.

Results: We found that polygenic scores (β = .12), perceptions of peer drinking (β = .37), and roommates' self-reported drinking (β = .10) predicted alcohol use (all ps < .001), while average

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alcohol use across residence hall did not (β = −.01, p = .86). We found no evidence for interactions between peer influence and genome-wide polygenic scores for alcohol use.

Conclusion: Our findings underscore the importance of genetic predisposition on individual alcohol use and support the potentially causal nature of the association between peer influence and alcohol use.

Keywords

Alcohol; College Students; Peer Drinking; Genetic Predisposition; Gene-Environment Interaction

College students engage in high rates of alcohol use and suffer a variety of alcohol-related consequences (Hingson et al., 2009). In 2015, 58.0% of college students reported drinking alcohol and 37.9% reported engaging in binge drinking during the past month (National Institute on Alcohol Abuse and Alcoholism, 2017). Alcohol misuse is associated with a variety of negative consequences, including memory blackouts (Hingson et al., 2009; Wechsler et al., 2000; Wilhite and Fromme, 2015), unplanned sexual encounters (Hingson et al., 2009; Townshend et al., 2014; Wechsler et al., 2000), physical and sexual victimization (Hingson et al., 2009), legal trouble, personal injuries (Hingson et al., 2009; Wechsler et al., 2000), and death (Hingson et al., 2009). College students who engage in binge drinking are also more likely than those who do not binge drink to fall behind in their classes (Wechsler et al., 2000), and those who do not binge drink may suffer from secondhand effects of alcohol use, such as disrupted sleep or study (Boekeloo et al., 2009; Wechsler and Nelson, 2008). Given the prevalence of alcohol misuse and the associated potential ramifications, it is critical to identify modifiable risk factors associated with alcohol use among college students.

Peer Influence on Alcohol Use

Peer drinking is one of the most robust predictors of alcohol misuse among college students (Perkins, 2002), as peer influences become increasingly important during late adolescence and emerging adulthood (Arnett, 2000; Perkins, 2002). Studies of peer influence on individuals' alcohol use consistently find that higher peer drinking is associated with higher levels of one's own use (see Borsari and Carey, 2001, and Borsari et al., 2007 for review). The most commonly used measure of peer drinking is asking individuals about their perceptions of their peers' alcohol use (Borsari et al., 2007; Perkins, 2002). Perceptions of peer use are especially salient during the first year of college, as new students turn to and observe their peers for cues about normative alcohol use behaviors (Borsari et al., 2007). This method of measuring peer influence is easy to capture through self-report surveys. However, one major drawback of this method is that perceptions of peer drinking may not accurately reflect actual peer-reported drinking. Some findings indicate that individuals tend to overestimate the extent to which their peers drink (Perkins, 2002; Wechsler and Kuo, 2000). Those who drink more (Baer, 1994; Borsari et al., 2007) and engage in riskier patterns of use (Wechsler and Kuo, 2000) also tend to have more inflated perceptions of peer use. Other studies, however, found no significant difference between perceptions and peer-reported drinking (Bauman and Fisher, 1986; Deutsch et al., 2015).

Another, less common, method of measuring peer influence is to ask peers directly about their own alcohol use (Borsari et al., 2007; Perkins, 2002). Peer-reported drinking is more often used in social network analyses to provide a more accurate estimation of the normative alcohol behaviors (Bauman and Ennett, 1996; Deutsch et al., 2015), which play a role in shaping both perceptions of peer alcohol use and individuals' own alcohol use (Perkins, 2002). Measuring peer influence via peer-reported drinking provides the opportunity to collect data directly from the source; however, it is often more difficult to collect for this same reason. Despite substantial research showing that both perceptions of peer alcohol use (Borsari et al., 2007; Borsari and Carey, 2001; Perkins, 2002) and peer-reported alcohol use (Carter et al., 2010; O'Hare, 1997; Wechsler and Kuo, 2000) are associated with higher levels of one's own drinking, few studies examine these multiple measures of peer influence simultaneously.

College is a unique setting in that individuals who are entering a critical developmental period are surrounded by an entire community of their peers. Living in on-campus housing is associated with increases in alcohol consumption (Carter et al., 2010; Cross et al., 2009; O'Hare, 1990), but the community in which a student lives can impact the extent to which alcohol consumption increases (Wechsler and Nelson, 2008). College student alcohol initiation and consumption can vary greatly depending on contextual factors that shape a college's drinking culture, such as college location, alcohol outlet density, social affiliations (e.g., Greek life), type of institution, residence hall configurations, and level of supervision (Borsari et al., 2007; Wechsler and Nelson, 2008). In light of the various factors that can influence the drinking culture at a given college, it is important to consider the community in which students live when studying alcohol use.

