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Understanding Associations among Family Support, Friend Support, and Psychological Distress

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Abstract

Emotional support from family and friends is associated with lower psychological distress. This study examined whether genetic and environmental influences explain associations among family support, friend support, and psychological distress. Data were drawn from the Midlife Development in the United States (MIDUS) study and included 947 pairs of MZ, same-sex DZ, and opposite-sex DZ twins. Results showed that a genetic factor explains the relationship between friend support and psychological distress, independent of family support. Alternatively, a nonshared environmental factor accounts for an association among family support, friend support, and psychological distress. Thus, heritable factors shape a distinct relationship between friend support and psychological distress, but unique experiences contribute to a link among family support, friend support, and psychological distress.

Greater emotional support from friends is consistently linked to lower levels of psychological distress (e.g., Cohen, 2004; Norton et al., 2005; Lepore, Evans, & Schneider, 1991; Ritsner, Modai, & Ponizowsky, 2000). A frequent explanation for this association is one focusing on environmental sources, such that friends engage in behaviors that help to alleviate individuals' psychological distress. A recent genetically informed study, however, demonstrated that the relationship between friend support and psychological distress is attributable to genetic influences (Horwitz, Reynolds, Neiderhiser, & Charles, in press). This suggests that the same set of genes that influence friend support also contribute to psychological distress. A new question that arises from this finding is: what types of genetically-based mechanisms explain this link? For example, heritable tendencies to evoke more or less support from others may be responsible for an association between general aspects of social support (i.e., with family and friends) and psychological distress. Alternatively, heritable tendencies to seek out supportive friends may account for a distinct relationship between friend support and psychological distress that is not shared with other forms of social support, including family support. Thus, additional research is needed to assess whether genetic contributions to the link between friend support and psychological

distress are shared with family support. The current study examined whether genetic and environmental influences explain associations among family support, friend support and psychological distress in a sample of adult twins in the United States.

Genetically informed designs are used to examine potential genetic influences on phenotypes. Phenotypes refer to any observable characteristic, such as hair color, cognitive ability, personality (e.g., extraversion), reported social support, or reported psychological distress. In twin studies, genetic factors reflect the influence of the whole genotype on the measured phenotype, rather than the effects of any particular genes (Reiss & Leve, 2007). The twin-based method has been posited to be particularly useful for examining how genetic factors shape complex traits, which are likely influenced by many (polygenic) genes (McGue & Bouchard, 1998). As described in detail in the Method section, twin studies compare covariances for a trait or set of traits among genetically identical (monozygotic, MZ) twins versus fraternal (dizygotic, DZ) twins. For example, twin designs can be used to assess whether identical twins and their co-twins are more alike on a particular phenotype compared to fraternal twins and their co-twins. If identical twins are more alike on the given phenotype, this indicates the influence of genetic effects on that phenotype.

Twin-based methods have been used to understand how mental health outcomes, including psychological distress, are shaped. Indeed, previous research has shown that approximately 44% of the individual variance in psychological distress is ascribable to genetic effects (Rijsdijk et al., 2003). This suggests that psychological distress is, at least in part, a heritable characteristic.

Likewise, twin-based methods have been used to understand how social support arises. This research has shown that genetic factors explain approximately 17 to 38% of the individual variance in both family support and friend support (e.g., Kendler & Baker, 2007). When genetic influences are found to contribute to social support, this may reflect the influence of genotype-environment correlation (r_{GE}) on social support (e.g., Horwitz & Neiderhiser, 2011). Genotype-environment correlation refers simply to a correlation between an individual's genotype and environment (Plomin, DeFries, & Loehlin, 1977; Scarr & McCartney, 1983). For example, an underlying heritable characteristic (e.g., personality) may be correlated with an individual's exposure to certain environmental experiences (e.g., the type of social support that the individual receives).

Two types of r_{GE} that are relevant for understanding how genetic factors shape social support include evocative and active r_{GE} . Evocative r_{GE} is defined as a phenomenon where individuals' heritable characteristics are likely to elicit certain responses from others. For example, previous research has suggested that people with higher levels of heritable aggressive or externalizing behaviors tend to elicit more negative responses from others (e.g., Ganiban et al., 2009; Marceau et al., 2013). Evocative r_{GE} is relevant for understanding both friend and family support because family and friends may react in similar ways to individuals' heritable characteristics. Alternatively, active r_{GE} occurs when individuals select relationships that are correlated with their own heritable characteristics. Prior work has suggested that adolescents' heritable characteristics (e.g., personality traits) are related to the particular peer groups they select (e.g., Brendgen, 2012). For example,

adolescents with higher levels of heritable aggressive personality may tend to select peers with similar aggressive tendencies (Brendgen, 2012). Active rGE is relevant for explaining friend support because friends are selected but not family support because family members are ascribed. To illustrate, individuals with higher levels of heritable extraversion may tend to select more supportive friends.

