Developing a Genetically Informative Measure of Alcohol Consumption Using Past-12-Month Indices*

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ABSTRACT. Objective: The goal of this study was to develop a factor score derived from measures of past-12-month alcohol consumption. **Method:** Data were drawn from two studies—the Adult and Family Development Project (N = 734) and the Missouri Adolescent Female Twin Study (N = 3,787). Data on four indices of alcohol consumption (quantity, frequency, frequency of drinking to intoxication, and frequency of five or more drinks/day) were factor analyzed, and differences in factor loadings across gender, race/ethnicity, and study were tested. Correlations between these factors were computed across three assessments and between parent and offspring self-reports. Finally, using the classical twin design, variance in the past-12-month alcohol consumption factor was decomposed into additive genetic (A), shared environmental (C), and nonshared environmental (E) influences, and the extent to which these factors overlap with those influencing lifetime heaviest drinking were examined. **Results:** Factor loadings across all groups were high (.69–.95), with some evidence for differing factor loadings across gender, race/ethnicity, and study. The across-wave correlations for the factor ranged from .22 to .62. The within-wave correlation between parental and offspring drinking was .25, suggesting the importance of familial influences, which genetic analyses attributed to both additive genetic (31%) and shared environmental (17%) factors. The overlap between genetic influences on past-12-month and lifetime heaviest drinking was 0.97. **Conclusions:** A factor score derived from past-12-month drinking measures is heritable and is largely influenced by those genetic factors that influence heaviest drinking, at least in young adults. It also shows moderate across-wave stability. This will allow for large- and small-scale genomic studies to use past-12-month drinking measures in data analysis of similar cohorts. (*J. Stud. Alcohol Drugs, 72,* 444–452, 2011)

EXCESSIVE ALCOHOL CONSUMPTION is the third leading contributor to preventable death in the United States (Centers for Disease Control and Prevention, 2004). In addition to an elevated risk for alcohol abuse and dependence and related physical consequences, such as cirrhosis, drunk driving was responsible for 40% of traffic-related accidents across the United States (National Highway Traffic Safety Administration, 2007). With these serious public health implications in mind, investigators have aimed to identify the biological and environmental underpinnings of excessive alcohol consumption. It is now well known that alcohol consumption is heritable (Heath and Martin, 1994; Heath et al., 1991), with a host of studies showing that individual indices (e.g., quantity, frequency) and factors representing lifetime alcohol consumption during an individual's heaviest period of drinking are influenced by genetic factors that strongly overlap with heritable influences on alcohol abuse and dependence (Grant et al., 2009; Kendler et al., 2010). In the context of gene-finding efforts, the observation that a quantitative measure such as lifetime heavy alcohol consumption is a robust indicator of genetic vulnerability to alcoholism has been reassuring because such quantitative indices can augment power to detect genomic signals.

However, not all studies, particularly those that do not have a primary focus on the study of alcoholism, necessarily ascertain alcohol consumption across the lifetime, nor do they necessarily focus on an individual's period of heaviest drinking (Block and Subar, 1992). Lifetime heavy drinking may be computed by extracting the maximum value reported across several shorter intervals, but this involves the unreliability associated with the heaviest period of drinking occurring between periods queried about in consecutive interviews (e.g., two waves of data, collected 5 years apart, querying past-12-month drinking with heaviest drinking occurring in the second year subsequent to the first interview). Other studies may only collect past-12-month assessments, which is particularly true of genomic studies, where alcohol involvement is measured only as a covariate. These studies may assume that past-12-month drinking is a stable indicator of lifetime typical alcohol consumption; however, given the role of varying environmental influences on current drinking, such measures may be more greatly influenced by individual-specific factors and, consequently, also be less heritable. This raises the question of the feasibility of using past-12-month indices of alcohol consumption in genetic and genomic analyses.

In previous publications, we reported on an alcohol consumption factor score, derived from drinking measures

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from an individual's lifetime heaviest period of drinking. We demonstrated its measurement characteristics and showed that this factor was heritable (50%) (Agrawal et al., 2009) and that these genetic influences explained nearly all of the genetic variation in alcohol abuse and dependence (Grant et al., 2009). However, similar studies of past-12-month drinking are lacking. Therefore, in this study, using two independent datasets, we examined the following: (a) the factorial structure of past-12-month alcohol consumption; (b) the stability of alcohol consumption in the past 12 months across multiple waves of data collection; (c) parent–offspring correlations for past-12-month alcohol consumption; and (d) heritability, using the classical twin design, of past-12-month alcohol consumption and its genetic overlap with alcohol consumption during the period of heaviest drinking.

Method

Samples

Adult and Family Development Project (AFDP). The AFDP is a longitudinal study of familial alcoholism across three generations. At Wave 1 (1988), the total sample consisted of 454 "target" adolescents and their parents; 246 adolescents had at least one biological alcoholic parent who was also a custodial parent, and 208 adolescents were demographically matched controls without an alcoholic parent (Chassin et al., 1991). Data were collected annually for Waves 1 through 3 and at 5-year intervals for Waves 4 through 6. To augment sample size, biological full siblings were also invited to participate at Wave 4 (n = 327), Wave 5 (n = 346), and Wave 6 (n = 349) if they were within the same age range as the original participants. As a consequence, Wave 4 consisted of 734 subjects, including 407 of the originally targeted adolescents and their age-eligible siblings (n = 327). In general, sample retention was excellent (90% or greater).