Peer influence on college student alcohol use is a complex factor. First, it is difficult to determine the nature of the association (i.e., correlational versus causal) between peer influence and alcohol. We know that homophily occurs among heavy drinkers, such that heavy-drinking individuals are more likely to self-select into peer groups whose members hold similar values, beliefs, attitudes, and interests toward substance use (Kandel, 1978; Oetting and Donnermeyer, 1998). This pattern of self-selection based on homophily persists across development, as college students tend to recreate their high school peer group in the college environment. Individuals who associated with substance-using peers in high school self-select into substance-using peer groups in college (Kendler et al., 2015). It is thus unclear if affiliation with heavy-drinking peers is causally related to an increase in college students' own alcohol use.

Because association with peers who use substances is relatively stable, it is possible that peer influence on alcohol use in college students may simply reflect confounded selection processes, whereby individuals with externalizing predispositions select into more deviant peer groups (Kendler et al., 2015). Much of the prior literature on peer group influence has been unable to directly test the causal versus correlational nature of this relationship due to this self-selection aspect. The random assignment of college roommates represents an opportunity to overcome this limitation through a natural experimental design. In contrast to previous work, studying randomly assigned roommate pairs reduces the confounding

influence of self-selection into peer groups on alcohol use, and increases confidence in potential conclusions about the causal association between peer influence and alcohol use.

Second, we know that individuals are not equally susceptible to the effects of peer influences. Genetic influences play a significant role in alcohol use outcomes (Hart and Kranzler, 2015; Verhulst et al., 2015), and appear to increase in importance under particular high-risk environmental conditions (Dick et al., 2007; Harden et al., 2008; Kendler et al., 2011). Proximal peer substance use is a consistent environmental moderator of genetic influences on alcohol use, with genetic factors accounting for more variance in alcohol use in environments with more substance-using peers (Dick et al., 2007; Kendler et al., 2011; Latendresse et al., 2011). Considering the increasing importance of peers during emerging adulthood (Arnett, 2000; Perkins, 2002), genetic influences may be more pronounced for those who associate with deviant peers (Dick et al., 2007; Harden et al., 2008; Kendler et al., 2011).

Few studies of gene by environment interactions have examined peer effects as a moderator of genetic predisposition among college students, and of those, most focused primarily on candidate genes (Guo et al., 2015). However, candidate gene approaches no longer reflect the state of the science, as they have not replicated in large-scale studies (Duncan and Keller, 2011). Alcohol use behaviors are genetically complex, in that they are influenced by many genetic variants of small effects (Dick and Agrawal, 2008; Hart and Kranzler, 2015; Plomin et al., 2009); thus, there is a need to move beyond candidate genes. Genome-wide association studies (GWAS) reflect the current state-of-the-science approach to identify genetic variants associated with a phenotype. In particular, GWAS allow researchers to calculate genome-wide polygenic scores (GPS), which are aggregate scores created by summing the number of “risk” (i.e., trait-associated) alleles an individual carries, weighted based on information from an independent discovery sample, typically using regression coefficients (Bogdan et al., 2018; Salvatore et al., 2014).

The current design provided us with a unique opportunity to study multiple dimensions of peer influence on college students’ alcohol use within a genetically-informed, university-wide study, Spit for Science. As part of this study, participants responded to baseline and follow-up surveys and were given the opportunity to provide salivary DNA samples. From the DNA samples, we were able to calculate GPS for alcohol consumption as our measure of genetic propensity. Through collaboration with our university, we used university records to match Spit for Science participants with their roommates and group them within their residence halls. We then measured and operationalized peer influence in three different ways: target individuals’ perceptions of their college peers’ drinking; their roommates’ self-reported drinking; and the average of the self-reported drinking of all individuals living in the target’s residence hall. Finally, we limited our sample to participants who lived with a randomly assigned roommate to eliminate the effects of self-selection into peer groups. The structure of our study allowed us to examine peer influence while addressing a number of the limitations of prior research in this area.