Genetically informed studies also provide the capability of investigating the extent to which genetic factors explain associations among phenotypes. Using this approach, several previous studies have shown that genetic factors explain links between social support and symptoms of psychological distress (e.g., Bergeman, Plomin, Pederson, & McClearn, 1991; Spotts et al., 2005; Yuh et al., 2008). These studies often use general measures of social support that include both family and friend support in one composite measure. Thus, it is difficult to determine from this work whether genetic influences contribute to associations among symptoms of psychological distress and general aspects of support, or more specific forms of support from family or friends. A more recent study demonstrated that the link between friend support and psychological distress is also ascribable to genetic effects (Horwitz et al., in press). This finding helped to clarify that the same heritable characteristics that are important for shaping friend support also contribute to psychological distress.

Yet questions remain about what genetically-based mechanisms explain the relationship between friend support and psychological distress. Specifically, genetic influences may give rise to associations among general aspects of support (i.e., from family and friends) and psychological distress. A plausible explanation for these genetic influences would be evocative rGE . For example, the same heritable characteristics in individuals that tend to elicit less support from both family and friends may also lead to greater levels of psychological distress. Alternatively, genetic influences may shape a distinct relationship between friend support and psychological distress that is independent of support from family members. These genetic influences may reflect the role of active rGE . That is, individuals' heritable characteristics may tend to influence their friend choices and, in turn, their friend support and psychological distress. Thus, a genetically informed design is needed to investigate whether genetic influences contribute to a relationship among family support, friend support, and psychological distress, or to a unique association between friend support and psychological distress.

In addition to genetic influences, twin studies also provide information about the role of environments, including shared and nonshared environments, in shaping phenotypes. Shared environmental influences, described in more detail in the Method section, are ascertained in twin studies by the degree of similarity that twin pairs share with each other that does not stem from genetic influences (e.g., twins' rearing environment). For example, growing up in a highly supportive environment where parents encouraged and nurtured friendships may give rise to strong supportive relationships from both family and friends and lower levels of psychological distress (Shaw, Krause, Chatters, Connell, Ingersoll-Dayton, 2004). In this way, shared environmental influences may shape links among general aspects of individuals' social support from family and friends and psychological distress. Nonshared environmental influences may also account for an association among family support, friend support, and psychological distress. Nonshared environmental influences are those unique

environmental experiences that twins do not share with their co-twins (e.g., negative life events unique to the individual). For example, job loss may lead to increased psychological distress and social withdrawal (Russell, 1999), which may influence how people perceive support from family and friends.

The current study examined the degree to which genetic and environmental (both shared and nonshared) factors contribute to the association among family support, friend support, and psychological distress. The sample was drawn from Midlife Development in the United States (MIDUS) study, which was the same sample of adult twins that was used in the investigation by Horwitz and colleagues (in press). The current study builds on Horwitz, in press, by examining whether genetic contributions to the link between friend support and psychological distress are explained by or distinct from support from family members. We also assessed the extent to which environmental factors explain associations among family support, friend support, and psychological distress.

Method

Participants

The sample consisted of 998 twin pairs from the MacArthur Foundation Survey of Midlife in the United States (MIDUS) study (Kessler, Gilman, Thornton, & Kendler, 2004). Data on the twins were collected primarily from 1995 to 1996. Both members of each twin pair participating in the study met overall study eligibility criteria and criteria specific to the twin sample. These criteria included being at least first-degree relatives of the original contact or his or her spouse or partner, being aged between 25 and 74, having a residential telephone number; living in the continental United States, and speaking English. Zygosity was determined using self-report questions that asked about similarity in traits such as eye and hair color and issues such as whether the twins were mistaken for one another as children. Such techniques are generally more than 90% accurate (Lykken, Bouchard, McGue, & Tellegan, 1990). Twin pairs were randomly designated as either Twin 1 or Twin 2.