Alcoholic families were recruited using court records, health maintenance organization wellness questionnaires, and community telephone surveys. To qualify, parents had to live in Arizona, be of non-Hispanic White or Hispanic ethnicity, be born between 1926 and 1960, and meet Diagnostic and Statistical Manual of Mental Disorders, Third Edition (American Psychiatric Association, 1980), criteria or family history research diagnostic criteria (Endicott et al., 1975) for lifetime alcohol abuse or dependence (219 biological fathers and 59 biological mothers). Matched nonalcoholic families (matched on child's age, family composition, ethnicity, and socioeconomic status) were recruited by using directories to find families living in the same neighborhoods as the families ascertained for alcoholism.

The two primary sources of potential recruitment biases were selective contact and refusal to participate (see Chassin et al., 1992, for a complete description of sample recruitment and representativeness). Potential participants who were and were not successfully contacted did not differ on alcoholism indicators from available archived information, but those who were not contacted were more likely to be younger, from court sources, Hispanic, and unmarried and had a lower socioeconomic status rating associated with their residence. Individuals who refused to participate were more likely than were participants to be Hispanic and married, but they did not differ in age, sex, socioeconomic status, or alcoholism.

Data were collected in person using computer-assisted interviews or via telephone for families who were located out of the geographic region. To prevent contamination and encourage self-disclosure, family members were interviewed in separate rooms, and a Department of Health and Human Services Certificate of Confidentiality was used to emphasize confidentiality.

For the factor analyses, participants (N = 734) were drawn from Wave 4 because this assessment was closest in age to the Missouri Adolescent Female Twin Study (MOAFTS; AFDP M_{age} = 22 years, range: 17–27). Data (excluding age-ineligible siblings) from Wave 5 (M_{age} = 26.6 years, range: 22–39) and Wave 6 (M_{age} = 32.9, range: 28–41) were also included to examine the stability of past-12-month drinking.

Missouri Adolescent Female Twin Study. Data for these analyses were drawn from the first full-length follow-up interview of the MOAFTS. MOAFTS consists of a cohort of female same-sex twin pairs born between July 1, 1975, and June 30, 1985, who were identified from birth records (Heath et al., 2002). Twins were eligible to participate if both members of the twin pair had survived past infancy, were not adopted, and if their biological parents were Missouri residents at the time of the twins' birth. Using a cohort-sequential sampling design, twins and at least one biological parent (typically the biological mother) were invited to participate in the baseline interviews during 1994 to 1999, when the twins were 13, 15, 17, or 19 years old. Recruitment of additional 13-year-olds continued over a 2-year period as twins became age-eligible. A telephone diagnostic interview—based on the Semi-Structured Assessment for the Genetics of Alcoholism (Bucholz et al., 1994)—was administered, first to the parents, and subsequently, after obtaining parental permission, to the twins (minors). Further details regarding sample recruitment and characteristics of this first wave of interview data, which are not used in the current study, are given elsewhere (Heath et al., 1999; Knopik et al., 2005). During 2002–2005, the first full-length follow-up interview was completed, which included a detailed assessment of alcohol consumption. All eligible twins, including those who may not have completed a baseline assessment, were invited to participate in the follow-up, provided they or their parents had not previously indicated an unwillingness to partici-

pate in future studies. A total of 3,787 twins, ages 18–29 (*Mdn* = 22) years, completed follow-up interviews.

Of the 734 Wave 4 AFDP and 3,787 MOAFTS subjects, 517 and 2,904 subjects in AFDP and MOAFTS, respectively, reported drinking at least six times across their lifetime and were used for factor analysis. Of the 517 AFDP subjects, 502 could be classified as White or Hispanic; 15 subjects reported that they were another ethnicity, even though their parents reported being either Hispanic or non-Hispanic Whites, and 2 individuals did not self-report ethnicity at any wave. To avoid any confounds associated with self-reported ethnic affiliation and its cultural influences on drinking, these 15 subjects were excluded. For analyses of across-wave stability in the AFDP data, all individuals reporting a lifetime history of alcohol use at that wave (Wave 4: $n = 631$; Wave 5: $n = 669$; Wave 6: $n = 667$) were used.

Measures

The primary measures used for analyses were reports of alcohol consumption in the past 12 months.

Quantity. The quantity measure reflects the number of drinks consumed on a typical drinking day. In AFDP, separate questions were asked about typical (not past-12-month) number of drinks of wine or beer and distilled spirits, with responses ranging from none to nine or more, which were summed. In MOAFTS, a single question was asked about typical drinks per day in the past 12 months, with responses ranging from 1 to 2 drinks up to 31 or more drinks. The quantity item was uniformly scaled across both studies and log-transformed (with the addition of 1 to account for those who never drank in the past 12 months).

Frequency. In AFDP, subjects were queried separately about how often they drank wine or beer and distilled spirits in the past 12 months ("never" to "every day"). A maximum value across the two responses was used. In MOAFTS, a single item with responses ranging from 1 day per year to every day was used, with those not drinking in the past 12 months being coded as "never." Variables were uniformly scaled across studies.

Frequency of five or more drinks. How often an individual had consumed five or more drinks in a day was similarly assessed across MOAFTS and AFDP, with responses ranging from "never" (AFDP: explicit; MOAFTS: reported as no alcohol use in the past 12 months) to "every day."

Frequency of intoxication. Similar to the other frequency measures, in both interviews, subjects were asked on how many days/how often they got drunk (ranging from "never" to "every day").