Hypotheses

In the present study, we examined the associations between peer influence and alcohol use and whether peer influence moderated genetic predispositions (indexed using a genome-wide polygenic score) to predict alcohol use. We had two primary hypotheses, which were pre-registered with the Open Science Framework at osf.io/5phvu/:

1. Higher polygenic scores, perceptions of peer drinking, roommate drinking, and residence hall drinking would predict higher levels of alcohol use.
2. The association between polygenic scores and alcohol use would be stronger for individuals who perceived their peers as drinking more, whose roommates report drinking more, and who lived in a residence hall with residents who report drinking more.

Method

Participants

Data come from the Spit for Science project, a university-wide initiative focused on college students' substance use and behavioral health outcomes at a large, urban four-year university (Dick et al., 2014). The Spit for Science project launched in fall 2011 and new cohorts of freshmen were recruited in 2012, 2013, and 2014, resulting in four cohorts as of spring 2017. All incoming freshmen over age 18 were invited to participate in a baseline survey at the beginning of the fall semester (i.e., August) and were given the opportunity to provide a DNA (saliva) sample. Participants were invited to complete follow-up surveys every subsequent spring semester around February to March. Study data were collected and managed using REDCap electronic data capture tools hosted at Virginia Commonwealth University (Harris et al., 2009). REDCap (Research Electronic Data Capture) is a secure, web-based application designed to support data capture for research studies, providing 1) an intuitive interface for validated data entry; 2) audit trails for tracking data manipulation and export procedures; 3) automated export procedures for seamless data downloads to common statistical packages; and 4) procedures for importing data from external sources. The full sample included 9,923 participants whose demographic makeup is comparable to that of the larger student body (Dick et al., 2014).

We used university records and Spit for Science data to first match all participants into their rooms and residence halls. Next, we retained participants in our analytic sample if they met the following inclusion criteria: provided genetic data; lived with a randomly assigned roommate; lived in the same on-campus housing with the same roommate for both the fall and spring semester of freshman year; lived with a roommate who was also a participant in the Spit for Science study. Approximately 48.7% of participants who met all other inclusion criteria (n = 4,128) lived with one or more randomly assigned roommates during their freshman year. Roommates were randomly assigned by Residential Life and Housing using a computer algorithm that matched students based on responses to basic lifestyle questions (e.g., general cleanliness, preference for staying up late). Only cohorts one through three were included in the present study because genotypic data for cohort four was not available at the time of analysis. Participants self-reported whether they were randomly assigned a

roommate during the fall semester of freshman year, with the exception of cohort one for whom this question was only asked in the spring.

Based on the inclusion criteria above, the analytic sample included 755 participants (367 roommate pairs and 7 triples). The analytic sample was comprised of 65.70% females, 34.04% males, and 0.26% who did not provide sex information. Approximately half (51.52%) of all participants self-identified as White, followed by 25.43% who identified as Black, 12.05% as Asian, 4.77% as more than one race, 4.77% as Hispanic/Latino, 0.53% as another race/ethnicity, and 0.93% of participants chose not to report or had missing race/ethnicity data. The mean age of participants was 18.47 years (SD = .33). The number of individuals sharing a room ranged from two to three (M = 2.03, SD = .16).

Measures

Perceptions of peer alcohol use.—Perceptions of peer use was one of our predictors of college students' drinking. Perceptions of peer drinking was calculated as an individual-level composite score based on questions asked during spring of freshman year regarding how many college friends the target individual perceives had (1) "drunk alcohol," (2) "got drunk," and (3) "had problems with alcohol (like hangovers, fights, accidents)." College friends were defined as "people who you would have seen regularly and spent time with in school and outside of school" since starting college. Participants responded to each of the three stems using a Likert-type scale that ranged from one to five, with one indicating "none of my friends" and five indicating "all of my friends." Perceived peer alcohol use was calculated as the sum of the endorsed items (ranging from 3 to 15), with higher totals indicating higher levels of perceived peer alcohol use (Kendler et al., 2008).

Alcohol use.—Self-reported alcohol use was a calculated measure of the grams of ethanol consumed per month based on the consumption items from the Alcohol Use Disorders Identification Test (AUDIT-C; Bush et al., 1998). See Salvatore et al., 2016 for additional details about how this variable was calculated. This was measured for target individuals (i.e., each participant), as an average for the roommate(s) of the target individual, and as an average for the target's residence hall.

Individual alcohol use.—Target individuals' alcohol use was measured as self-reported alcohol consumption, reported separately for fall and spring. Grams of alcohol use consumed were natural log-transformed after adding a constant of one to adjust for the positive skew and to retain individuals who drank zero grams of alcohol.

