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## Marriage and Divorce: A genetic perspective

**Beth A. Jerskey, Ph.D.<sup>(1),(2)</sup>, Matthew S. Panizzon, Ph.D.<sup>(1),(3)</sup>, Kristen C. Jacobson, Ph.D.<sup>(4)</sup>, Michael C. Neale, Ph.D.<sup>(5)</sup>, Michael D. Grant, Ph.D.<sup>(1)</sup>, Mark Schultz, M.A.<sup>(1)</sup>, Seth A. Eisen, M.S., M.D.<sup>(6)</sup>, Ming T. Tsuang, M.D., Ph.D.<sup>(3),(7)</sup>, and Michael J. Lyons, Ph.D.<sup>(1),(7)</sup>**

<sup>(1)</sup> Department of Psychology, Boston University, Boston, MA

<sup>(2)</sup> Department of Psychiatry and Human Behavior, The Warren Alpert Medical School of Brown University, Providence, RI

<sup>(3)</sup> Department of Psychiatry, University of California San Diego, La Jolla, CA

<sup>(4)</sup> University of Chicago, Chicago, IL

<sup>(5)</sup> Virginia Institute of Psychiatric and Behavioral Genetics, Virginia Commonwealth University, Richmond, VA

<sup>(6)</sup> Department of Internal Medicine, Washington University School of Medicine, St. Louis, MO

<sup>(7)</sup> Harvard Institute of Psychiatric Epidemiology and Genetics, Boston, MA

### Abstract

Marriage is considered one of the most important sources of social support that an individual receives as an adult. Although hypotheses have been formulated as to why individuals may dissolve a marriage, the determinants of marital success or failure are still relatively unknown. Behavioral geneticists have found that both marriage and divorce are, in part, genetically influenced. The goal of this research was to determine the degree of shared genetic and environmental variance between the two marital statuses. Participants were 6,225 twin pairs from the Vietnam Era Twin Registry. Data were obtained on marital history, and if the individual was no longer married, how the marriage ended. Univariate analyses were performed to determine the extent of genetic and environmental influences each of the marital statuses (i.e., marriage and divorce), followed by a novel bivariate analysis to test the shared variance between marriage and divorce. Results from this analysis revealed that the two different marital statuses were influenced by entirely distinct genetic and environmental factors.

### Keywords

marriage; divorce; twins; stage modeling

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Marriage is considered one of the most important forms of social support for adults, and population-based studies have found that most adults will marry at some point in their lifetime (Bjorksten & Stewart, 1984). Despite the benefits of marriage, the divorce rate has been rising since the middle of the twentieth century (Coontz, 2007). One potential origin

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Corresponding author: Beth A. Jerskey, Butler Hospital, 345 Blackstone Blvd, Weld Building, Room 210 (TRG), Providence, RI 02912, tel: 401-455-6640, fax: 401-455-6618, Beth\_Jerskey@Brown.edu.

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for this trend is the genetic influence on getting married and ultimately divorced. Johnson and colleagues (2004) found considerable genetic influences on the propensity to marry over the course of the lifespan. Longitudinally, the genetic influences on getting married have been found to increase at midlife and then decrease in older adulthood (Trumbetta, Markowitz, & Gottesman, 2007). Divorce, like marriage, has also been found to be highly heritable. McGue and Lykken (1992) found the proportion of genetic variance in the risk of getting a divorce was slightly greater than 50%. In addition, D'Onofrio and colleagues (2007) reported an increased risk of marital instability in offspring of divorced parents (i.e., intergenerational transmission).

Jockin and colleagues (1996) found that up to 40% of the variance in the heritability of divorce is from genetic factors that affect the personality of one spouse. Traditionalism and social potency were the most important correlates of divorce risk, as were high scores in both neuroticism and extraversion. Spotts and colleagues (2004) found that the way that spouses interact with one another stems from genetically influenced characteristics; however, they posit that the same influences do not always operate similarly in different social settings. In addition, various pathologies may have negative effects on marital quality or vice versa. For example, Dehle and Weiss (1998) found that low marital quality predicted an increase in depressed mood and at the same time initially higher scores of depression predicted greater decline in marital quality. Divorced individuals have also shown increases in various pathologies such as affective disorders, gambling and substance abuse (Jerskey et al. 2001) all of which have shown to have genetic influences (e.g., see Plomin, DeFries, McClearn, & Rutter, 1997).

