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Religious attendance and frequency of alcohol use: same genes or same environments: a bivariate extended twin kinship model

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Religious attendance has been shown to correlate negatively with alcohol use. We investigated whether this relationship is driven by genetic or environmental factors. Data on frequency of church attendance and frequency of alcohol use were obtained from twins and their families in the Virginia 30 000 study. A comprehensive bivariate model of family resemblance was fitted to the data using Mx. This model is described in detail. Results indicate that genetic factors primarily account for the relationship between alcohol and church attendance in males, whilst shared environmental factors, including cultural transmission and genotype-environment covariance, are stronger determinants of this association in females.

Keywords: religious attendance, alcohol use, genetics, twins, model, Mx, genetic and environmental factors

Introduction

A negative relationship between religious attendance and alcohol use has been shown in a number of recent articles.[1–9] People who frequently attend religious services tend to drink less alcohol. Whether this observed correlation is due to genetic or environmental factors has received little attention. In another paper in this issue,[10] we examine the role of genetic and environmental factors for religious attendance using an extended kinship design. This design allows the simultaneous testing of additive and non-additive genetic, shared and individual-specific environmental factors, as well as sex differences in the expression of genes and environment in the presence of assortative mating and combined genetic and cultural transmission. In addition, the consistency of these parameters over a large range of relationships can be evaluated. We have extended this three-generational model to the multivariate case, thereby providing a tool to test hypotheses about the relationship between variables. The method allows the simultaneous estimation of a range of genetic and environmental parameters and an overall goodness-of-fit test of the model.

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In this paper, we explain the various aspects of the multivariate extended twin kinship model and describe an implementation of this model in the statistical modeling package Mx.[11] We illustrate the model with data from the Virginia 30 000[12] on religious attendance and alcohol use.

Materials and methods

The Virginia 30 000

The Virginia 30 000 sample contains data from 14 763 twins, ascertained from two sources.[12,13] Public birth records and other public records in the Commonwealth of Virginia were used to obtain current address information for twins born in Virginia between 1915 and 1971, with questionnaires mailed to twins who had returned at least one questionnaire in previous surveys. A second group of twins was identified through their response to a letter published in the newsletter of the American Association of Retired Persons (AARP, 9476 individuals). Twins participating in the study were mailed a 16 page 'Health and Lifestyles' questionnaire, and were asked to supply the names and addresses of their spouses, siblings, parents and children for the follow-up study of relatives of twins. Completed questionnaires were obtained from 69.8% of twins invited to participate in the study, which was carried out between 1986 and 1989.

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The original twin questionnaire was modified slightly to provide two additional forms, one appropriate for the parents of twins and another for the spouses, children and siblings of twins. Modifications affected only those aspects of the questionnaire related to twinning, in order to obtain self-report data. The response rate from relatives (44.7%) was much lower than that from the twins. Of the complete sample of 28 521 individuals (from 5670 extended kinships) with valid church attendance and alcohol use data, 59.7% were female, with 50% of respondents under 50 years of age.

Zygosity determination

Zygosity of twins was determined on the basis of responses to standard questions about similarity and the degree to which others confused them. This method has been shown to give at least 95% agreement with diagnosis based on extensive blood typing.[14,15]

Measures

In all questionnaires mailed to twins and their relatives, self-report data on church attendance were obtained from a single item which asked respondents to indicate the number corresponding to the frequency of which they attend church services. The six possible response values were: 'never', 'rarely', 'a few times a year', 'once or twice a month', 'once a week' and 'more than once a week'. Several questions were asked regarding the frequency and quantity of the respondents' alcohol use. We analyzed the frequency measure with response values ranging from 'more than once a day', 'every day', '3–4 times a week', 'once or twice a week', 'once or twice a month', 'less often' to 'not at all'.

Statistical methods

The entire data set has been corrected for the linear and quadratic effects of age, sex, twin status, source of ascertainment (Virginian birth records versus AARP) and interactions between these effects, using SAS 6.12.[16] Subsequent analyses are based on the normalized residuals from this regression analysis.