For the twin analyses that examined the genetic and environmental correlation between past-12-month and lifetime heaviest alcohol consumption, variables identical to those above—but indicating lifetime heaviest drinking (defined as a period lasting at least 12 months when the respondent drank the most alcohol)—were created. For instance, for "frequency," respondents were asked on how many days they had had any alcoholic drink during their period of heaviest use, with response categories, identical to those for past-12-month drinking, ranging from "1 day/year" to "every day." If individuals reported that their heaviest drinking occurred in the past 12 months, then those reports were used; otherwise, reports from the period of heaviest drinking were used. A factor similar to the one developed for past-12-month drinking (and discussed in considerable detail in Agrawal et al., 2009), representing lifetime heaviest alcohol consumption, was created for the genetic analyses.

Analyses

Measurement of alcohol consumption. Because four alcohol consumption indices were used, exploratory factor analyses were not performed (i.e., too few variables for more than one factor to be extracted; Velicer and Fava, 1998). To confirm that underlying the four indices of alcohol consumption was a single factor, tests of internal consistency in SAS Version 8.2 (SAS Institute Inc., Cary, NC), using Cronbach's α, were conducted. Subsequent to this, confirmatory factor analysis of the single factor model was conducted in Mplus Version 5.1 (Muthén and Muthén, 2007) across subgroups of data. The estimated factor loadings were compared across these subgroups to determine if, after allowing for intercepts to vary, differential factor loadings contributed to the absence of measurement invariance. Measurement invariance reflects the statistical test of whether individual indices of alcohol consumption have differing measurement characteristics across subpopulations of individuals. For the purposes of our analyses, six groups were defined: MOAFTS Whites and MOAFTS African Americans, reflecting the racial composition of MOAFTS; and AFDP male-White, AFDP male-Hispanic, AFDP female-White, and AFDP female-Hispanic, reflecting gender and ethnicity (White vs. Hispanic) in the AFDP cohort. For the purposes of model identification, variances were constrained to 1.0 and means were constrained to 0 across all groups. The baseline model constrained raw estimates of both intercepts (related to means) and factor loading parameters across all six groups. Next, an omnibus test that allowed all intercepts and factor loadings to differ was fit. Leaving the intercepts free across groups, we individually tested the equality of factor loadings of each of the individual indices of alcohol consumption across groups. When constraints no longer resulted in a nonsignificant change in model fit, the next alcohol consumption index was considered. To account for familial clustering, the maximum likelihood robust estimator was used. All chi-square difference test statistics were computed using scaling parameters and equations available at statmodel.com (Satorra and Bentler, 1999).

Stability. Using SAS, correlations were computed in the AFDP data for Waves 4–6 for the individual indices and the

underlying alcohol consumption factor score. Paired *t* tests were used to compare means for the individual indices of alcohol consumption and for the factor score across waves.

Parent–offspring correlations. SAS was used to compute correlations between parental reports of their own alcohol use in the past 12 months at Wave 4 and the offspring report of their own alcohol consumption, which are the main outcomes for these analyses.

Heritability and genetic overlap. We used the MOAFTS twin data to decompose familial similarity into genetic and familial environmental sources. In the classical twin design, individual differences can be attributed to additive genetic (A), shared environmental (C), and nonshared environmental (E) factors (Neale and Cardon, 1992). Monozygotic and dizygotic twins shared 100% and 50% of their segregating genes, respectively. C influences are correlated to the same extent across monozygotic and dizygotic twins, whereas E influences are uncorrelated across members of twin pairs. A bivariate Cholesky (Benoit, 1924) model was used to examine the extent to which common A, C, and E factors influenced the covariance between the alcohol consumption factor score assessed using past-12-month measures and a comparable factor created using reports from the period of heaviest drinking.

Results

Sample characteristics

Table 1 presents means for the past-12-month quantity measure and for drinking frequency, frequency of five or more, and frequency of intoxication in MOAFTS and AFDP across the six groups. Men consumed more alcohol than women, drank more frequently than women, and were intoxicated more often than women. MOAFTS African American women had the lowest mean quantity of alcohol consumed and drank less frequently than their White counterparts. In AFDP, Hispanic women reported drinking as much as their White counterparts; however, AFDP Hispanic women tended to consume alcohol less frequently than the MOAFTS White women but were comparable to the African American women. There was very little evidence for differences in quantity or frequency of alcohol consumption across White and Hispanic males.

Table 1. Mean and frequency of four indices of alcohol consumption in the past 12 months across the Missouri Adolescent Female Twin Study (MOAFTS) and the Arizona Family Development Project (AFDP, Wave 4)