Trumbetta and Gottesman (2000) proposed two distinct 'endophenotypes' for marital status; one oriented toward pair-bonding and the other toward mate diversification. Pair-bonding would reflect a greater likelihood of maintaining a marriage over a lifespan, while mate diversification is associated with the greater likelihood of multiple marriages. They found significant genetic influences on both endophenotypes with unique environmental influences accounting for the remainder of the variance. However, it is unclear the extent to which both phenotypes might share genetic variance.

While influences on marriage and divorce can be separately evaluated using traditional twin and non-twin approaches, the analysis of *shared* risk or protective factors across marriage and divorce poses a unique methodological dilemma, as divorce is contingent upon having ever married. Indeed, in studies of unrelated individuals, determining the influence of shared factors on marriage and divorce is an intractable problem. In contrast, twin studies have advantages over non-twin designs in that data on a co-twin's marital status can also be used simultaneously with data on the twin's own marital status. Nevertheless, standard multivariate twin models are not designed to assess covariation among two traits in which the status of one trait is conditional upon the other. A similar situation has been observed in substance use literature when modeling the relationship of substance initiation to various outcomes (Heath & Martin, 1993, Koopmans, Slutske, Heath, Neale, & Boomsma 1999; Madden et al., 1999).

In such cases, a specific type of bivariate analysis is needed to determine the degree of covariance between the two traits. This "stage" approach, which is captured by the Causal-Contingent-Common (CCC) pathway model, may be used to accurately describe the degree to which the variables are independent constructs from one another (Kendler et al., 1999). While these CCC models have been applied to prior studies of substance use (e.g., Maes et al., 2004), to our knowledge, this would be the first study to use the CCC approach to determine the extent of shared genetic and environmental influences on the social constructs of marriage and divorce. Thus, the purpose of the present study was to explore the genetic

and environmental influences on marriage and divorce, with a particular emphasis on the nature of the relationship between the two constructs. We hypothesized the existence of genetic and environmental factors specific to both marital statuses as well as a significant phenotypic association.

## Methods

### Sample

Participants were members of the Vietnam Era Twin (VET) Registry, a population based cohort of roughly 6,300 male-male twin pairs (Goldberg, Curran, Vitek, Henderson, & Boyko, 2002). Detailed information on ascertainment procedures have been published elsewhere (Eisen, True, Goldberg, Henderson, & Robinette, 1987; Hendersen et al., 1990). Participation in the VET Registry is largely unbiased with regard to demographic characteristics (Goldberg, Eisen, True, & Hendersen, 1987). At the time of data collection, 92.6% were employed full-time and 1.8% part-time. In terms of occupational status, 45% describe themselves as “blue collar” while 45% could be classified as “white collar” workers; 33.3% were high school graduates and 38.6% college graduates. The distribution of race and ethnicity was relatively similar to the total population of men who served in the military during the Vietnam era with the majority (90.4%) identifying themselves as non-Hispanic white. The mean age at the time of data collection was 38 years old ( $SD \pm 2.7$ , range = 30–48).

### Measures

Marital history was obtained in 1987 as part of a 24-page questionnaire that asked participants a broad spectrum of demographic and health questions including a subsection specific to questions about marital status (Eisen et al., 1987). Specifically, participants were asked if they had ever married, whether they were still in the marriage and, if not, how the marriage ended (e.g., death of spouse, divorce).

### Data Analysis

Biometrical modeling was utilized to estimate the relative contributions of genes and environment to marital outcomes. In the conventional univariate analysis (i.e., the ACE model) the total phenotypic variance of a trait is partitioned into additive genetic effects (A or  $a^2$ ), common environmental effects (C or  $c^2$ ) that are shared equally between members of a twin pair, and unique environment effects (E or  $e^2$ ) that are uncorrelated between twins. The E term consists of all influences that are specific to the individual rather than the twin pair, thus promoting dissimilarity between twins, and includes random error (Neale & Cardon, 1992). Nested models are also compared to the full ACE model.