Our primary outcome measure was target individuals' alcohol use in the spring. We measured this by creating residualized values of spring alcohol use to account for random variation allele frequencies across on ancestral background, which can be amplified when using genome-wide polygenic scores to make cross-ancestry predictions. Although there are greater within-group genetic differences, allele frequencies can vary across groups due to genetic drift (random variation), a phenomenon referred to as population stratification (Peterson et al., 2017; Rotimi and Jorde, 2010). If not controlled for, population stratification can result in false positives (Martin et al., 2017; Peterson et al., 2017; Rotimi and Jorde, 2010). To overcome this issue, we controlled for ancestral principal components, which

adjusts for structural genetic differences by super-population to account for the variation attributable to each ancestral group (Peterson et al., 2017).

We accounted for population stratification by including ancestry-specific principal components derived from the genetic data. Categories included those of primarily African (n = 1,069), admixed from the Americas (n = 444), East Asian (n = 426), European (n = 2,211), and South Asian ancestries (n = 367). See Peterson et al., 2017 for additional details about how principal components were derived in the Spit for Science sample. For each ancestral group, we first conducted a linear regression of the 10 standardized principal components on the centered log of spring drinking. Next, we identified the principal components associated with spring drinking for each ancestral group and extracted the spring drinking residualized values (from a multiple regression that included only the significantly associated principal components). In effect, this process created a spring drinking measure that statistically controlled for ancestry-specific population stratification. The residualized spring alcohol use variable was used as our outcome variable in all subsequent inferential analyses.

Roommate alcohol use.—As some participants lived with more than one roommate, we calculated the average alcohol consumption in the fall semester for all individuals living in a room. To utilize all available data, roommate averages were calculated using alcohol consumption data for the full Spit for Science sample. The target individual's alcohol consumption was dropped before calculating each roommate average. Grams of alcohol use were natural log-transformed after adding a constant of one to adjust for the positive skew and to retain individuals who drank zero grams of alcohol.

Residence hall alcohol use.—For residence halls, we calculated the average alcohol consumption in fall for all individuals living in a residence hall. Again, to utilize all available data, residence hall averages were calculated using alcohol consumption data for the full Spit for Science sample. The target individual's alcohol consumption was dropped before calculating each residence hall average.

Covariates.—We included the following covariates in our analyses: age, sex, self-identified race/ethnicity, cohort, count of single nucleotide polymorphisms (SNPs), and individuals' fall drinking. All covariates, with the exception of cohort and count of SNPs, were self-report measures. Participants indicated their age, sex, and self-identified race/ethnicity during the fall of their freshman year. Sex was coded as male (0) or female (1). Race/ethnicity was coded American Indian/Native Alaskan, Asian, Black/African American, Hispanic/Latino, more than one race, Native Hawaiian/Pacific Islander, White, or unknown. White was set as our reference group for all subsequent analyses. Due to small counts, we collapsed American Indian/Native Alaskan and Native Hawaiian/Pacific Islander into "Other race/ethnicity." Participants who reported their race/ethnicity as unknown or chose not to answer were categorized as "Missing." Cohort was included as a covariate because preliminary analyses (see below) revealed cohort differences in average alcohol consumption across residence halls. Cohort one was set as our reference group. The count of SNPs refers to the number available for scoring, which we included to account for variation in the number of alleles across participants (e.g., SNPs dropped as a result of quality control following imputation).

Genotyping and Polygenic Score Creation

Genotyping was performed at Rutgers University Cell and DNA Repository using the Affymetrix Biobank array (653 k variants). SNPs with a Hardy-Weinberg Equilibrium (HWE) p-value of p <= 1×10^{-6} and a minor allele frequency (MAF) of <= 0.005 were removed. Additionally, after removing palindromic SNPs (which can be ambiguous with respect to the reference allele when going across samples), there were 63,826 independent SNPs remaining for polygenic scores after quality control and linkage disequilibrium (LD) pruning. Genotypes were imputed to the 1000 genomes Phase 3 reference panel. For additional details regarding sample genotyping and quality control, see Webb et al., 2017.