Variable	MOAFTS White women (n = 2,575)	MOAFTS African American women (n = 329)	AFDP White women (n = 156)	AFDP Hispanic women (n = 65)	AFDP White men (n = 200)	AFDP Hispanic men (n = 81)
Drinks/day, *M* (*SD;* range)	3.29 (2.50; 0–17)	2.33 (2.07; 0–17)	3.91 (2.32; 0–10)	3.95 (2.44; 1.5–13.5)	6.43 (4.1; 0–17)	6.27 (3.71; 0–17)
Frequency						
Never	6.9	10.1	4.5	4.6	4.5	2.5
1–2 times	6.3	11.6	10.3	10.8	5.0	6.2
3–5 times	9.4	14.3	21.8	32.3	12.0	18.5
>5 to less than monthly	13.5	14.3	21.2	18.5	15.0	14.8
1–3 times/month	33.2	28.7	26.3	21.5	29.5	25.9
1–2 times/week	23.1	16.5	10.9	12.3	22.0	23.5
3–5 times/week	7.5	3.4	5.1	0.0	9.5	7.4
Every day	0.2	1.2	0.0	0.0	2.5	1.2
Frequency of five or more						
Never	30.4	61.4	43.0	50.8	24.0	17.3
1–2 times	17.6	16.1	30.1	23.1	19.0	29.6
3–5 times	8.5	4.6	7.7	10.8	15.0	11.1
>5 to less than monthly	7.1	1.5	7.1	7.8	8.5	9.9
1–3 times/month	21.9	10.0	3.4	3.1	16.5	14.8
1–2 times/week	11.7	4.3	6.4	4.6	12.5	9.9
3–5 times/week	2.7	1.5	1.9	0.0	2.4	6.2
Every day	0.08	0.6	0.0	0.0	2.1	1.2
Frequency of intoxication						
Never	35.2	65.8	37.8	46.2	30.5	33.3
1–2 times	20.4	15.9	34.6	40.0	22.0	19.8
3–5 times	11.1	6.4	11.5	6.2	16.0	17.3
>5 to less than monthly	7.8	2.5	4.5	3.1	6.9	11.1
1–3 times/month	17.6	6.4	5.1	1.5	16.6	8.7
1–2 times/week	6.7	2.5	6.4	3.1	6.0	6.2
3–5 times/week	1.4	0.3	0.0	0.0	2.0	3.7
Every day	0.0	0.3	0.0	0.0	0.0	0.0

TABLE 2. Standardized factor loadings, intercepts, and residual variances with their 95% confidence intervals (CIs) across six subgroups

Variable	Raw intercept [95% CI]	Raw estimate [95% CI]	Factor loading [95% CI]
MOAFTS White women			
Quantity	1.30 [1.27, 1.33]	0.39 [0.37, 0.42]	.70 [.67, .73]
Frequency	3.60 [3.51, 3.69]	1.23 [1.16, 1.29][a]	.77 [.74, .79]
Intoxication	1.78 [1.67, 1.88]	1.48 [1.41, 1.54][c]	.84 [.81, .86]
Five or more	2.19 [2.07, 2.30]	1.78 [1.73, 1.84][e]	.92 [.91, .94]
MOAFTS African American women			
Quantity	1.06 [0.98, 1.14]	0.39 [0.37, 0.42]	.75 [.68, .82]
Frequency	3.09 [2.83, 3.35]	1.23 [1.16, 1.29][a]	.75 [.70, .79]
Intoxication	0.79 [0.57, 1.01]	0.87 [0.59, 1.14][d]	.63 [.50, .76]
Five or more	1.05 [0.79, 1.31]	1.29 [1.03, 1.55][f]	.76 [.67, .85]
AFDP White women			
Quantity	1.48 [1.38, 1.59]	0.39 [0.37, 0.42]	.71 [.64, .78]
Frequency	3.05 [2.73, 3.37]	1.13 [0.94, 1.32][b]	.73 [.65, .81]
Intoxication	1.22 [0.90, 1.53]	1.48 [1.41, 1.54][c]	.94 [.90, .97]
Five or more	1.23 [0.87, 1.59]	1.78 [1.73, 1.84][e]	.95 [.91, .98]
AFDP Hispanic women			
Quantity	1.50 [1.36, 1.64]	0.39 [0.37, 0.42]	.75 [.65, .85]
Frequency	2.79 [2.36, 3.21]	1.13 [0.94, 1.32][b]	.74 [.62, .87]
Intoxication	0.83 [0.47, 1.19]	0.87 [0.59, 1.14][d]	.72 [.58, .87]
Five or more	1.03 [0.57, 1.49]	1.29 [1.03, 1.55][f]	.87 [.75, .99]
AFDP White men			
Quantity	1.83 [1.71, 1.95]	0.39 [0.37, 0.42]	.61 [.53, .68]
Frequency	3.77 [2.45, 4.09]	1.23 [1.16, 1.29][a]	.74 [.68, .81]
Intoxication	1.81 [1.46, 2.16]	1.48 [1.41, 1.54][c]	.81 [.76, .87]
Five or more	2.30 [1.90, 2.70]	1.78 [1.73, 1.84][e]	.91 [.86, .96]
AFDP Hispanic men			
Quantity	1.82 [1.63, 2.00]	0.39 [0.37, 0.42]	.67 [.55, .79]
Frequency	3.60 [2.13, 4.08]	1.23 [1.16, 1.29][a]	.80 [.73, .87]
Intoxication	1.72 [1.18, 2.26]	1.48 [1.41, 1.54][c]	.83 [.74, .92]
Five or more	2.36 [1.79, 2.93]	1.78 [1.73, 1.84][e]	.88 [.80, .96]

Note: Superscripts ([a, b, c, d, e, f]) indicate specific patterns of equality constraints across raw estimates—these are only shown when estimates could not be equated across all groups.