Multivariate analyses extend the ACE model to elucidate the degree to which genetic and environmental influences overlap between traits, as well as contribute to the observed phenotypic correlation. However, when an individual's status for one trait is conditional upon their status for another trait, standard multivariate approaches are no longer effective. As described by Heath and colleagues (2002) in reference to substance use, “the same person cannot be simultaneously a non-user and a persistent or a dependent user (p. 114).” Similarly, it is impossible for an individual to provide data pertaining to the liability for divorce if they have never married. We therefore applied a CCC model to the data in order to determine the extent to which genetic and environmental influences on getting married are the same as the genetic and environmental influences of divorce (Figure 1). The CCC model is an improvement over standard Cholesky models because it tests the contingent nature between marriage and divorce. Indeed, Cholesky models cannot be used to model the relationship between marriage and divorce, as individuals who have divorced, have by

definition been married as well, which leads to no variation in marital status among individuals who have been divorced.

The CCC model was developed as a means of capturing the covariance between conditionally related traits (Kendler et al., 1999). Detailed descriptions of the model's implementation and applications are available elsewhere (e.g., Neale, Aggen, Maes, Kubarych, & Schmitt, 2006). Briefly, the model assumes a direct causal path ( $b$ ) linking the liability of getting married and getting divorced. This  $b$ -pathway represents a single regression parameter which specifies that the causal contributions of A, C and E on marriage are proportional to their effects on divorce. When squared, the causal parameter estimates the proportion of the phenotypic variance in divorce accounted for by ever marrying. Thus the total phenotypic variance for divorce ( $\text{var}_d$ ) is calculated as the sum of four variance components ( $\text{var}_d = b^2 + a^2 + c^2 + e^2$ ) when the variance for marriage is equal to 1, and when the variance components are uncorrelated between liability to marriage and to divorce. Critical to the CCC model is that data for the down stream variable (i.e., divorce) are structurally missing for those who never married. Intuitively this would set up a zero-variance problem; it would be impossible to estimate the covariation between getting married and getting divorced since participants who answered "yes" to the progression item (i.e., divorce) show no variation in the initiation item. However, by virtue of having data from co-twins the path is identifiable (see Neale et al., 2006).

In the current analysis, models were fit to ordinal data using the maximum likelihood based structural equation modeling software package Mx (Neale, Boker, Xie, & Maes, 2002).

The difference in the log-likelihood between the full model and a reduced model is distributed as a chi-square, which when used in conjunction with the difference in degrees of freedom between the models can be used to assess whether a reduced model provides a good fit to the data, as indicated by a non-significant  $p$  value. In addition, the Akaike Information Criterion (AIC; Akaike, 1987) was used to identify the most parsimonious model. The smallest AIC indicates the "best fitting" model or the most balanced model between fit and parsimony. This metric penalizes highly parameterized models relative to simpler ones (Tanaka, 1993).

It should be noted that the first stage in the model is the same as the univariate analyses on ever married and will, therefore, provide the same A, C, and E estimates, while the second stage is influenced by the shared variance between marriage and divorce reflected in a regression coefficient ( $b$ ). The data for the secondary outcome (i.e., divorce in this model) are structurally missing for those who never married in the first place.

## Results

Prior to beginning our univariate and bivariate analyses, we ran fully saturated<sup>1</sup> models which estimated thresholds for both marriage and divorce separately for twin 1 and twin 2, as well as for MZ and DZ twins. We then systematically tested whether the thresholds could be equated across each member of the pair and across zygosity. These threshold-equal models fit the data well, indicating that rates of marriage and divorce do not systematically differ across twins within a pair, or among MZ versus DZ twins.

<sup>1</sup>Due to the conditional nature of the two phenotypes, there is no information to estimate the within-person covariance between the marriage and divorce liabilities. Thus, the model is not identified with respect to this parameter. However, the optimization algorithm used in Mx (Gill et al., 1998) is able to find one of the many equivalent solutions, so it remains only to adjust the df by the requisite number of underidentified covariance parameters, which is four in this case (within person covariances for twins 1 and 2 in both MZ and DZ groups).

### Univariate Analyses of ever-married

The full univariate model reflected a substantial contribution of genes and unique environmental influences. Table 1 displays the parameters estimates for the univariate analyses and Table 2 displays the results for the biometrical model fitting. The best fitting model for ever married was the AE model suggesting that twins' resemblances to each other were due to genetic and non-shared environmental factors.

### Univariate Analyses for ever-divorced

Similar to the univariate results for ever marrying, the full univariate model reflected a substantial contribution of genes and unique environmental influences with less common environmental influences. Again, the AE model fit the data the best once the common environmental influences were removed. Tables 3 and 4 reflect the parameter estimates and modeling fitting for ever divorced.