Structural modeling of the data was undertaken using methods described in Eaves et al[12] and Truett et al,[13] which assess the contributions of additive and dominant genetic effects in the presence of effects such as vertical cultural inheritance, phenotypic assortative mating, shared twin and sibling environments and within-family environment. Phenotypic assortment occurs when mate selection is based at least partly on the trait being studied, and is evidenced by a correlation between the observed phenotypes of spouses. Vertical cultural inheritance is the transmission of non-genetic information from parent to child, and refers to the environmental effects the parents create for their children based on their phenotype. A model which assumes that assortment and cultural transmission are based on the measured phenotype is only one of the possible mechanisms for family resemblance.[17,18] Between-family environmental effects make family members relatively more similar, whereas sibling environments are those environmental factors shared between all types of offspring. A special twin environment is an additional correlation between the environment of twins (in addition to the sibling environment) which makes both MZ and DZ twins more alike than ordinary siblings even in the absence of genetic effects.[19] Where all these sources of common environment contribute to variation among individuals regardless of relationship, they differ in their effect on the covariation between types of relatives. The contribution of genetic and environmental factors may be dependent upon sex, both in their magnitude and nature. Figure 1 presents a path diagram of the so-called 'Stealth' model.

A FORTRAN program 'Famfit' was originally written by one of us (LJE) to fit this extended twin kinship model to correlations of twins and their first degree and collateral relatives, including parents, siblings, spouses and children. A mathematically equivalent version of the model was implemented in Mx[11] for three main reasons. First, Famfit used correlations between the twins and any available relative, thereby using the same individuals in multiple correlations, which overestimates statistical precision. Mx can fit models directly to the raw data to obtain maximum likelihood estimates of the model parameters with appropriate confidence intervals.[20] This method has the added advantage of handling data that are missing at random or completely at random.[21] Second, Famfit only allowed the analysis of one variable at the time, and would have required major additions to include multiple variables. In contrast, the Mx version is written using the rules of multivariate path analysis,[22] so that it can handle more than one variable, limited only by the speed of computers. Third, the Mx version is intended to be more readily communicated and thus easier for others to develop and modify as necessary for other pedigree structures and other models of familial resemblance. To help with this goal, we will describe here how the program is constructed.

The principles behind the Mx version, which can be freely obtained from the author, are simple. The complete model is broken up into a number of building blocks which are precalculated in the top part of the program. The expectations of each of the existing relationships including twins and their first

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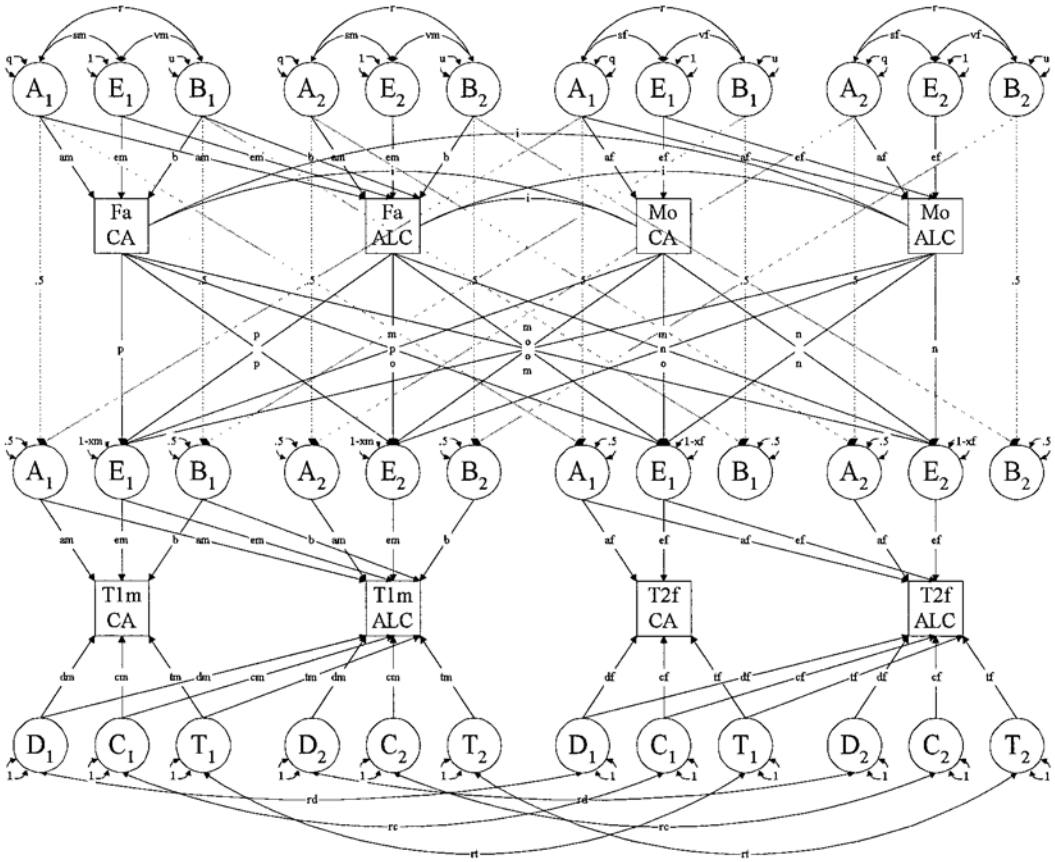