Measurement of alcohol consumption

As shown in Table 2, factor loadings were uniformly high across all subsets of individuals. Computation of Cronbach's α (range: .80–.86 for AFDP and .81–.87 for MOAFTS) indicated high internal consistency, which was consistent with the single factor models (and visually verified by inspection of screen plots in SAS). Despite the single factor solution being optimal across all six groups, there was modest evidence for different factor loadings by sample and ethnicity, but only in women. Allowing intercepts and factor loadings to vary freely across groups resulted in a significant improvement in fit ($\Delta\chi^2$ = 402.8 for 20 *df;* comparative fit index [CFI] increases from .91 to .99; Tucker–Lewis index [TLI] increases from .94 to .98; root mean square error of approximation [RMSEA] decreases from .13 to .07). Next, we attempted to constrain the factor loadings across groups. For quantity, factor loadings could be constrained across groups ($\Delta\chi^2$ = 10.6 for 5 *df*). For both frequency of intoxication and frequency of five or more drinks, factor loadings across all groups were not equal ($\Delta\chi^2$ = 23.1 and 25.2 for 5 *df*); however, allowing the MOAFTS African American and AFDP female-Hispanic samples to have different (but equal to each other) factor loadings from the other groups (which could be constrained to each other) allowed for satisfactory model fit ($\Delta\chi^2$ = 0.12 and 6.8 for 4 *df*). Finally, for frequency of use, constraining the AFDP female-White and MOAFTS female-African Americans to have equal factor loadings and allowing for MOAFTS women to have similar factor loadings to the AFDP men led to reasonable model fit ($\Delta\chi^2$ = 7.1 for 4 *df*). The overall best-fitting model showed a modest improvement in CFI and TLI (.99) and a reduction in RMSEA (.05).

Stability

The top half of Table 3 shows the correlations, across three waves of assessment, for the individual indices of alcohol consumption and for the composite factor score assessed for the 12 months before the assessment. Pearson correlations suggest that across-assessment correlations were highest between past-12-month reports at Waves 5 and 6, intermediate between past-12-month reports at Waves 4 and 5, and lower between Waves 4 and 6. Paired *t* tests revealed some significant across-wave differences (bottom half of Table 3). Quantity of alcohol consumed and frequency of intox-

Table 3. Mean differences and correlations between past-12-month indices of alcohol consumption, in non-abstainers, across three waves of AFDP assessments

	Pearson correlations across waves		
Variable	Wave 4 and Wave 5	Wave 5 and Wave 6	Wave 4 and Wave 6
Quantity	.44	.45	.32
Frequency	.40	.53	.23
Five or more	.45	.57	.30
Intoxication	.46	.57	.32
Factor score	.51	.62	.22
	Differences across waves, *M* (*SD*)		
Variable	Wave 4 – Wave 5	Wave 5 – Wave 6	Wave 4 – Wave 6
Quantity	0.02 (0.70)	0.31 (0.63)*	0.35 (0.72)*
Frequency	-0.36 (1.93)*	-0.06 (1.87)	-0.39 (2.29)*
Five or more	-0.14 (1.90)	0.04 (1.70)	-0.03 (2.18)
Intoxication	-0.05 (1.63)	0.13 (1.44)*	0.10 (1.78)
Factor score	-0.06 (0.91)	-0.003 (1.06)	0.03 (0.80)

*Significant difference using *t* test at $p < .05$. Negative coefficients represent increase across waves (e.g., Wave 5 – Wave 6 is < 0 because Wave 5 < Wave 6), and positive coefficients represent decrease across waves (e.g., Wave 5 – Wave 6 is > 0 because Wave 5 > Wave 6).

ication, in the past 12 months, decreased from one wave to the next, whereas frequency of alcohol use increased across waves. For quantity, alcohol consumption at Wave 4 ($M_{\text{Wave 4}} = 1.54$) was significantly greater than quantity reported in the 12 months preceding Wave 6 ($M_{\text{Wave 6}} = 1.20$), with similar differences between Waves 5 ($M_{\text{Wave 5}} = 1.50$) and 6. Waves 4 and 5 did not differ from each other. Frequency of intoxication at Wave 4 ($M_{\text{Wave 4}} = 1.30$) was greater than that reported at Wave 6 ($M_{\text{Wave 6}} = 1.20$) but not when comparing Waves 4 and 5 ($M_{\text{Wave 5}} = 1.31$). For frequency of use, Wave 4 ($M_{\text{Wave 4}} = 3.02$) reports were significantly lower than those at Wave 5 ($M_{\text{Wave 5}} = 3.29$) and at Wave 6 ($M_{\text{Wave 6}} = 3.35$). Despite these fluctuations in drinking patterns, mean factor scores remained stable across assessments.

Parent–offspring correlation

Data on quantity, frequency, and frequency of five or more drinks were available, at Wave 4, via self-report, from the biological mother and father of the AFDP subjects. Parental measures were highly correlated ($r = .40$) with each other for quantity and frequency and less so for five or more ($r = .14$). We computed a factor score using these three measures across both parents; factor loadings were high, ranging from .47 for maternal reports of five or more drinks to .84 for quantity. The correlation between Wave 4 parental drinking and offspring drinking at Waves 4–6 was significant (correlations of .25–.31), suggesting the role of familial influences on past-12-month drinking.

Table 4. Role of additive genetic, shared environmental, and nonshared environmental influences, with their 95% confidence intervals (CIs), of past-12-month and heaviest alcohol consumption

Variable	Additive genetic (A) [95% CI]	Shared environment (C) [95% CI]	Nonshared environment (E) [95% CI]
Past 12 months	.31 [.23, .43]	.17 [.07, .22]	.52 [.47, .58]
Heaviest period	.53 [.48, .58]	–	.47 [.42, .52]
Correlation	.97 [.82, 1.00]	–	.56 [.51, .61]

Heritability and genetic overlap

Results from the bivariate genetic model are presented in Table 4. Thirty-one percent of the variance in past-12-month drinking was attributable to additive genetic influences. Additive genetic and nonshared environmental influences contributed to 53% and 47%, respectively, of the variance in the factor score drawn from the heaviest drinking period. Although shared environmental factors were not found to play a role in alcohol consumption during heaviest drinking, 17% of the variance in alcohol consumption during the past 12 months was because of shared environment.