In the current analyses, twin pairs were excluded if they had missing or unknown values for zygosity or sex or if they came from families with data from two or more pairs. After these exclusions, the present study included 947 twin pairs, including 362 monozygotic (MZ) ($n = 168$ MZ males, $n = 194$ MZ female pairs), 335 same-sex dizygotic (DZ) ($n = 129$ DZ males, $n = 206$ DZ female pairs), and 250 opposite-sex DZ pairs. The sample included more women (55%) than men (45%) and ranged in age from 25 to 74 years old ($M = 45, \pm 12.05$). The ethnic breakdown included Caucasian = 92.0%, African-American = 4.5%, Native-American/Eskimo = 0.8%, multiracial = 0.3%, other = 1.0%, and unreported = 1.6% individuals. Most individuals were married (71%), with the rest not married (28%), or who did not report on their marital status (1%), and over half the sample had at least 1 to 2 years of college education (58%). Finally, 12.94% of the sample reported symptoms that classified them as having had a major depressive disorder, dysthymia, or generalized anxiety disorder within the past year. This is consistent with a recent study using the non-twin MIDUS sample which also reported that 12.20% of the sample had a major depressive disorder, dysthymia, or generalized anxiety disorder (Charles, Piazza, Mogle, Sliwinski, & Almeida, 2013). These MIDUS twin sample characteristics are summarized in Table 1.

Measures

Family support—Family support (6 items, $\alpha = .89$) measured the degree of emotional support provided by family members, including brothers, sisters, parents, and children who do not live with them (Brim, Ryff, & Kessler, 2004). On a 4-point scale from 1 (a lot) to 4 (not at all), respondents rated how much family members really care about you; understand the way you feel about things; you can rely on them for help if you have a serious problem; open up to them if you need to talk about your worries. Items were reverse-scored and averaged together to create a composite scale, in which higher scores indicated greater family support.

Friend support—Friend support (4 items, $\alpha = .81$) assessed the degree of emotional support provided by close friends (Brim et al., 2004). On a 4-point scale from 1 (*a lot*) to 4 (*not at all*), respondents rated how much close friends really care about you; understand the way you feel about things; can you rely on them for help if you have a serious problem; open up to them if you need to talk about your worries. Items were reverse-scored and averaged together to create a composite scale, in which higher scores indicated higher levels of friend support.

Psychological distress—The Non-Specific Psychological Distress Scale (Kessler et al., 2002; Mroczek & Kolarz, 1998) (6 items, $\alpha = .87$) was used to measure psychological distress. Respondents were asked to rate how much of the time during the last 30 days from 1 (*none of the time*) to 5 (*all of the time*) they felt so sad that nothing could cheer them up, nervous, restless or fidgety, hopeless, that everything was an effort, and worthless. This scale was developed using item response models and factor analysis, yielding a single factor structure representing current, general psychological distress. Each item was selected because of its high utility in identifying symptoms common to many DSM-IV-TR disorders, including depressed mood, motor agitation, fatigue, nervousness, and worthless guilt. The measure was validated in eight administrations using samples from different populations (Kessler et al., 2002; Mroczek & Kolarz, 1998). The measure was developed as a screening tool for quickly identifying people with mental health issues in the general population (Kessler et al., 2002). Items were averaged together to create a composite scale, with higher scores indicating higher levels of psychological distress. To correct for positive skewness, psychological distress was transformed prior to analyses using log transformation.

Data Analysis

Twin Design—Twin designs include pairs of monozygotic (MZ) twins who share 100% of their genes and dizygotic (DZ) twins who share, on average, 50% of their segregating genes. Initial genetic, shared environmental, and nonshared environmental estimates, based on twin correlations (i.e., intra-class correlations), can provide a preliminary understanding of their contributions to a trait. Specifically, comparing intra-class correlations between MZ twins to those between DZ twins allows for initial estimates of these influences for a single phenotype. For example, suppose a study reveals that MZ twins have an intra-class correlation of .40 for a single phenotype and the DZ twins have an intra-class correlation of .25. The MZ correlation of .40 reveals that .60 or 60% of the variability of the phenotype in question is ascribable to nonshared environmental effects. This is because MZ twins share

100% of their genetic material, so any factors contributing to their dissimilarity are attributable to the nonshared environment. Of the remaining 40%, researchers can compare estimates of the MZ twins to those intra-class correlations of the DZ twins to evaluate heritable and shared environmental contributions. Higher correlations for MZ versus DZ twins indicate genetic contributions. The total genetic contribution is estimated by doubling the difference between MZ and DZ pairs, i.e. $(0.40 - 0.25) \times 2 = .30$, or 30% of the variance. Hence, the remaining 10% of the variance shared by twin pairs stems from shared environmental variance (i.e., $.40 - .30 = .10$). These initial estimates, within-trait and even across traits, are useful in guiding expectations from formal model estimation, but which is appropriately conducted on covariance matrices and takes into account sample sizes, missing data, etc.