af = gender-common additive genes – females
am = gender-common additive genes – males
b = male-specific additive genes – males
r = induced correlation between gender-common and male-specific additive genetic effects
df = non-additive genes – females
dm = non-additive genetic parameter – males
rd = correlation between male and female non-additive genetic effects
cf = common environment – females
cm = common environment parameter – males
rc = correlation between male and female common environment
tf = special twin environment – females
tm = special twin environment parameter – males
rt = correlation between male and female special twin environmental effects
n = maternal cultural transmission - females
m = maternal cultural transmission - males
o = paternal cultural transmission - females
p = paternal cultural transmission - males
ef = specific environment parameter - females
em = specific environment parameter - males
i = assortative mating parameter
sf = correlation between gender-common additive genetic effects and environment - females
sm = correlation between gender-common additive genetic effects and environment - males
vf = correlation between male-specific additive genetic effects and environment - females
vm = correlation between male-specific additive genetic effects and environment - males

Figure 1 Full extended family resemblance model for opposite-sex DZ twins and their parents. Path coefficients are the same in both generations, and gene–gene and gene–environment correlations occur in both generations (dominance, shared environment and twin environment not shown for the parental generation)

degree and collateral relatives can then be formed by combining the building blocks in the appropriate way, each of which is done in a separate calculation group. The constraints necessary to identify uniquely all the parameters in the model are specified in the following groups. The data groups then provide the observed data as well as the expected covariance matrices in terms of the precalculated expectations. Finally, calculation groups are added to print the various parameter estimates and to derive components of variance. The full model allows for a complete treatment of sex differences, both in the magnitude and the kind of effect. This implies that both the building blocks and the

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expectations for the relationships have to be specified for the four combinations (male–male, female–female, male–female and female–male).

Each of the 150 groups are referred to by name declared with #define statements to make it easier to insert or delete groups without extensive renumbering. The first calculation group 'mf' specifies the assortment paths (matrix I) between spouses and implicitly contains the expectation for spouse covariance. Groups 'apm', 'bpm', 'apf' and 'bpf' declare matrices for additive genetic – both common to both sexes (matrix A) and male-specific (matrix B) – and unique environmental (matrix C) latent factors and calculate the covariance between an individual's genotype and his/her phenotype for the four combinations by sex. This covariance includes paths through a correlated set of genes and through genotype–environment covariance resulting from the combined presence of genetic and cultural transmission. Groups 'aim', 'aif', 'aimf' and 'aifm' compute the covariance between the genotypes of sibling, which may include effects due to phenotypic assortment. These building blocks are then used in groups 'aaim', 'aaif', 'aaimf' and 'aaifm' to calculate the covariance between the genotypes of cousins. The covariance between genotype and environment is calculated in groups 'acm', 'acf', 'acmf' and 'acfm', both within the same generation (using an algebra section) and across generations, eg between aunt and niece (using the compute statement). Parameters for the environmental covariance due to vertical cultural transmission are declared in groups 'cim', 'cif', 'cimf' and 'cifm'. The following four groups ('pmj', 'pfg', 'pmg' and 'pfj') precalculate the covariance between the phenotype of the parents and the genetic and environmental latent factors of the children (partly with algebra and partly with compute). Two groups ('calcdz', 'calcmz') then summarize all the building blocks separately for relationships through MZ and DZ twins.