Polygenic scores were constructed using summary statistics from a recent GWAS of alcohol consumption (Clarke et al., 2017). We created scores using the *clump* and *score* procedures in PLINK 1.9 (Chang et al., 2015; Purcell et al., 2007) as a linear function of the number of score alleles an individual possesses weighted by the product of the sign of the SNP effect (beta) and the negative logarithm (base 10) of the associated GWAS *p*-value. Clumping was performed with respect to the LD pattern in the 1000 Genome Phase 3 sample using a 500kb physical distance and an LD threshold of r^2 >= 0.25. Thus, the polygenic scores were constructed of SNPs that capture independent genetic association signals from the discovery GWAS. We calculated GPS at increasingly lenient *p*-value thresholds from the discovery GWAS sample ($p < .0001$, $p < 0.001$, $p < 0.01$, $p < 0.10$, $p < 0.20$, $p < 0.30$, $p < 0.40$, $p < 0.50$).

Data Analysis Plan

As our multi-ancestry sample required careful consideration and control for population stratification within each ancestral super-population, we first created residualized values of spring alcohol use that controlled for within-ancestry principal components, which we used as our outcome variable in all subsequent analyses. We then conducted a series of linear regressions for each of the GWAS discovery sample GPS thresholds to determine which one was most predictive in the full Spit for Science sample, identified by R^2, controlling for sex, self-reported race/ethnicity, and the count of SNPs (see Appendix A). The GPS that included all independent SNPs meeting a threshold of $p < .01$ in the UK Biobank discovery sample was most strongly associated with spring alcohol consumption in our sample ($\beta = .04$, $p = .01$, 95% CI: [.01, .07]). Thus, we carried forward this GPS into our main analyses, which we conducted using the final analytic sample. We tested our research questions using multilevel models with random intercepts for residence halls, and the nesting structure defined as individuals nested within rooms nested within residence halls. We used the nlme package (Pinheiro et al., 2018) to run analytic models and the MuMIn package (Bartoń, 2018) to calculate R^2 values in *R* (R Core Team, 2017). Predictor variables were centered prior to analysis.

Results

Table 1 presents the descriptive statistics and zero-order correlations for continuous and dichotomous variables. Individuals' alcohol use in fall ($M = 145.68$, $SD = 368.66$) did not significantly differ from that of their roommates ($M = 145.38$, $SD = 361.38$), $t(1185.70) =$

−0.63, $p = .531$. Asian students demonstrated a substantial increase in spring drinking compared to White students (see Table 2). In response to this somewhat surprising finding, we conducted a series of supplementary analyses to probe this increase in drinking among Asian students more specifically. First, we calculated the within-group change in alcohol consumption between fall and spring semester for Asian and White students. Next, we conducted an independent samples t-test to examine whether the increase in drinking from fall to spring differed between Asian and White students. The increase in drinking between fall and spring for those who self-identified as Asian (MDiff = .85) was larger compared to those who identified as White (MDiff = .63); however, the difference in increase between the two groups was not significant t(107.13) = 0.86, p = .390 in this simple model (i.e., without all of the other covariates included in Table 2). White students reported drinking more grams of alcohol per month (M = 209.91, SD = 467.3) upon entering college compared to Asian students (M = 77.33, SD = 252.09); thus, our results may reflect that Asian students "caught up" to their White peers in the amount of alcohol consumed by the end of their freshman year. Individuals' alcohol use in fall, perceptions of college peer alcohol use, and roommates' self-reported alcohol use in the fall were positively correlated with individuals' alcohol use in the spring. Residence hall alcohol use in the fall, however, was not significantly associated with individuals' alcohol use in the spring.

Cohort Effects and Representativeness Analyses

We first ran a series of analyses to determine whether there were any significant differences by cohort. There was a significant difference in average residence hall alcohol use between cohorts, $F(2, 752) = 60.97$, $p < .001$, with residence halls in cohort two reporting significantly more alcohol use than in cohort one ($M_{Diff} = 35.97$) and three ($M_{Diff} = 41.48$). Perceptions of peer alcohol use also significantly differed between cohorts, $F(2, 741) = 3.33$, $p = .037$, with greater perceptions of peer drinking in cohort one than in cohort two ($M_{Diff} = 0.67$). There was no evidence of cohort differences for roommate or individual alcohol use. Next, we compared the analytic sample to the full sample, but found no evidence of systematic differences on any of the key study variables. Finally, we compared participants who lived with a randomly assigned roommate to those who lived with a non-random roommate, but found no significant differences on any study variables. The full results from the cohort effects and representativeness analyses are available upon request from first author.