Biometric model-fitting—A biometric model-fitting approach, Cholesky decomposition, was used to estimate simultaneously the relative additive genetic (A), shared environmental (C), and nonshared environmental (E) contributions to the associations between family support, friend support and psychological distress by maximum likelihood estimation of the raw data in Mx (Neale, Boker, Xie, & Maes, 2003). This approach extends the univariate model (described above) to examine associations between phenotypes, or variables. Mx is statistical software program commonly used for structural equation modeling (Neale et al., 2003). As displayed in Figure 1, this model includes three variables: family support (variable 1), friend support (variable 2), and psychological distress (variable 3). Family support was entered prior to friend support and psychological distress to test the extent to which family support account for the genetic covariance between friend support and psychological distress. Furthermore, friend support was entered prior to psychological distress, consistent with theoretical explanations that friend support influences psychological distress (e.g., Cohen, 2004).

Prior to model-fitting, psychological distress was reverse-scored (higher levels = lower psychological distress) to be positively associated with family and friend support. This model includes genetic (A1, A2, A3), shared environmental (C1, C2, C3), and nonshared environmental (E1, E2, E3) factors. As depicted in Figure 1, A1, C1, and E1 explain variance in family support. The relative contributions of A1, C1, and E1 to family support are estimated by paths a_{11} , c_{11} , and e_{11} . A1, C1, and E1 may also explain variance in friend support (paths a_{21} , c_{21} , and e_{21}) and psychological distress (paths a_{31} , c_{31} , and e_{31}). The factors A2, C2, and E2 explain variance in friend support. The relative contributions of these factors to friend support are estimated by paths a_{22} , c_{22} , and e_{22} . A2, C2, and E2 also account for variance in psychological distress via the paths a_{32} , c_{32} , and e_{32} . Finally, A3, C3, and E3 account for residual variance in psychological distress, independent of family and friend support, denoted by the paths a_{33} , c_{33} , and e_{33} .

The extent to which the genetic, shared environmental, and nonshared environmental factors associated with family and friend support account for variance in psychological distress is computed as: $(a_{21}^2 + a_{31}^2 + c_{21}^2 + c_{31}^2 + e_{21}^2 + e_{31}^2)$. The degree to which genetic and environmental influences related to friend support explain psychological distress, independent of family support, is computed as: $(a_{32}^2 + c_{32}^2 + e_{32}^2)$. Residual variance in

psychological distress unrelated to both family and friend support is computed as: $(a_{33}^2 + c_{33}^2 + e_{33}^2)$.

Tests of model fit—We tested a full model, where all possible genetic, shared environmental, and nonshared environmental paths were estimated. We then systematically dropped paths that were not significantly different from zero, as indicated by 95% confidence intervals. Model differences were explored using a nested model approach that compared constrained models (where parameters were dropped that were not significantly different from 0) to the full model. Differences in χ^2 values of the models (χ^2) in relation to differences in their degrees of freedom were tested to determine whether constrained models resulted in a significant decrement in model fit compared to the full model. If the χ^2 value for a nested model to the full model is non-significant, the nested model accurately represents the data and is, therefore, a preferable fit compared to the full model. We dropped each non-significant path individually. If there was a significant decrement in model fit (despite non-significant confidence intervals in the full model) the path was considered significant. We also tested dropped paths in larger groups until we arrived at the best-fitting model.

We also calculated the Bayesian Information Criteria (*BIC*) fit statistic (Raferty, 1995). We did so because the χ^2 statistic, which is likely to reject a model that fits the data well but imperfectly, is highly sensitive to sample size, and is more likely to favor saturated models (Mulaik et al., 1989; Neale & Cardon, 1992). The Mx-provided *BIC* statistic evaluated the χ^2 statistic for a model minus the product of the degrees of freedom and the natural log likelihood of the sample size. Negative or smaller *BIC* values across a series of models fitted to the same data are suggestive of a preferable fit, reflecting model parsimony for large sample sizes.

Model assumptions—Twin models rely on several key assumptions that, if violated, could impact genetic and environmental estimates (e.g., Johnson, 2007). One key assumption (i.e., the equal environment assumption) is that environmental effects are the same across twin types. Violations of this assumption could occur if MZ twins are more likely to be treated similarly than DZ twins, and if these environmental influences lead to greater similarity in MZ than DZ twins' friend support and psychological distress. The validity of this assumption has been supported in twin studies of psychiatric disorders (e.g., Hettema, Neale, & Kendler, 1995; Neiderhiser et al., 2004). Another assumption is that assortative mating (i.e., when individuals select partners with similar traits) is not present. Assortment for similar heritable traits has implications for subsequent generations (i.e., genetic transmission) because this form of assortment leads to correlated genetic influences amongst parents and as a consequence, increases genetic relatedness amongst their offspring than would be otherwise expected. In contrast, friend selection does have not implications for future generations in terms of direct genetic transmission and therefore, is not relevant for the present study. Finally, twin models rely on the assumption that the effects of gene \times environment interaction ($G \times E$) in any of the key phenotypes of interest are negligible.