The expectations for each of the 88 sex-specific relationships in the extended twin kinship design – except for the spousal correlation which is declared in the first group – are specified in the following groups. The first degree relationships include parent–offspring relatives (groups 'ms', 'fs', 'md', 'fd'), twins (groups 'mzm', 'dzm', 'mzf', 'dzf', 'dzmf'), and siblings (groups 'sim', 'sif', 'simf'). The parent–offspring correlations are made of building blocks from groups 'pmj', 'pfg', 'pmg', 'pfj' between the parental phenotype and latent factors of the children and the matrices defining the links between the latent factors and phenotypes (matrices Y for males and X for females in groups 'apm' and 'apf' respectively). The expectations for the correlations between twins use the blocks for genetic covariance (groups aim, aif, aimf and aifm), genotype–environment covariance (groups acm, acf, acmf and acfm) and environmental covariance (groups cim, cif, cimf and cifm). In addition, matrices are declared for latent factors representing genetic dominance (matrix K), non-parental shared environment (matrix L) and special twin environment (matrix M). The correlations between these factors in males and females are declared in the group for opposite-sex twins (dzmf). The sibling expectations are similar to those for twins except for the special twin environment contribution.

The next 20 groups complete the expected covariances for avuncular relationships through DZ twins (groups unedzm–anidzmf), MZ twins (groups unemzm–animzf) and siblings (groups unesim–anisimf). The matrix algebra for each of these correlations consists of five matrices: i) a twin or sibling correlation from an uncle/aunt to his/her co-twin, combined with ii) parent phenotype–child's latent factor correlations from the parent (= co-twin) to his/her child (= niece/nephew), and iii) additional paths from the phenotype of an uncle/aunt to his/her latent factors, combined with iv) paths from the latent factors to the genetic latent factors of a niece/nephew, multiplied finally by v) a matrix of paths from the latent factors in the child to his/her phenotype. For an example of the expected covariance between uncle and nephew through a male DZ twin, see Figure 2. The cousin relationships are specified in the next 16 groups, which may exist through DZ twins (groups comdzm–cofmdzmf) or MZ twins (groups commzm–comfmzf). These are also built up by combining the various building blocks in the appropriate fashion, in a similar way to the avuncular relationships. Groups 'msw' through 'hanimzf' formulate the expectations for all the relationships through marriage: first degree relatives and their spouse (groups msw–sifmw), spouses through twins (groups wmzmw–wdzmfh) and nieces/nephews and the spouse of their uncle/aunt (groups wunedzm–hanimzf).

The final eight groups specifying correlations between relatives deal with three generational relationships between grandparents and their grandchildren (groups gmps–gfmd). The Famfit program did not include expectations for these relationships as the number of observed pairs of these relationships was relatively small the VA 30 000 sample. However, when fitting to the raw data, all possible relationships have to be explicitly specified. Given the assumption that the correlation between the twins and their parents is identical to the correlation between the twins and their children, the grandparent–grandchild correlations can be computed by combining the expected parent–offspring correlations in the appropriate way.