We also examined the extent to which genetic influences on the past-12-month alcohol factor score overlapped with genetic influences on a factor score derived from measures of lifetime heaviest drinking. There was significant correlation ($R_g = .97$); and squaring this estimate we can conclude that 94.1% of the genetic factors influencing past-12-month drinking are shared with those influencing lifetime heaviest alcohol consumption. The nonshared or individual specific environmental factors on the factor score derived from past-12-month and lifetime heaviest drinking were also correlated, albeit to a lesser degree—31.3% of the environmental factors not shared by members of a twin pair overlapped across past-12-month and heaviest drinking.

Of those who drank, 27.9% of the subjects reported that they drank as much in the past 12 months as during their period of heaviest alcohol consumption. To avoid any confounds in the genetic correlation between alcohol consumption during the past 12 months and the period of heaviest use, we also re-ran twin analyses after excluding these subjects. Estimates remained unchanged ($A_{\text{past12}} = .34$, 95% CI [.25, .53]; $C_{\text{past12}} = .15$, 95% CI [.05, .32]; $A_{\text{heavy}} = .51$, 95% CI [.44, .59]), with the genetic correlation being .98, 95% CI [.78, 1.00].

Discussion

We sought to characterize the measurement characteristics, stability, and heritability of alcohol consumption in the past 12 months. Our analyses suggest that although a single factor—characterized by high factor loadings for quantity, frequency, frequency of five or more, and frequency of intoxication—characterizes alcohol consumption, factor loadings

may vary across female samples. We noted some differences with respect to women of African American descent and Hispanic ethnicity having lower estimates for factor loadings when compared with White men and women; for frequency of use, factor loadings were lower in the Arizona women. After we allowed for differing intercepts, however, these cultural and regional differences were modest. It is therefore recommended that formal tests of differential measurement be conducted and the resulting factors generated from the best-fitting model be used for subsequent analyses before combining data on composite measures derived from past-12-month or current drinking indices, such as factor scores.

Past-12-month drinking was moderately stable across the three waves, with increasing stability between Waves 5 and 6 when participants were older (mean ages of 27 and 33 years, respectively). Similar stability has been reported by Dawson and colleagues (2008) in those not meeting criteria for alcohol use disorders (or remitting from it) during either wave of the National Epidemiologic Survey of Alcohol and Related Conditions, although whether the stability in our sample would be modified by accounting for onset and offset of alcohol dependence remains to be investigated. However, our findings suggest some caution in assuming that past-12-month drinking, particularly when assessed during young adulthood, is a reasonable indicator of lifetime typical drinking, because the lower correlations between drinking at Wave 4 (age range: 17–27 years) and Wave 6 (age range: 28–41 years) do suggest that developmental factors continue to modify drinking patterns well into adulthood. The variation in drinking between young and later adulthood may reflect exposure to pro-drinking milieus in college (Bartholow et al., 2003; Sher et al., 2001), which may contribute to some of the specificity of past-12-month alcohol consumption at Wave 4, as well as the transition to employment and parenthood in later adulthood (Christie-Mizell and Peralta, 2009; Gotham et al., 1997; Little et al., 2009; Richman et al., 1995) that may have had an impact on the emerging stability in Waves 5 and 6.

The parent–offspring correlation in AFDP suggested the role of familial influences on past-12-month drinking, whereas application of standard genetic modeling techniques to the MOAFTS data indicated that a large component of this familiality could be attributed to genetic factors, at least in women. An important implication of this finding is that past-12-month drinking measures may be used in genetic and genomic analyses of alcohol consumption. Heritability of this measure was considerably lower than that reported for alcohol consumption during the period of lifetime heaviest use; however, the high degree of genetic overlap between past-12-month drinking and alcohol consumption during the heaviest period (which could have been, but was not always, during the past 12 months) suggests that when assessments of the heaviest period of alcohol consumption are unavailable, past-12-month measures may be used to provide a reasonable estimation of genetic liability to alcohol consumption. This may be of utility to ongoing meta-analyses of genomewide association studies of alcohol consumption that are reliant on past-12-month measures of alcohol consumption, primarily from dietary intake sections. Although considerable caution is still warranted in interpreting results from those genomic analyses as representative of genetic vulnerability to alcohol consumption at its peak or to alcohol use disorders, it is likely that some genomic factors that jointly influence current and lifetime heavy drinking (e.g., alcohol dehydrogenase genes that metabolize alcohol; Macgregor et al., 2009; Whitfield et al., 1998) would be successfully identified by such endeavors.

Whereas it appears that a large proportion of the genetic influences on past-12-month drinking overlap with genetic influences on lifetime heaviest drinking, these genetically informative analyses were restricted to a sample of 18- to 29-year-old women with moderate levels of alcohol consumption. It is plausible that during this developmental period, heaviest drinking occurs in the past 12 months. This is only partially supported by our data, in which 27.9% of the women reported their drinking in the past 12 months to be equivalent to their heaviest drinking, and the exclusion of these subjects does not modify the genetic correlation. However, as noted in analyses of the AFDP data, mean levels of past-12-month alcohol consumption do change over time, as indicated by the correlations suggesting that although past-12-month drinking may be a reasonable phenotypic and genetic proxy for lifetime heaviest drinking in young cohorts, it may not serve as an equally good indicator in older cohorts, particularly if alcohol consumption measures are only queried in a subset of individuals (e.g., those reporting a lifetime history of a certain frequency of drinking).