Results

Corrections for the effects of twins' age, sex, marital status, and frequency of contact with co-twins were made by computing standardized residuals from the regression of scores on these variables (McGue & Bouchard, 1984). Table 2 displays summary statistics, including the means, standard deviations, and ranges for family support, friend support, and psychological distress for the entire sample. We next randomly selected twins to compare the means of friend support and psychological distress between MZ and DZ twin groups. Results showed no differences in means between MZ and DZ groups for family support, $t(839) = 1.35$, friend support, $t(842) = -1.48$, or psychological distress, $t(839) = -1.71$, $p > .05$. This suggests that MZ and DZ twins do not differ, on average, in their friend support or psychological distress. Furthermore, correlation analyses demonstrated significant associations among these variables. Specifically, greater family support was correlated with greater friend support ($r = .32$, $p < .0001$), and lower psychological distress was correlated with greater family support ($r = -.22$, $p < .0001$) and greater friend support ($r = -.21$, $p < .0001$).

Intra-Class Correlations

Results from the intra-class correlations suggested that genetic influences are present in the phenotypes of family support, friend support, and psychological distress. This was suggested by MZ correlations for family support ($r = .34$, $p < .0001$), friend support ($r = .18$, $p < .0001$), and psychological distress ($r = .36$, $p < .0001$) that were nearly twice the magnitude of DZ correlations for family support ($r = .21$, $p < .0001$), friend support ($r = .10$, $p = .013$), and psychological distress ($r = .20$, $p < .0001$). Therefore, genetic influences account for approximately 26% [$(.34 - .21) \times 2 = .26$] of the variance in family support, 16% of the variance in friend support [$(.18 - .10) \times 2 = .16$], and 32% [$(.36 - .20) \times 2 = .32$] of variance in psychological distress.

Model Fitting Results

Prior to biometric model fitting, we tested for the presence of sex limitation, a phenomenon where the degree of genetic and environmental influences on phenotypic associations varies by sex. We compared a model where paths for men and women varied to one that constrained genetic and environmental paths to be the same in males and females (Neale, Roysamb, & Jacobson, 2006). The results showed no significant evidence of the presence of sex limitation in the associations among family support, friend support, and psychological distress; thus, we present analyses from biometric model fitting that constrained estimates to be equal across same-sex and opposite-sex twin groups.

Table 3 summarizes the parameter estimates and 95% confidence intervals from both the full model (model fit: $-2LL = 1356.85$, $df = 3315$, $BIC = -10609.39$) and the best-fitting model (model fit: $-2LL = 1359.79$, $df = 3319$, $BIC = -10621.54$, $\chi^2 = 2.94$, $p = 0.568$). In the best-fitting model, all shared environmental paths (c_{11} , c_{21} , c_{31} , c_{22} , c_{32} , c_{33}) could be dropped without resulting in a significant degradation in model fit (see Table 3 and Figure 2). As such, findings from the present investigation suggest that associations among family

support, friend support, and psychological distress are not explained by contributions from the shared environment.

Results from the best-fitting model further showed that genetic factors accounted for 36% of the total variance in psychological distress $[a_{31}^2 + a_{32}^2 / (a_{31}^2 + a_{32}^2 + e_{31}^2 + e_{33}^2) = (.04 + .32) / (.04 + .32 + .01 + .62) = .36]$. A genetic factor (A1) that was related to family support, but unrelated to friend support contributed to psychological distress, suggesting that genetic influences contribute to an association between family support and psychological distress, independent of friend support. Factor A1 explained 11% of the genetic variance $[a_{31}^2 / (a_{31}^2 + a_{32}^2) = .04 / (.04 + .32) = .11]$ and 4% of the total variance in psychological distress $(a_{31}^2 = .21^2 = .04)$. Another genetic factor (A2) that was related to friend support, but unrelated to family support accounted for a majority (88%) of the genetic variance in psychological distress $[a_{32}^2 / (a_{31}^2 + a_{32}^2) = .32 / (.04 + .32) = .88]$ and 32% of the total variance in this phenotype $(a_{32}^2 = .57^2 = .32)$. As such, genetic influences on the link between friend support and psychological distress are distinct from family support. Furthermore, a majority (63%) of the total variance in psychological distress was ascribable to nonshared environmental effects $[e_{31}^2 + e_{33}^2 / (a_{31}^2 + a_{32}^2 + e_{31}^2 + e_{33}^2) = (.01 + .62) / (.04 + .32 + .01 + .62) = .63]$. A nonshared environmental factor (E1) that was related to family support also contributed to friend support and psychological distress. This indicates that nonshared environmental influences explain the association among family support, friend support, and psychological distress. Factor E1 accounted for 1% of the nonshared environmental variance in psychological distress $[e_{31}^2 / (e_{31}^2 + e_{33}^2) = .01 / (.01 + .62) = .01]$, as well as 1% of the total variance in this phenotype $(e_{31}^2 = .11 = .01)$. An additional nonshared environmental factor (E3) contributed the remaining variance in psychological distress. This factor was responsible for a majority (98%) of both the nonshared environmental variance in $[e_{33}^2 / (e_{31}^2 + e_{33}^2) = .62 / (.01 + .62) = .98]$ and total variance $(e_{33}^2 = .79 = .62)$ in psychological distress. This finding indicates that residual variance in psychological distress is explained by the nonshared environment.