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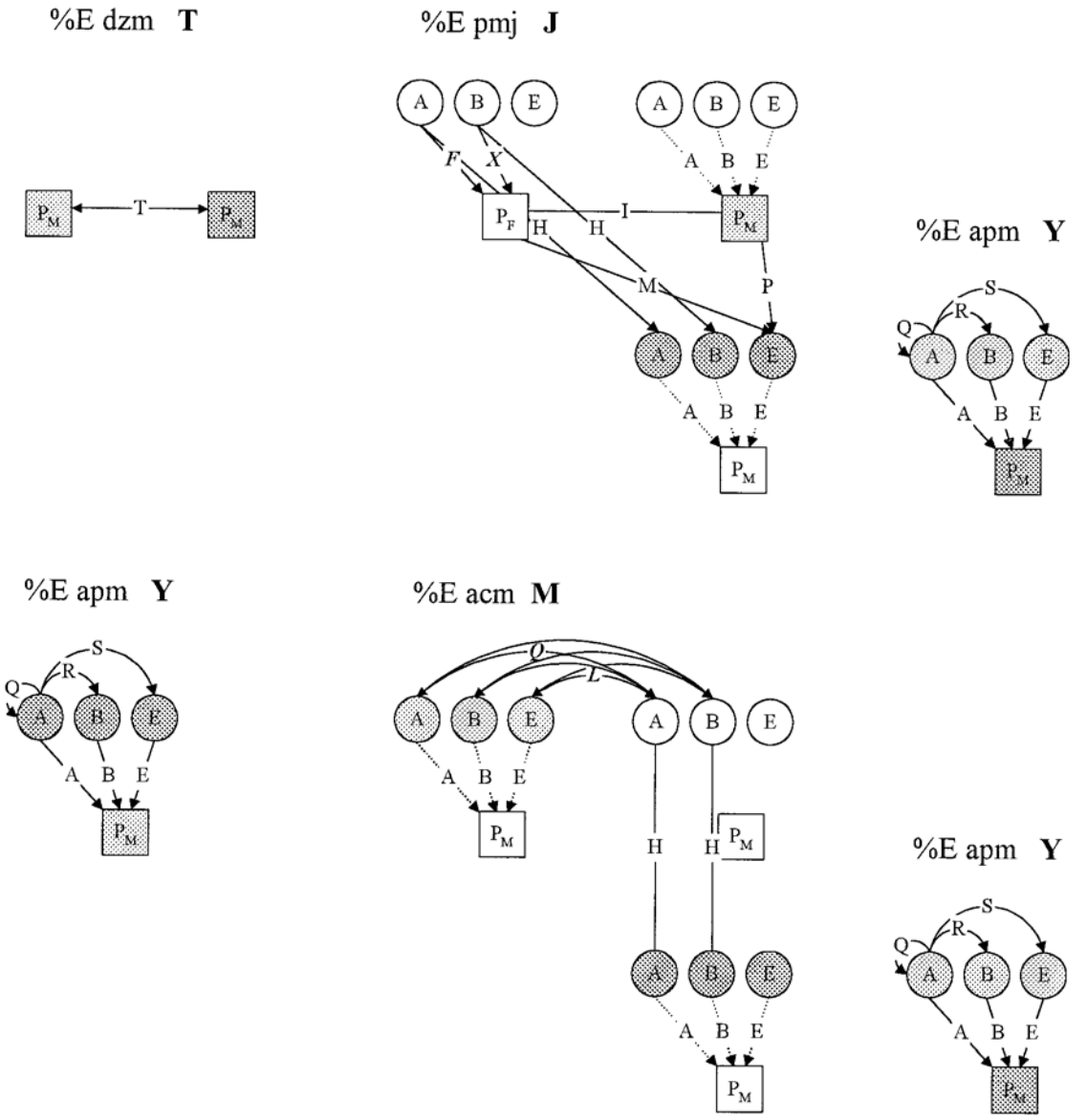

Figure 2 Example of building blocks for the expectation of the avuncular relationship between uncle and nephew through male DZ twins

To identify all the parameters of the model with the 88 available relationships, a total of 12 constraints have to be implemented, which is done in the following 12 groups. The assumption of equilibrium of variance components over generations requires constraints on the variances and the covariances of the latent factors in consecutive generations. For the genetic latent factors, group 'aco' specifies the constraint for the common set of genes, group 'bco' for the male-specific genes and group 'abco' for the covariance between the common and male-specific genetic factors. The constraints for the residual environmental covariance (groups cco–cdco) and the covariance between the genetic and environmental factors are sex-specific (groups acco–bdco). The total phenotypic variances are also constrained across generations in group 'pvm' for males and group 'pvf' for females. The expected phenotypic variances are the same as the expected covariance of MZ twins except for the environmental covariance which is fixed to 1. This implies that the unique environment is estimated as 1 minus the residual environmental covariance due to cultural transmission as specified in groups 'cco' to 'cdco'.

The data groups that read the observed raw data for all the relatives are 'mzmef', 'dzmef', 'mzfef', 'dzfef' and 'dzmfef'. Each of these is preceded by three (four for opposite sex twins) groups which

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combine the expectations between i) twins, their parents and sibs, ii) twins/parents/sibs and spouses/children, and iii) spouses and children. In addition to specifying the model for the covariances between relatives, the data groups also contain models for the means. Each selected variable is assigned a free parameter for its mean. The order of the relatives in the expected mean and covariance statements is identified by identification codes which match those in the variable length observed data files. The final data group also includes boundary statements to limit the range of values for the parameter estimates, and option statements for the output.