However, since ever divorcing is dependent on getting married, the univariate model may be misleading given that there may be a strong shared genetic and environmental influence between getting married and subsequently getting divorced. Thus, the last analysis was the bivariate CCC model to determine the extent to which there are overlapping determinants.

### Bivariate Analysis of ever-married and ever-divorced

We ran three alternative versions of the CCC model. The first model assumes that the determinants for divorce are solely related to the genetic and environmental influences on getting married (i.e., having ever married and ever divorced on the same continuum). In this model, a good fit to the data would suggest that marriage and divorce share a substantial proportion of the same genetic and environmental influences. However, this model was not a good fit to the data given the significant p-value and AIC ( $X^2 = 107.72$ ;  $p = 0.00$ ;  $AIC = 97.77$ ). The second model allows the b-pathway to be free to determine the extent of shared variance between ever married and ever divorced. Table 5 lists the model fitting results for bivariate analyses on ever-married and ever-divorced. Due to the underidentification of the model noted above, there is no saturated model comparison to the CCC model.

The results from the full CCC model suggest that almost all the variance in divorce is independent of that for ever getting married. This was reflected in the b-parameter estimate which was close to zero ( $b = 0.0854$ ). In other words, 0.7% of the variance in ever getting divorced ( $0.085^2 = 0.0072$ ) is in common with ever marrying (Figure 2).

The last model set the regression pathway to zero (i.e.,  $b = 0$ ), under the assumption that the genetic and environmental influences on marriage and divorce are completely independent. This model fit the data better than the previous two models (Figure 3,  $p = 0.579$ ,  $AIC = -4.031$ ). Since the variance attributed to the regression of divorce on marriage in the full CCC model was so small, the parameters estimates were almost identical for the full CCC model and the CCC model in which b was set to zero.

## Discussion

Consistent with past findings, results from the present study indicate that both getting married and ending a marriage by divorce are significantly influenced by genetic factors. However, it was also found that the genetic and environmental influences responsible for getting married are independent from those that influence divorce. Several possible explanations exist for the genetic and environmental independence of marriage and divorce. There is evidence to suggest that after the selection of a mate, there may be some factors that are protective for a couple (e.g., same religious background) and others that place the couple

at greater risk for future problems (e.g., increased alcohol consumption in one spouse). In some cases, the concordance of risk factors between spouses may lead to increased marital quality (e.g., shared phobias; McLeod, 1994).

While some features in a marriage appear to be assortative (Heath, Kendler, Eaves, Markell, 1985), other features such as personality tend not to be (Eaves, Eysenck, & Martin, 1989). However, it is possible that more extreme fluctuations in some personality features make someone less likely to marry in the first place (e.g., low levels of social closeness), while other personality factors with different modes of genetic transmission increase an individual's potential for divorce (e.g., low levels of traditionalism). Studies of personality assortment may be only getting a snapshot at some time during the marriage which may not be truly representative. Personality factors related to selecting a mate may be very different from factors that increase the likelihood of keeping a mate. In addition, it is possible that individual factors that may lead to divorce may be more persistent and those individuals who remain married may have characteristics that are more malleable (Spotts et al., 2005; 2004).

In addition, a moderate degree of assortment exists within and across psychiatric conditions (Maes et al., 1998) in that individuals select mates similar to themselves. However, the quality and strength of the marriage, not the existence of the marriage per se, may be the necessity to keeping problematic behavior to a minimum with the inverse effect for marriages of poor quality (Laub, Nagin, & Sampson, 1998). It may also be that certain personality traits influence less adaptive and more problematic behaviors leading to increased marital discord (i.e., low harm avoidance may be associated with increased alcohol consumption and gambling).

### Methodological Limitations

The results of this research should be interpreted in the context of two study-specific methodological limitations. The participants in this study were: 1) all male and 2) relatively young (mean age 38). Thus these results may not generalize to women or samples from different age cohorts. Spotts and colleagues (2006) found that men's reports of marital warmth and conflict were influenced by the same genetic factors; however, different genetic factors were responsible for these same constructs in women. McGue and Lykken (1992) found relatively little genetic difference regarding divorce between males and females in their sample. They also determined, via cross-sectional data, that the genetic influence on divorce increased with age. Contrary to this, using longitudinal data, Trumbetta and Gottesman (1997) found stronger genetic influences when their sample was younger; citing possible greater mortality risks to divorced individuals, age-related changes in motivations to divorce and an overall increase in the divorce rate as factors that may account for the declining heritability.