Discussion

The current study demonstrated that genetic contributions explain an association between emotional support from friends and psychological distress that is independent of emotional support from family members. This suggests that genetically-based mechanisms that cannot explain family support are important for understanding how the link between friend support and psychological distress arises. Findings from the present study also revealed that nonshared environmental influences explain a relationship among family support, friend support, and psychological distress. This suggests a new mechanism relating distress and social support, such that nonshared environmental influences shape links among general aspects of social support from different interpersonal relationships and psychological distress.

The current study showed that the genetic link between friend support and psychological distress is not shared with social support from family members. Active *r*GE may explain the distinct genetically-based association for friend support because friendships are selected, but family relationships are ascribed. An active *r*GE explanation for the current findings is

consistent with previous studies that have suggested that adolescents' heritable characteristics influence what particular peer groups the adolescents tend to select (e.g., Brendgen, 2012). Thus, individuals' heritable characteristics (e.g., heritable personality traits) may influence their choices of certain friendships over others and, in turn, their friend support and psychological distress. Since personality traits were not measured in the present study, it is only possible to speculate what traits may play a role in individuals' friend choices. Extraversion is one plausible candidate given that previous research has shown that individuals with higher levels of heritable extraversion may tend to select friends who are also more extraverted (Selfhout, 2010). In turn, these individuals may experience higher levels of support from the friends they have selected and lower psychological distress.

A nonshared environmental factor accounted for an association among family support, friend support, and psychological distress. This suggests that nonshared environmental influences operate in shaping general aspects of social support in relation to psychological distress. Accordingly, previous research showed that nonshared environmental factors accounted for similarities in the quality of children's relationship with their family and friends (Pike et al., 2003). With respect to the current findings, nonshared environmental influences may include individuals' unique environmental experiences during adulthood. Such unique experiences (e.g., negative life events) may operate by shaping psychological distress and perceptions of support from family and friends, in turn. For example, psychological distress triggered by job loss is often associated with social withdrawal (Russell, 1999). Thus, individuals' own negative life events may lead to increased psychological distress and social withdrawal, which may influence how individuals perceive their social support networks. Nonshared environmental factors may also involve the impact of unique experiences during childhood. For example, differential parental treatment of each twin has been linked to later psychological distress (Reiss et al., 1995). Therefore, individuals' own experiences in childhood may give rise to later psychological distress and their perceptions of family and friends.

Implications

An implication of the current results is that interventions focused on reducing psychological distress may need to consider how heritable characteristics, that are unrelated to family support, shape perceived and received friend support. In addition, future research needs to assess specific heritable characteristics underlying the unique association between friend support and psychological distress. Furthermore, when nonshared environmental factors are found to contribute to associations between measures of social support and adjustment, this suggests the important role of environments that are unique to each individual in these associations (Leve, Harold, Ge, Neiderhiser, Patterson, 2010). As such, the current results also indicate that environments unique to each individual are important in the consideration of how support from both family and friends is tied to psychological distress. Additional research is needed to examine what particular aspects of each person's unique environments are critical for shaping his or her family support, friend support, and psychological distress.

Limitations

Certain limitations of the current study need to be addressed. First, the current study used a community-based sample, which warrants caution about generalizing findings to clinical populations. For example, the extent to which genetic factors shape the association between family, friendships, and psychological distress may vary between community and clinical populations. At the same time, the strength of using a community-based sample is the ability to shed light on how family support and friend support are linked to psychological distress in the general population. Second, given that psychological distress is a general measure of mental health (Kendler et al., 1994), caution is warranted about generalizing findings to links between family support, friend support, and specific mental disorders. Third, the closeness of the twins may vary by the size of the twins' family; therefore, future studies should include family size as a control variable. Fourth, due to the self-report nature of the data, associations among family support, friend support, and psychological distress are potentially vulnerable to inflation (Lindell & Whitney, 2001). At the same time, one possible way that common method variance operates is via genetically influenced self-report tendencies. For example, the same genetic influences that shape tendencies to report lower levels of support may also influence greater psychological distress. Genetically informed designs that use multi-informant and observational reports of the study variables would afford more stringent tests of their inter-correlations. Fifth, current analyses used cross-sectional data; thus, conclusions about the direction of effects between family support, friend support, and psychological distress and whether the relative influences from genetic and environmental effects on this association vary over time cannot be drawn.