Eight groups are added to summarize the parameter estimates and calculate derived parameters. Groups 'parest' and 'parest2' list all the parameter estimates; groups 'varcom' to 'varcom3' compute variance components separately for males and females; groups 'constra' lists the results of the constraints groups to make it easy to check that all constraints are satisfied; and group 'prt' calls up all the computed matrices to print. Finally, confidence intervals around parameters of interest are requested in group 'conf'. Given the number of parameters in the bivariate full model (220) and the size of the observed dataset (1 or 2 variables in 30 000 individuals), it is wise to restrict the number of requested confidence intervals until after the evaluation of the model.

Although the model was written for the extended kinships of twins, additional relationships could be included or a reduced model could be fitted if fewer relationships are available. For example, if data are available for MZ and DZ twins and their parents, a simplified version could be used which has mostly the same building blocks as those specified in the first 25 groups of the full 'Stealth' model. One would have to choose between fitting a model with genetic dominance versus one with cultural transmission. Unless siblings are available as well, the parameters for a special twin environment are not identified in the twin–parent design.

Results

Response frequencies

Response frequencies for the church attendance and alcohol use questionnaire items and their cross-tabulation are listed in Table 1. This cohort demonstrated a marked difference between the church attendance behavior of men and women, with greater frequency of church attendance among women. The frequency of alcohol use was, however, much greater in men vs women. A significant negative association was observed between frequency of church attendance and of alcohol use in males (–0.27) and females (–0.25).

Maximum likelihood estimation from individual observations

Due to advances in computational speed and efficiency it is now feasible to use maximum likelihood methods in modeling genetic and environmental effects in pedigrees of this complexity, allowing us to obtain unbiased estimates and confidence intervals of all parameters. Table 2 lists the model parameter estimates obtained using maximum likelihood methods. For each of the major sources of variation – gender-common additive genetic (A), male-specific additive genetic (B), non-additive genetic (D), unique environment (E), common environment (C) and twin environment (T) – a Cholesky decomposition was used to model the covariance between church attendance and alcohol use. The covariances between the two additive genetic sources, between additive genetic and environmental sources and due to assortative mating are fully specified. Cultural transmission paths may be dependent on the sex of the parents and the offspring and both within and across phenotypes.

Most of the off-diagonal paths in the Cholesky and full matrices were estimated to be negative in males and females, reflecting the negative association between church attendance and alcohol use. Assortment was shown to exist primarily within phenotypes but some cross-assortment may exist. The pattern of the cultural transmission estimates indicated mostly negative transmission for church attendance and positive transmission for alcohol use. Parental alcohol use appeared to have a negative effect on church attendance, while the path from church attendance in parents to alcohol use in children is positive for male and negative for female offspring.

Maximum likelihood estimates of the proportions of variance for the genetic and environmental effects from the analysis of individual observations are shown in Table 3. The 95% confidence intervals could be obtained from Mx using the method of Neale and Miller.[20] However, given the large number of estimated parameters in the full bivariate model, estimating confidence intervals requires extensive computer time.

Additive genetic effects accounted for 53% of the variance in church attendance in males and 44% in females, with dominance explaining an additional 6% in females only. These proportions include the effects due to assortative mating (about 15%), given the highly significant spousal correlation. The environmental effects on church attendance were primarily individual specific (47% in males, 40% in

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Table 1 Response frequencies (%) of self-reported frequency of church attendance and alcohol use in the Virginia 30 000

Religious attendance	Response frequencies						
	Never	Rarely	Few times a year	Once or twice a month	Once a week	More than once a week	
Females (n=17 218)	7.1	17.4	17.0	11.0	31.2	16.2	
Males (n=11 643)	9.2	23.0	18.5	11.0	25.2	13.1	
Alcohol use	Not at all	Less often	Once or twice a month	Once or twice a week	3-4 times a week	Every day	More than once a day
Females (n=17 340)	32.5	29.3	10.0	14.3	7.4	5.8	0.8
Males (n=11 727)	24.7	19.2	11.0	18.9	13.7	10.2	2.2