Association and Gene by Environment Analyses

We conducted our analyses in two stages, first examining the main effects of our hypothesized polygenic score and peer variables (Research Question 1) and then the interactions between the peer variables and the polygenic score (Research Question 2). As shown in Table 2, Model 1, having a higher polygenic score, perceiving higher levels of peer drinking, and living with a roommate who drank more in the fall were associated with higher levels of alcohol consumption in spring of freshman year. Perceptions of peer drinking was the strongest predictor of alcohol use in the spring. Polygenic score uniquely accounted for approximately 1.18% of the variation in spring drinking (semi-partial $R^2 = .01$). Fall residence hall drinking was not associated with spring alcohol use. Approximately 18.86% of the variance in individual alcohol use in spring could be explained by grouping at the

room level (ICC = .19), and 0.32% of the variance in roommate alcohol use could be explained by grouping at the residence hall level (ICC = .00). As shown in Table 2, Model 2, we observed no interactions between peer measures and polygenic score on predictions of spring drinking.

In light of concerns that gene-by-environment effects may be impacted by the potentially confounding effects of gene-by-covariate interactions (Keller, 2014), we also conducted a series of supplemental analyses to examine whether our pattern of results was robust when controlling for all 10 ancestral principal components and all gene-by-principal component interactions (see Supplementary Material). None of our effects significantly changed with the inclusion of these covariates (see Supplementary Tables 1 and 2), which guided our decision to report the results with the fewest parameters in this paper.

Discussion

Peer influences are one of the most robust predictors of drinking among college students; however, we know that both genetic predisposition and the drinking culture in which students live are also critical to consider. To that end, we capitalized on a genetically-informed, university-wide study to examine multiple dimensions of peer influence and whether peer influence moderated genetic predisposition to predict college students' alcohol use. We found partial support for our hypotheses: perceptions of more peer drinking, higher levels of roommate drinking, and higher polygenic scores were associated with higher levels of spring drinking, but alcohol consumption at the residence hall level was not associated with spring alcohol use. We found no evidence that peer influence moderated genome-wide polygenic scores.

Our findings are consistent with previous literature, suggesting the importance of peer influence (Borsari and Carey, 2001) and genetic predisposition (Dick et al., 2007; Kendler et al., 2011; Latendresse et al., 2011) on alcohol use. More importantly, however, our findings add to the literature regarding the role of roommates and residence halls on college students' alcohol use, such that alcohol use among roommates is influential, while alcohol use across residence halls is not. As all roommates were randomly assigned, we can rule out the influence of self-selection into peer groups on alcohol use as a confound. Thus, our findings support the potentially causal nature of the association between peer influence and alcohol use, a notable distinction from previous research in this area. Future replication of our findings using similar quasi-experimental designs would confirm the nature of this association.

The present findings highlight the importance of considering a multidimensional assessment of peer drinking, as both perceptions of peer drinking and roommates' own self-reported drinking independently influenced college students' alcohol use. This underscores the importance of considering both how much individuals think their peers drink and how much their peers actually drink when looking at college student alcohol use. In contrast, residence hall drinking did not significantly influence college students' alcohol use. This null finding may result from the fact that residence halls include many students living across multiple floors; thus, it is likely that students may not have much interaction with many of their peers

who live in the same residence hall. We may also be underpowered to detect differences across residence halls, as not all individuals living in a residence hall participated in the present study and there were relatively few ($n = 9$) higher level units. Additional research using multidimensional assessments of peer drinking can further inform and advance the peer influence literature.

Although we found evidence for polygenic association with alcohol use, we did not find the expected gene by environment interaction effects. Previous studies that focused on peer influence as a moderator of genetic risk used younger age groups (Dick et al., 2016, 2007; Latendresse et al., 2011); therefore, it is possible that the same effects may not apply in college students due to potential gene by environment by development effects on alcohol use. It is also possible that college itself is an extreme social environment that promotes alcohol use, which may make it difficult to distinguish the differences in genetic risk as a function of environment due to the lack of heterogeneity (Boardman et al., 2013). Finally, as previously mentioned, alcohol use behaviors are influenced by many genetic variants of small effects (Hart and Kranzler, 2015; Plomin et al., 2009); however, gene by environment interaction effects are typically even smaller (Boardman et al., 2013), underscoring the need for a larger sample to discern potential interaction effects.