It is also noteworthy that the role of shared environmental influences on past-12-month drinking could not be excluded. These factors make members of monozygotic and dizygotic twin pairs equally similar to each other. They may include environmental influences experienced by both members of a twin pair, or they could be related to diverse environmental cues that are perceived similarly by the twins. Possible contributors to shared environments for current drinking may include drinking habits and rules regarding responsible alcohol consumption learned from parents; however, because the twins are young adults, it is likely that a majority of them would live away from home. To some extent, lingering effects of parental values and attitudes regarding drinking may continue to influence the drinking habits of twins, to a similar extent, even when living apart (Abar and Turrisi, 2008; Boyle and Boekeloo, 2009; Walls et al., 2009). Another possible contributor to shared environment in these young adult twins may be affiliating with similar peer networks and maintaining similar peer niches, even when going to different colleges. Whereas these putative shared environmental factors appear to have no statistical effects on the heaviest

period of alcohol consumption or on alcohol use disorders, it appears that past-12-month drinking is influenced by shared (and nonshared) environment.

Some caveats and limitations of this study are noteworthy. First, some of the subgroups (e.g., AFDP female-Hispanic) were small and may not have been adequately powered to detect nuanced statistical differences in the measurement invariance models. Second, we did not include a measure of maximum drinks in a single 24-hour period (maxdrinks) in these analyses. There were two reasons for this. First, AFDP did not include an assessment of maxdrinks for the past 12 months. Second, and perhaps more importantly, our previous analyses (Agrawal et al., 2009) showed that maxdrinks had a lower factor loading on the underlying consumption factor and was more likely to be influenced by genetic factors that did not overlap with the other measures of alcohol consumption. Relatedly, in these analyses, we separated quantity from frequency (instead of Quantity × Frequency). This was largely motivated by the fact that some studies only collect data on quantity (e.g., drinks per day), and we were interested in examining the differential measurement properties of these two indices.

We conclude that although past-12-month alcohol consumption may vary across populations (e.g., gender, ethnicity, region, and across the lifetime), genetic factors play an essential role in their etiology. This is comforting for genetically informative studies in which only current drinking is available. However, it is also important to recognize that this high degree of overlap may be restricted to young adult cohorts, and past-12-month drinking in older cohorts may be less representative of lifetime heaviest alcohol consumption. Furthermore, although there appears to be genetic overlap across the two measures, past-12-month drinking was less heritable, and the extent to which this limits our power to detect genomic signals needs to be explored. It may be hypothesized that although lifetime measures (and indeed, well-constructed, psychometrically valid indices of alcohol consumption) continue to serve as the "gold standard" for genetic analyses, in their absence, investigators may use measures of current drinking.

Finally, perhaps of more considerable interest, such studies may also wish to examine the extent to which environmental exposures experienced in those past 12 months modify the action of latent or measured genetic influences. In other words, given the importance of shared and nonshared environment on past-12-month drinking, Gene × Environment analyses may reveal more precisely the extent to which environment moderates biological influences on current drinking.

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References

Abar, C., & Turrisi, R. (2008). How important are parents during the college years? A longitudinal perspective of indirect influences parents yield on their college teens' alcohol use. *Addictive Behaviors, 33,* 1360–1368.

Agrawal, A., Grant, J. D., Littlefield, A., Waldron, M., Pergadia, M. L., Lynskey, M. T., . . . Heath, A. C. (2009). Developing a quantitative measure of alcohol consumption for genomic studies on prospective cohorts. *Journal of Studies on Alcohol and Drugs, 70,* 157–168.

American Psychiatric Association. (1980). *Diagnostic and statistical manual of mental disorders* (3rd ed.). Washington, DC: Author.

Bartholow, B. D., Sher, K. J., & Krull, J. L. (2003). Changes in heavy drinking over the third decade of life as a function of collegiate fraternity and sorority involvement: A prospective, multilevel analysis. *Health Psychology, 22,* 616–626.

Benoit, C. (1924). Note sur une méthode de résolution des équations normales provenant de l'application de la méthode des moindres carrés à un système d'équations linéaires en nombre inférieur à celui des inconnues—Application de la méthode a la résolution d'un système defini d'équations linéaires (Procédé du Commandant Cholesky). *Bulletin géodésique, 2,* 67–77.

Block, G., & Subar, A. F. (1992). Estimates of nutrient intake from a food frequency questionnaire: The 1987 National Health Interview Survey. *Journal of the American Dietetic Association, 92,* 969–977.

Boyle, J. R., & Boekeloo, B. O. (2009). The association between parent communication and college freshmen's alcohol use. *Journal of Drug Education, 39,* 113–131.

Bucholz, K. K., Cadoret, R., Cloninger, C. R., Dinwiddie, S. H., Hesselbrock, V. M., Nurnberger, J. I., . . . Schuckit, M. A. (1994). A new, semi-structured psychiatric interview for use in genetic linkage studies: A report on the reliability of the SSAGA. *Journal of Studies on Alcohol, 55,* 149–158.

Centers for Disease Control and Prevention (CDC). (2004). Alcohol-Attributable Deaths and Years of Potential Life Lost—United States, 2001. *MMWR, 53,* 866–870.

Chassin, L., Barrera, M., Bech, K., & Kossak-Fuller, J. (1992). Recruiting a community sample of adolescent children of alcoholics: A comparison of three subject sources. *Journal of Studies on Alcohol, 53,* 316–319.