Alcohol use/ religious attendance	Not at all	Less often	Once or twice a month	Once or twice a week	3–4 times a week	Every day	More than once a day	
Females								
Never	251	337	118	215	147	131	21	1220 (7.17)
Rarely	580	922	333	550	308	240	42	2975 (17.49)
Few times a year	620	928	363	534	280	155	26	2906 (17.08)
Once or twice a month	433	613	242	345	139	100	8	1880 (11.05)
Once a week	1901	1586	530	651	321	286	24	5299 (31.14)
More than once a week	1683	607	130	155	80	72	7	2734 (16.07)
	5468 (32.14)	4993 (29.35)	1716 (10.09)	2450 (14.40)	1275 (7.49)	984 (5.78)	128 (0.75)	17014
Males								
Never	162	191	110	194	188	168	46	1059 (9.20)
Rarely	418	467	274	629	411	344	97	2640 (22.94)
Few times a year	309	399	288	513	374	204	46	2133 (18.34)
Once or twice a month	210	258	165	267	212	130	25	1267 (11.01)
Once a week	820	640	337	474	317	280	32	2900 (25.20)
More than once a week	896	259	99	114	77	57	6	1508 (13.11)
	2815 (24.46)	2214 (19.24)	1273 (11.06)	2191 (19.04)	1579 (13.72)	1183 (10.28)	252 (2.19)	11507

females). Shared environmental factors arose from special twin environment or cultural transmission. Genotype–environment covariance was estimated to be negative for males but positive for females.

For alcohol use, heritability estimates were more modest (25%) of which a small percentage was due to assortative mating or male-specific effects. Dominance variance was only observed for males (12%). Approximately the same amount of the variance of church attendance and alcohol use was explained by unique environmental factors in males and females, whereas shared environmental factors contributed a greater proportion to alcohol use (14% in males and 23% in females), consisting mostly of non-parental and special twin environmental factors. In females only, cultural transmission and genotype–environment covariance resulting from the combined effects of genetic and cultural transmission accounted for 8% and 11% of the variance respectively.

The covariance between church attendance and alcohol use was also partitioned into genetic and environmental components. In males, genetic factors explained the majority of the covariance (68%), which can be divided into gender-common and male-specific additive genetic factors and those arising from assortative mating. Unique (30%) and common (5%) environmental factors accounted for the remainder of the covariance in males, with a small negative component (–4%) due to genotype–environment covariance. The partitioning of the church attendance–alcohol use covariance in females was quite different. Only 17% of the covariance was attributed to genetic factors and 15% to unique environmental factors. With 13% of the

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Table 2 Parameter estimates of genetic and environmental effects on frequency of church attendance (CA) and alcohol use (ALC) in the Virginia 30 000, obtained using maximum likelihood methods

	Genetic effects								Environmental effects						Genotype–environment effects			
	Gender-common additive genetic (A_m)		Male-specific additive genetic (B_m)		Gender-common and male-specific genetic covariance		Non-additive genetic effects (D_m)		Unique environment (E_m)		Common environment (C_m)		Twin environment (T_m)		Common genotype–environment covariance		Male-specific genotype–environment covariance	
Males	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC
CA	0.575		0.201		0.101	0.000	0.001		0.710		0.020		0.162		–0.058	0.039	0.003	–0.000
ALC	–0.145	0.411	–0.216	0.001	–0.047	0.000	0.376	0.001	–0.139	0.719	–0.202	0.231	–0.001	0.246	–0.053	0.032	0.000	0.013
Females																		
CA	0.544		–		–		0.246		0.642		0.001		0.190		0.062	–0.212	0.035	–0.069
ALC	–0.018	0.439	–	–	–	–	–0.056	0.001	–0.113	0.647	–0.167	0.088	–0.132	0.286	–0.100	0.142	0.000	0.000

	Correlation between male and female factors						Assortment and Cultural Transmission effects									
	Non-additive genetic effects		Common environment		Twin environment		Assortative mating		Maternal cultural transmission to male offspring		Paternal cultural transmission to male offspring		Maternal cultural transmission to female offspring		Paternal cultural transmission to female offspring	
Male–Female–	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC
CA	1.000	–	1.000	–	–1.000	–	0.703	0.099	–0.084	–0.039	–0.040	–0.111	–0.020	–0.083	0.041	–0.150
ALC	–	0.999	–	1.000	–	0.131	0.096	0.485	0.031	0.045	0.049	0.049	–0.069	0.148	–0.151	0.143