Limitations

The findings from the present study should be considered in the context of its limitations. First, data were largely collected via self-report measures, which can be vulnerable to measurement error. Additionally, although we did the best we could to minimize self-report bias by reminding participants that their data was confidential, it is possible that some participants felt uncomfortable reporting their own alcohol use or perceptions of their peers' alcohol use truthfully. Second, the present study did not account for the frequency or type of interactions between individuals living in the same room or in the same residence hall. Despite living together, it is possible that roommates did not interact on a regular basis, and results may differ as a function of amount of interaction between individuals and their peers (Iannotti and Bush, 1992). Third, although perceptions of college peer alcohol use was a strong predictor of spring alcohol use, both variables were measured during the spring semester, and thus temporally confounded. Fourth, there was an imperfect match between the discovery sample used to calculate the polygenic scores, comprised entirely of individuals of European ancestry, and our sample in Spit for Science, which was more ancestrally diverse. This is problematic because power is limited when using GWAS summary statistics derived from European samples are used to make cross-ancestry predictions into non-European samples (Martin et al., 2017). As such, our polygenic risk inferences may be biased and should be interpreted with caution. Finally, the present study only included college students who lived with randomly assigned roommates. Importantly, randomly assigned roommates were matched based on responses to basic lifestyle questions, which may have resulted in some degree of self-selection, and this limits our confidence in the conclusions about the causal association between peer influence and alcohol use. Moreover, college students may differ from their non-college peers in their susceptibility to peer influence, as college students must learn and navigate new social norms upon arriving on campus. Additionally, students living with a random roommate may have a different

college experience compared to students who chose their own roommate. Thus, our findings may not generalize to the wider population.

Conclusions and Future Directions

Both peer drinking and genetic predispositions play an important role in college students' alcohol use. Peer drinking is most commonly measured via perceptions of peer drinking, and less commonly, via peer-reported drinking. Previous research rarely examined these dimensions of peer drinking simultaneously or within the context of students' genetic predisposition for alcohol use and the drinking culture in the community in which students live. Using a genetically-informed, university-wide study, we examined the associations between peer influence and alcohol use and whether peer influence moderated genetic predispositions to predict alcohol use. We found that genetic predisposition, perceptions of peer drinking, and roommates' self-reported drinking predicted alcohol use, but average alcohol use across residence hall did not. As information about the role of different groups of peers can inform and guide the implementation of prevention and intervention programs, future research should also examine the peer effects of self-selected roommates, as individuals are more susceptible to the influence of close friends (Kandel, 1978) compared to randomly paired roommates, suggesting that this is another important area of research. Future research should also examine the effects of residence floor on individual alcohol use to determine if there are intermediate effects of proximal and distal peers. Given that, contrary to previous literature, we did not find gene by environment effects on alcohol use, a gene by environment by development framework may provide better insight into whether an effect is observed in emerging adult populations. Although some college students may mature out of risky drinking (Lee et al., 2013; O'Malley, 2004), other research indicates that even after graduating from college, emerging adults continue to drink alcohol as frequently as they did while in college (Arria et al., 2016). Genetic predisposition plays an increasingly important role with age (Dick et al., 2007); therefore, future studies should examine the interplay between genetic risk and peer effects in a young adult sample. By examining these questions in young adults beyond the college years, we may better understand the ways in which peers, including cohabitating peers, may impact alcohol use and how this association changes across development.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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Appendix A

Table 1

Regression of GPS scores on spring drinking residuals

Variable	*B*	*CI*
Alc-GPS (*P* < .0001)	0.01	[−0.02, 0.04]
Alc-GPS (*P* < .001)	**0.03**	**[0.00, 0.06]**
Alc-GPS (*P* < .01)	***0.04***	***[0.01, 0.07]***
Alc-GPS (*P* < .05)	0.02	[−0.01, 0.06]
Alc-GPS (*P* < 1)	0.02	[−0.01, 0.05]
Alc-GPS (*P* < 2)	0.02	[−0.01, 0.05]
Alc-GPS (*P* < 3)	0.02	[−0.01, 0.05]
Alc-GPS (*P* < 4)	0.02	[−0.01, 0.05]
Alc-GPS (*P* < 5)	0.02	[−0.01, 0.05]
Observations	4,422	

Appendix A, Table 1: *P*-value in variable name denotes threshold from discovery sample. All continuous predictor variables were standardized and the outcome variable was standardized within ancestry. **Bold** type indicates $p <= .05$, and ***bold italic*** type indicates $p <= .01$.