Chassin, L., Rogosch, F., & Barrera, M. (1991). Substance use and symptomatology among adolescent children of alcoholics. *Journal of Abnormal Psychology, 100,* 449–463.

Christie-Mizell, C. A., & Peralta, R. L. (2009). The gender gap in alcohol consumption during late adolescence and young adulthood: Gendered attitudes and adult roles. *Journal of Health and Social Behavior, 50,* 410–426.

Dawson, D. A., Stinson, F. S., Chou, S. P., & Grant, B. F. (2008, November). Three-year changes in adult risk drinking behavior in relation to the course of alcohol-use disorders. *Journal of Studies on Alcohol and Drugs, 69,* 866–877.

Endicott, J., Andreasen, N., & Spitzer, R. L. (1975). *Family history-research diagnostic criteria.* New York, NY: Biometrics Research, New York State Psychiatric Institute.

Gotham, H. J., Sher, K. J., & Wood, P. K. (1997). Predicting stability and change in frequency of intoxication from the college years to beyond: Individual-difference and role transition variables. *Journal of Abnormal Psychology, 106,* 619–629.

Grant, J. D., Agrawal, A., Bucholz, K. K., Madden, P. A. F., Pergadia, M. L., Nelson, E. C., . . . Heath, A. C. (2009). Alcohol consumption indices of genetic risk for alcohol dependence. *Biological Psychiatry, 66,* 795–800.

Heath, A. C., Howells, W., Bucholz, K. K., Glowinski, A. L., Nelson, E. C., & Madden, P. A. (2002). Ascertainment of a mid-western US female adolescent twin cohort for alcohol studies: Assessment of sample representativeness using birth record data. *Twin Research, 5,* 107–112.

Heath, A. C., Madden, P. A., Grant, J. D., McLaughlin, T. L., Todorov, A. A., & Bucholz, K. K. (1999). Resiliency factors protecting against teenage alcohol use and smoking: Influences of religion, religious involvement and values, and ethnicity in the Missouri Adolescent Female Twin Study. *Twin Research, 2,* 145–155.

Heath, A. C., & Martin, N. G. (1994). Genetic influences on alcohol consumption patterns and problem drinking: Results from the Australian NH&MRC twin panel follow-up survey. *Annals of the New York Academy of Sciences, 708,* 72–85.

Heath, A. C., Meyer, J., Jardine, R., & Martin, N. G. (1991). The inheritance of alcohol consumption patterns in a general population twin sample: II. Determinants of consumption frequency and quantity consumed. *Journal of Studies on Alcohol, 52,* 425–433.

Kendler, K. S., Myers, J., Dick, D., & Prescott, C. A. (2010). The relationship between genetic influences on alcohol dependence and on patterns of alcohol consumption. *Alcoholism: Clinical and Experimental Research, 34,* 1058–1065.

Knopik, V. S., Sparrow, E. P., Madden, P. A. F., Bucholz, K. K., Hudziak, J. J., Reich, W., . . . Heath, A. C. (2005). Contributions of parental alcoholism, prenatal substance exposure, and genetic transmission to child ADHD risk: A female twin study. *Psychological Medicine, 35,* 625–635.

Little, M., Handley, E., Leuthe, E., & Chassin, L. (2009). The impact of parenthood on alcohol consumption trajectories: Variations as a function of timing of parenthood, familial alcoholism, and gender. *Development and Psychopathology, 21,* 661–682.

Macgregor, S., Lind, P. A., Bucholz, K. K., Hansell, N. K., Madden, P. A. F., Richter, M. M., . . . Whitfield, J. B. (2009). Associations of ADH and ALDH2 gene variation with self report alcohol reactions, consumption and dependence: an integrated analysis. *Human Molecular Genetics, 18,* 580–593.

Muthén, L. K., & Muthén, B. O. (2007). *Mplus user's guide* (5th ed.). Los Angeles, CA: Author.

National Highway Traffic Safety Administration. (2007). *Traffic safety facts research note: 2006 traffic safety annual assessment: Alcohol-related fatalities* (Report No. DOT HS, 810, 821). Washington, DC: NHTSA's National Center for Research and Statistics.

Neale, M. C., & Cardon, L. R. (1992). *Methodology for genetic studies of twins and families.* The Netherlands: Kluwer Academic Publishers.

Richman, J. A., Rospenda, K. M., & Kelley, M. A. (1995). Gender roles and alcohol abuse across the transition to parenthood. *Journal of Studies on Alcohol, 56,* 553–557.

Satorra, A. & Bentler, P. M. (1999). A scaled difference chi-square test statistic for moment structure analysis. Retrieved from: http://preprints.stat.ucla.edu/260/chisquare.pdf

Sher, K. J., Bartholow, B. D., & Nanda, S. (2001). Short- and long-term effects of fraternity and sorority membership on heavy drinking: A social norms perspective. *Psychology of Addictive Behaviors, 15,* 42–51.

Velicer, W. F., & Fava, J. L. (1998). Affects of variable and subject sampling on factor pattern recovery. *Psychological Methods, 3,* 231–251.

Walls, T. A., Fairlie, A. M., & Wood, M. D. (2009). Parents do matter: A longitudinal two-part mixed model of early college alcohol participation and intensity. *Journal of Studies on Alcohol and Drugs, 70,* 908–918.

Whitfield, J. B., Nightingale, B. N., Bucholz, K. K., Madden, P. A., Heath, A. C., & Martin, N. G. (1998). ADH genotypes and alcohol use and dependence in Europeans. *Alcoholism: Clinical and Experimental Research, 22,* 1463–1469.