Table 3 Variance components for genetic and environmental effects on frequency of church attendance (CA), alcohol use (ALC) and the covariance between church attendance and alcohol use (in italic) in the Virginia 30 000, estimated using maximum likelihood methods

	Genetic effects										Environmental effects									
	Gender-common additive genetic (A_m)		Male-specific additive genetic (B_m)		Gender-common and male-specific genetic covariance		Non-additive genetic effects (D_m)		Due to assortative mating		Unique environment (E_m)		Common environment (C_m)		Twin environment (T_m)		Cultural transmission		Genotype-environment covariance	
Males	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC	CA	ALC
CA	0.318		0.039		0.022		0.000		0.154		0.474		0.000		0.025		0.012		–0.044	
ALC	0.282	0.166	0.147	0.041	0.065	0.013	–0.001	0.124	0.191	0.038	0.303	0.463	0.014	0.082	0.004	0.053	0.032	0.007	–0.036	0.013
Females																				
CA	0.299				–		0.061		0.144		0.396		0.000		0.036		0.020		0.044	
ALC	0.040	0.218	–	–	–	–	0.055	0.004	0.082	0.034	0.157	0.408	0.001	0.040	0.100	0.111	0.133	0.078	0.432	0.108

covariance due to cultural transmission, the major source of covariation (43%) was genotype–environment covariance. The remainder (10%) was explained by special twin environment.

Discussion

Both genetic and environmental factors have been demonstrated to have a significant role in the frequency of church attendance, as well as of alcohol use. Major influences on individual differences in church attendance appeared to be additive genetic and unique environmental effects, with smaller contributions from assortative mating, non-additive genetic effects, twin environment (which could arise from genotype × age interaction), cultural transmission and resulting genotype–environment covariance. For frequency of alcohol use, most of the variance was explained by additive genetic, unique and shared (non-parental) environmental factors. These contributions are consistent with the limited available literature (Truett et al,[13] D'Onofrio et al,[23] Eaves et al[24] for religious attendance, Prescott et al[25] for alcohol use).

Although evidence is increasing of the negative association between church attendance and alcohol use, both in adult[1,4–7,9] and adolescent[2,3,8] populations, no studies have reported on the contribution of genetic and environmental factors to this association. In this paper, we extended the twin kinship model fitted to church attendance data, as described in Kirk et al,[10] to include a second phenotype, frequency of alcohol use. Strikingly different results were obtained for males and females. Whereas major sources of variance such as additive genetic and unique environmental factors accounted for most of the church attendance–alcohol use relationship in males, these contributions were minor in females. Cultural transmission and the resulting genotype–environment covariance, explained the majority of the association in females.

These results imply that in males the genetic factors responsible for individual differences in frequency of church attendance and of alcohol use are at least partly the same. In addition, some aspects of the environment that are specific to an individual influence increased church going and reduced alcohol use or vice versa. Whether there is any direct 'protective' effect of church attendance on alcohol use or whether people who drink alcohol are less likely to go to church cannot be determined from the model fitted here. In females, the co-occurrence of high church attendance and low alcohol use or the reverse appears to have some origin in the family environment. Effects of environmental transmission from parents to offspring and the resulting genotype–environment covariance appear much stronger in females. In contrast to the male offspring, females whose parents go to church more frequently tend to use less alcohol. Also, those whose parents drink more alcohol appear less likely to go to church. These results are consistent with common environmental effects (including cultural transmission) having a greater impact in females than in males. However, there is also genetic transmission from parents to female offspring; it is an essential ingredient in genotype–environment covariance.

Given the complexity of the model and the large number of estimated parameters, caution is needed in the interpretation of the results. Even with as large a sample as the Virginia 30 000, information may be limited to estimate some parameters, especially those which are highly correlated or only identified by one or few relationships. For example, the correlation between the male and female special twin environmental parameters is derived from the difference between the opposite sex dizygotic twin correlation and other same sex twin correlations. Although we believe that in theory the full bivariate 'Stealth' model is identified, any particular dataset may not have enough information to identify particular parameters.

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