### Directions for future research

Multivariate analyses utilizing personality factors or forms of psychopathology could be added to the model. However the temporal ordering of the personality and divorce measures is problematic; whether neuroticism and distress are the cause or consequence of an unhappy marriage is an open question (Gottman, 1998). This may also be the case for various forms of psychopathology (i.e., alcohol consumption leads to divorce or divorce prompts alcohol consumption). In addition, it may be the discordance between a husband and wife which leads to marital difficulties (i.e., gambling may only be a problem if one spouse is involved, if both spouses are gamblers there may be an equilibrium in the relationship); therefore, information from both spouses would be useful in trying to disentangle the factors related to divorce. More would also need to be known about which predisposing factors of personality



mixed with pathological factors contribute to problems with marital adjustment and ultimately marital dissolution. Future research is needed to continue to investigate factors that may contribute to the two distinct marital statuses.

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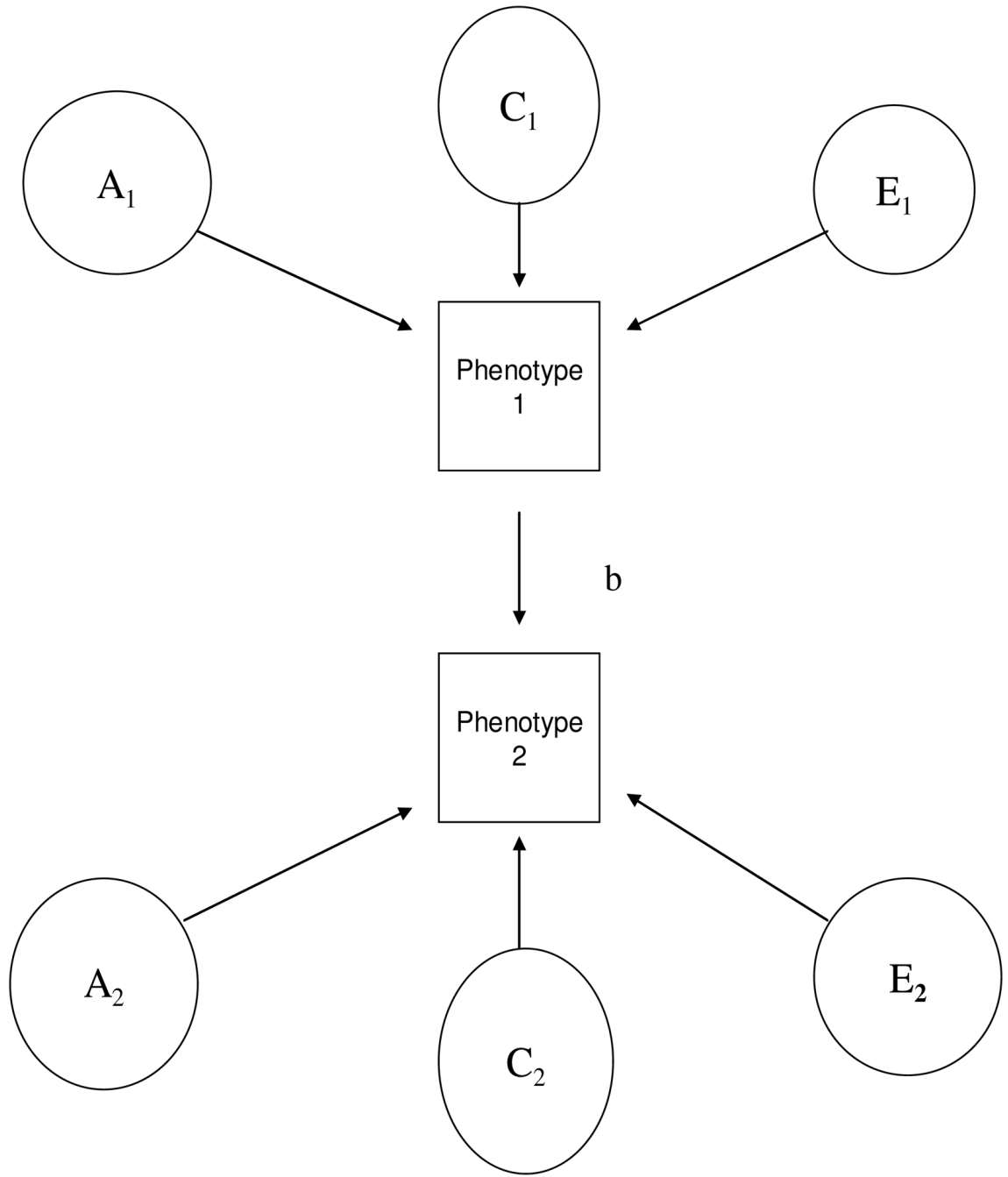
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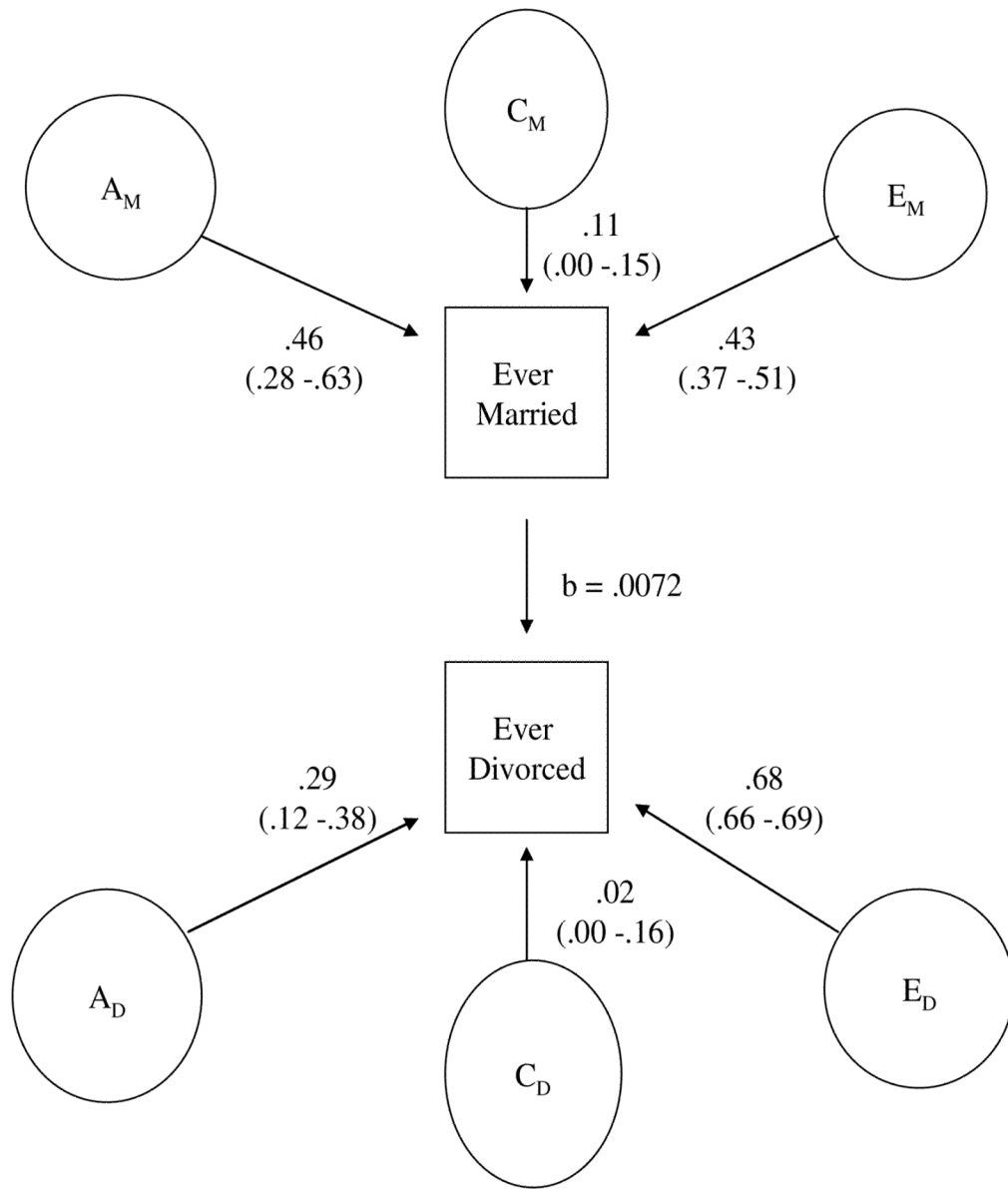
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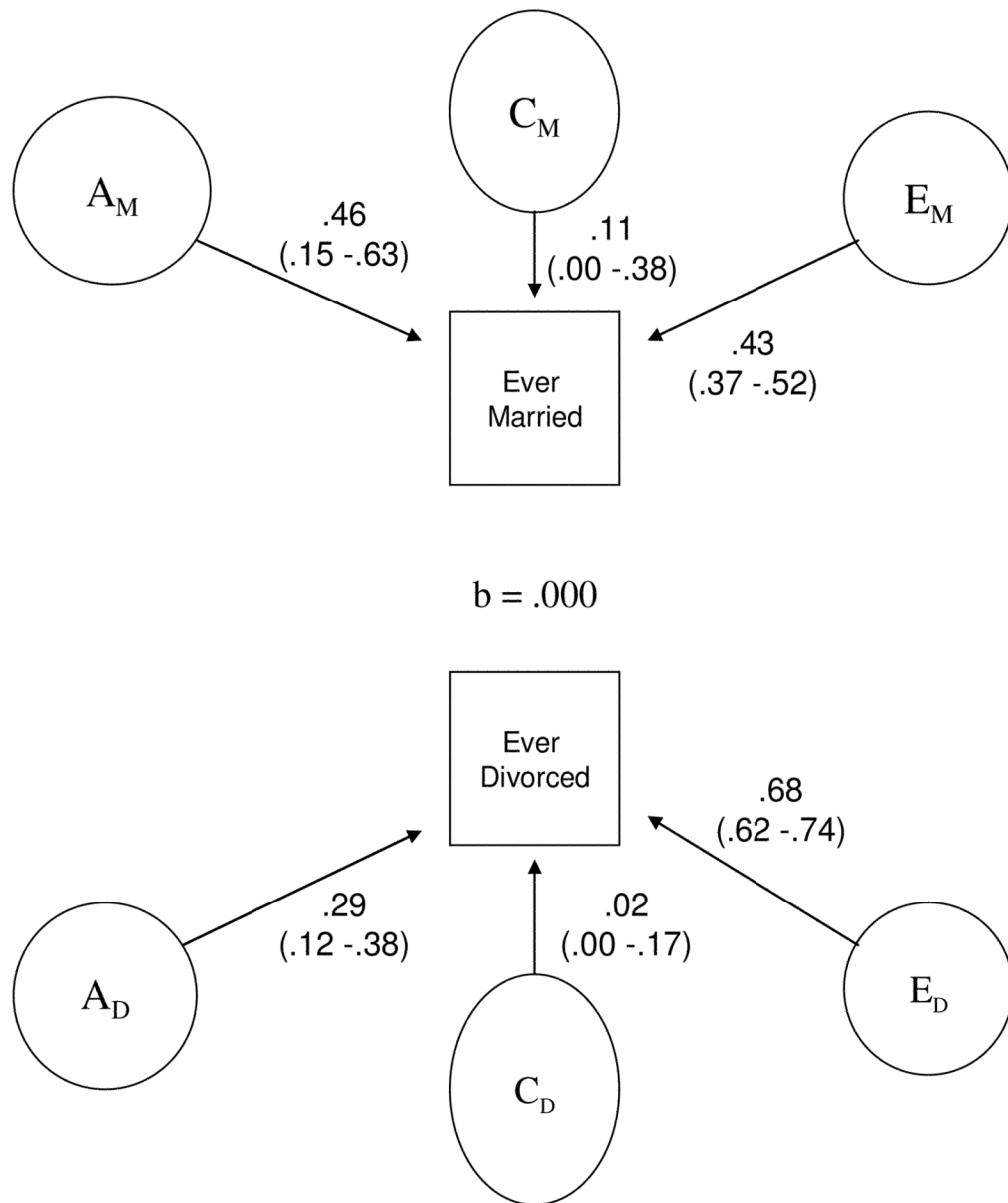
**Figure 1.**  
The CCC model (adapted from Kendler et al., 1999)