The current study demonstrated that the association between friend support and psychological distress is accounted for by genetic influences that are distinct from family support. This suggests novel genetically-based mechanisms on the link between friend support and psychological distress. For example, these heritable characteristics may play a role in shaping individuals' selection of certain friends over others and, in turn, their friend support and psychological distress. In addition, nonshared environmental contributions explained the association among family support, friend support, and psychological distress. As such, environmental influences that are unique to each individual (e.g., their unique relationships with family and friends) are also important for understanding how social support from both family and friends is related to psychological distress.

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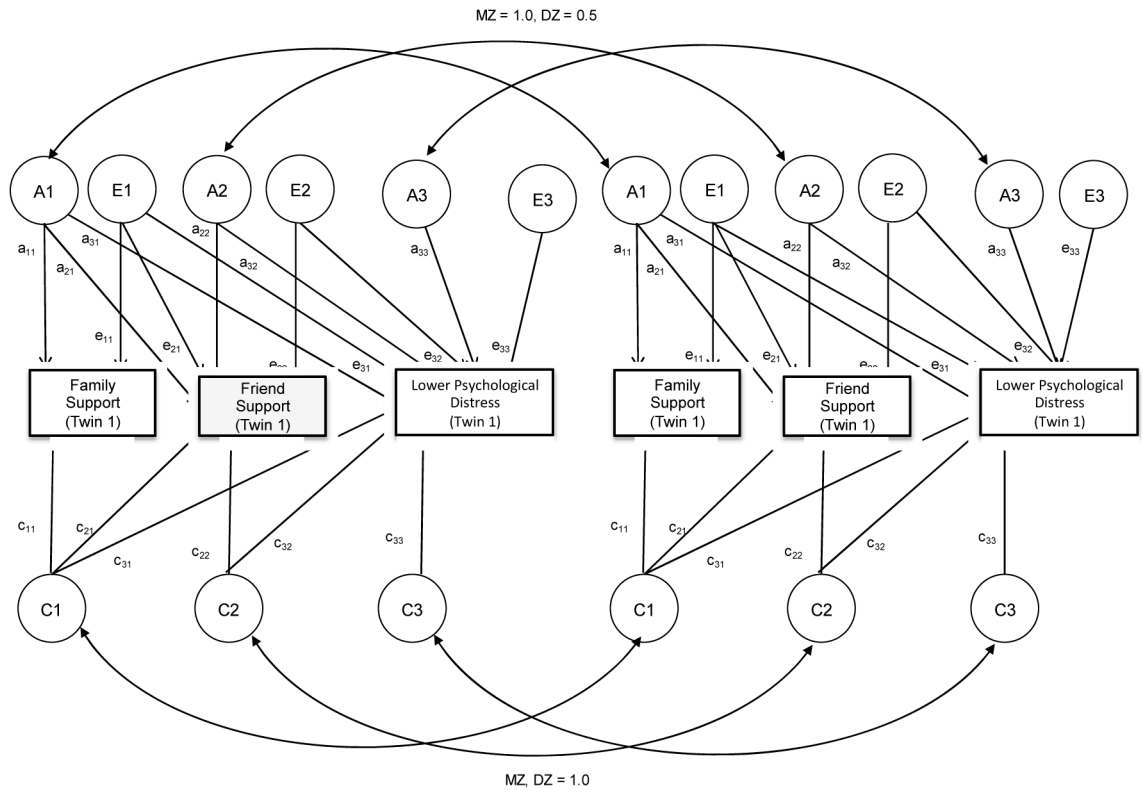


Figure 1. Cholesky Decomposition. This figure includes latent genetic (A1, A2, A3), shared environmental (C1, C2, C3), and nonshared environmental (E1, E2, E3) factors. The paths between factors A1, A2, and A3 for Twins 1 and 2 were constrained to 1.0 for monozygotic (MZ) twins and 0.5 for dizygotic (DZ) twins. The paths between factors C1, C2, and C3 for Twins 1 and 2 were constrained to 1.0 to reflect that shared environments are shared in common by twins. The paths between factors E1, E2, and E3 were not correlated to reflect that nonshared environments are not shared by twins and include measurement error. The paths estimates were constrained to be equal for Twin 1 and Twin 2. Genetic, shared environmental, and nonshared environmental influences on the associations among family support, friend support, and psychological distress are denoted by the path estimates a_{11} , a_{21} , a_{31} , c_{11} , c_{21} , a_{31} , e_{11} , e_{21} , e_{21} . Genetic, shared environmental, and nonshared environmental influences on the association between friend support and psychological distress, independent of family support, are denoted by the path estimates a_{22} , a_{32} , c_{22} , c_{32} , e_{22} , e_{32} . Residual variance in psychological distress is denoted by the path estimates a_{33} , c_{33} , e_{33} .