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Table 1

Descriptive statistics and zero-order correlations

Variable	1	2	3	4	5	6	7	8	9	10	11
Observed minimum	–0.05	0.00	0.00	3.00	0.00	0.00	0.00	0.00	0.00	0.00	18.00
Observed maximum	0.05	5108.18	8.54	15.00	5108.18	8.54	5108.18	8.54	230.53	1.00	19.71
M	–0.01	222.25	3.40	8.78	145.68	2.56	145.38	2.65	169.57	-	18.47
SD	0.02	511.01	2.45	2.93	368.66	2.51	361.38	2.49	41.01	-	0.33
n	755	755	755	744	592	592	596	596	755	753	645
1. *Alc-GPS*	-										
2. Spring Drinking	0.02	-									
3. Spring Drinking (log)	***0.12***	***0.58***	-								
4. Perceptions of College Peer Use	0.01	***0.36***	***0.59***	-							
5. Fall Drinking	0.01	***0.60***	***0.39***	***0.28***	-						
6. Fall Drinking (log)	0.04	***0.41***	***0.68***	***0.45***	***0.60***	-					
7. Avg. Roommate Fall Drinking	–0.08	***0.22***	***0.21***	***0.18***	***0.24***	***0.23***	-				
8. Avg. Roommate Fall Drinking (log)	0.00	***0.27***	***0.28***	***0.17***	***0.22***	***0.26***	***0.59***	-			
9. Avg. Residence Hall Fall Drinking	0.01	0.06	0.01	–0.02	0.00	0.04	0.04	0.07	-		
10. Sex (0 = Male)	–0.01	***–0.19***	**–0.09**	**–0.07**	***–0.14***	–0.05	***–0.15***	–0.06	0.04	-	
11. Age	–0.06	–0.03	0.02	0.02	0.02	0.02	0.04	0.00	–0.04	**–0.10**	-

M = Mean; *SD* = Standard deviation. *n* = Sample size. Computed correlation used Pearson-method with listwise-deletion. All continuous predictor variables were standardized and the outcome variable was standardized within ancestry. **Bold** type indicates $p <= .05$, and ***bold italic*** type indicates $p <= .01$.

Table 2

Results of mixed moderated models of peer effects, GPS, and their interactions

	Model 1		Model 2	
Variable	***B***	***CI***	***B***	***CI***
(Intercept)	0.10	[−3.61, 3.81]	0.03	[−3.70, 3.76]
Sex (0 = Male)	−0.09	[−0.22, 0.05]	−0.08	[−0.22, 0.056]
Race/Ethnicity (0 = White)				
Black	0.05	[−0.27, 0.38]	0.06	[−0.27, 0.39]
Asian	***0.49***	***[0.26, 0.73]***	***0.50***	***[0.27, 0.74]***
More than one race	−0.12	[−0.45, 0.20]	−0.11	[−0.44, 0.21]
Hispanic/Latino	−0.07	[−0.37, 0.23]	−0.08	[−0.38, 0.22]
Other race/ethnicity	0.32	[−0.49, 1.14]	0.35	[−0.47, 1.16]
Age	−0.01	[−0.21, 0.19]	0.00	[−0.21, 0.20]
Fall Drinking (log)	***0.49***	***[0.41, 0.56]***	***0.48***	***[0.41, 0.56***
GPS Count	**−0.16**	**[−0.29, −0.03]**	**−0.16**	**[−0.29, −0.03]**
Cohort (0 = Cohort 1)				
Cohort 2	0.01	[−0.16, 0.18]	0.00	[−0.17, 0.18]
Cohort 3	0.11	[−0.04, 0.25]	0.10	[−0.04, 0.25]
Perceptions of College Peer Use	***0.37***	***[0.30, 0.44]***	***0.37***	***[0.30, 0.44]***
Avg. Roommate Fall Drinking (log)	***0.10***	***[0.04, 0.17]***	***0.10***	***[0.03, 0.17]***
Avg. Residence Hall Fall Drinking	−0.01	[−0.08, 0.07]	−0.01	[−0.08, 0.07]
Alc-GPS	***0.12***	***[0.06, 0.19]***	***0.12***	***[0.06, 0.19]***
Perceptions**Alc-GPS*			0.00	[−0.07, 0.06]
Roommate Drinking (log)**Alc-GPS*			−0.01	[−0.08, 0.05]
Residence Hall Drinking**Alc-GPS*			0.02	[−0.05, 0.08]
Observations	482			
R^2	0.55			

Alc-GPS refers to the genome-wide polygenic risk score for alcohol; GPS Count refers to the number of SNPs available for scoring when calculating the GPS. All continuous predictor variables were standardized and the outcome variable was standardized within ancestry. **Bold** type indicates $p <= .05$, and ***bold italic*** type indicates $p <= .01$.