**Figure 2.**

Full CCC model

Note. With the exception of  $b$ , the values presented are the standardized variance components for each phenotype along with the 95% confidence intervals.



**Figure 3.**  
Best-fitting CCC model minus the regression line

**Table 1**

Parameter estimates for univariate analyses on ever-married

Full and nested models	Heritability $h^2$ (95% CI)	Family Environment $c^2$ (95% CI)	Non-Family Environment $e^2$ (95% CI)
ACE	.41 (.16-.62)	.15 (.00-.37)	.44 (.37-.51)
<b>AE</b>	<b>.58 (.51-.64)</b>	-	<b>.42 (.36-.49)</b>
CE	-	.48 (.42-.54)	.52 (.46-.58)
E	-	-	1.00 (1.00-1.00)

Note. Best-fitting model in bold.

Table 2

Univariate model fitting results for ever-married

Ever Married	Absolute Model Fit					Relative Model Fit			
	-2 LL	df	LRC <sup>a</sup>	$\Delta df^a$	p-value <sup>a</sup>	AIC	LRC <sup>b</sup>	LRC $\Delta^b$	p-value <sup>b</sup>
0 Saturated model	6500.936	9872	n/a	n/a	n/a	n/a	-	-	-
1 Full Model (ACE)	6503.377	9875	2.441	3	.486	-3.559	n/a	n/a	n/a
2 AE model	<b>6505.180</b>	<b>9876</b>	<b>4.244</b>	<b>4</b>	<b>.374</b>	<b>-3.756</b>	<b>1.803</b>	<b>1</b>	<b>.179</b>
3 CE model	6513.740	9876	12.804	4	.012	+4.804	10.363	1	.001
4 E model	6704.166	9877	203.230	5	<.001	+193.23	200.789	2	<.001

Note. LRC = Likelihood Ratio Chi-Square; df = degrees of freedom; AIC = Akaike's Information Criterion. Best-fitting model in bold.

<sup>a</sup>Significance of model is based on comparison with the saturated model.

<sup>b</sup>LRC obtained from comparison with Full Model (Model 1).

**Table 3**

Parameter estimates for univariate analyses on ever-divorced

Full and nested models	Heritability $h^2$ (95% CI)	Family Environment $c^2$ (95% CI)	Non-Family Environment $e^2$ (95% CI)
ACE	.32 (.13–.38)	.00 (.00–.16)	.68 (.62–.74)
<b>AE</b>	<b>.32 (.26–.38)</b>	-	<b>.68 (.62–.74)</b>
CE	-	.25 (.20–.30)	.75 (.70–.80)
E	-	-	1.00 (1.00–1.00)

Note. Best-fitting model in bold.



**Table 4**

Univariate model fitting results for ever-divorced

Ever Divorced	Absolute Model Fit					Relative Model Fit			
	-2 LL	df	LRC <sup>a</sup>	$\Delta df^a$	p-value <sup>a</sup>	AIC	LRC <sup>b</sup>	LRC df <sup>b</sup>	p-value <sup>b</sup>
0 Saturated model	11249.455	8819	n/a	n/a	n/a	n/a	-	-	-
1 Full Model (ACE)	11251.357	8822	1.902	3	.593	-4.098	n/a	n/a	n/a
<b>2 AE model</b>	<b>11251.357</b>	<b>8823</b>	<b>1.902</b>	<b>4</b>	<b>.754</b>	<b>-6.098</b>	<b>0.000</b>	<b>1</b>	<b>1.00</b>
3 CE model	11261.451	8823	11.996	4	.002	+3.996	10.094	1	.001
4 E model	11347.776	8824	98.321	5	<.001	+88.321	96.419	2	<.001

Note. LRC = Likelihood Ratio Chi-Square; df = degrees of freedom; AIC = Akaike's Information Criterion. Best-fitting model in bold.

<sup>a</sup>Significance of model is based on comparison with the saturated model.

<sup>b</sup>LRC obtained from comparison with Full Model (Model 1).

**Table 5**

Model fitting results for bivariate analysis

	EP	-2 log-likelihood	$\Delta\chi^2$	$\Delta$ df	p-value	AIC
1. Full CCC model with a free b parameter	9	17754.214	1.150	2	0.563	-2.850
2. Full model with b parameter set to zero	<b>8</b>	<b>17755.033</b>	<b>1.969</b>	<b>3</b>	<b>0.579</b>	<b>-4.031</b>

Note. Best-fitting model in bold. EP = estimated parameters; df = degrees of freedom; AIC=Akaike's Information Criterion; CCC = causal, contingent, common-pathway.