



## Marriage and divorce: A genetic perspective

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### 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 6225 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.

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### 1. Introduction

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 for this trend is the genetic influence on getting married and ultimately divorced. Johnson, McGue, Kreuger, and Bouchard (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 et al. (2007) reported an increased risk of marital

instability in offspring of divorced parents (i.e., intergenerational transmission).

Jockin, McGue, and Lykken (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 et al. (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,

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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.

## 2. Methods

### 2.1. Sample

Participants were members of the Vietnam Era Twin (VET) Registry, a population based cohort of roughly 6300 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).

### 2.2. 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).

### 2.3. 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, Martin, Lynskey, Todorov, and Madden (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 di-

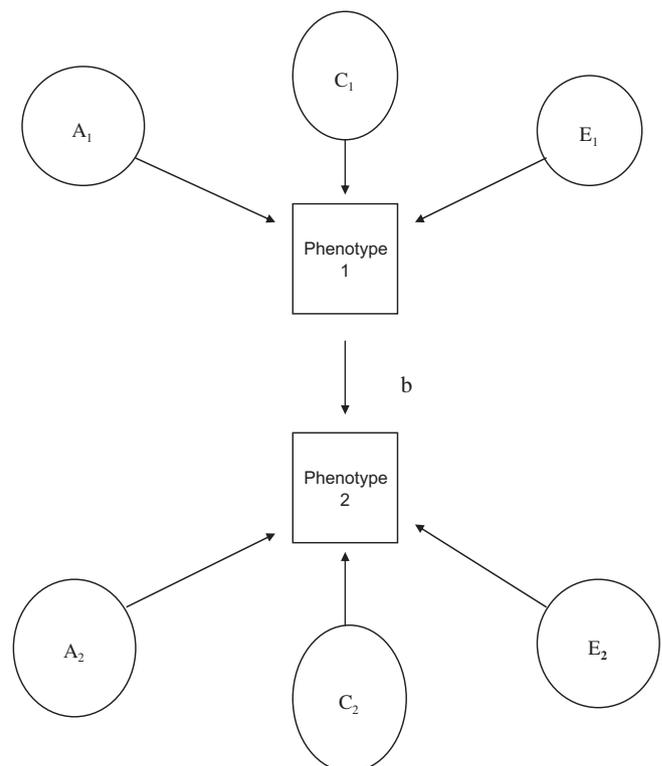


Fig. 1. The CCC model (adapted from Kendler et al., 1999).

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