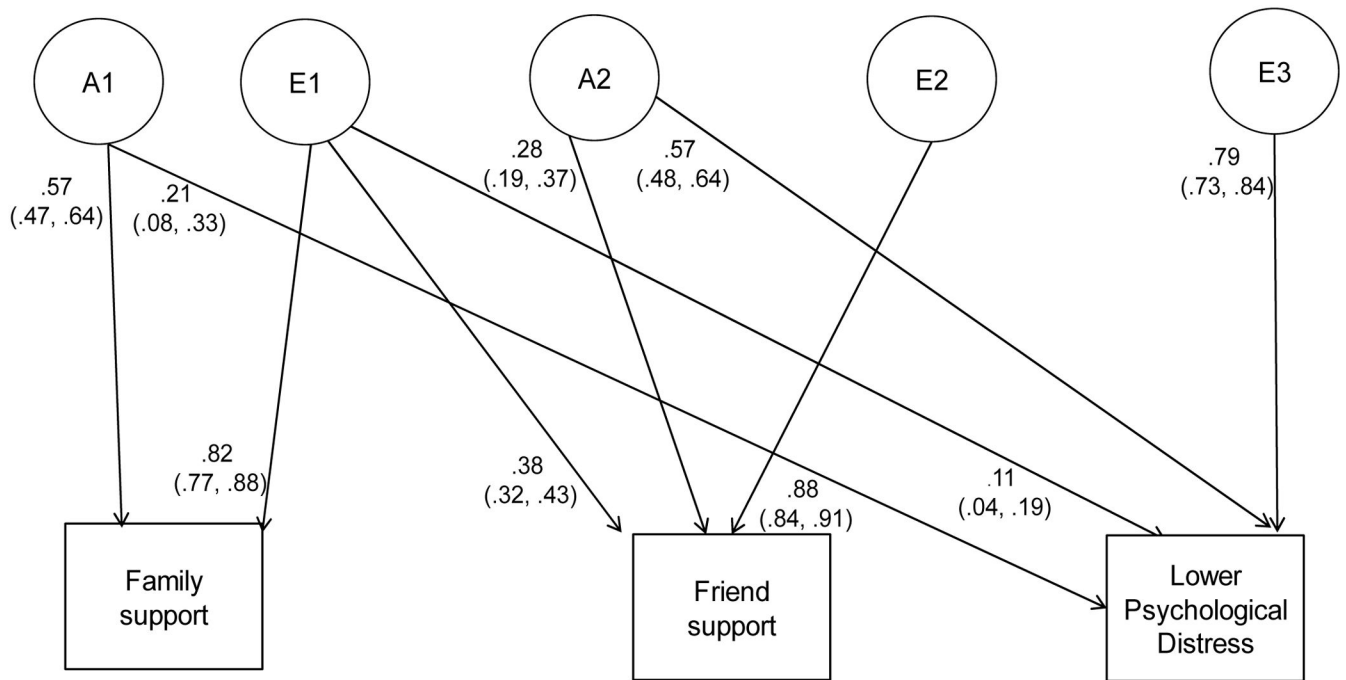


Figure 2. Parameter Estimates and 95% Confidence Intervals from the Best-Fitting Model for one twin in a pair. The best-fitting model included dropping all paths that were not significantly different from 0. Path estimates and 95% confidence intervals in parentheses correspond to results from the reduced model in Table 2. Path estimates that were not significantly different from 0 are not included in Figure 2.

Table 1

Sample demographic information

<i>Category</i>	<i>Percent</i>
Zygosity	
MZ	38.2
Same-sex DZ	35.4
Opposite-sex DZ	26.4
Sex	
Women	55.0
Men	45.0
Ethnicity	
Caucasian	92.0
African-American	4.5
Native-American Eskimo	0.8
Multiracial	0.3
Other	1.0
Not reported	1.6
Marital status	
Married	71.0
Not married	28.0
Not reported	1.0
Education	
Over 12 years	55.4
12 years	28.6
Under 12 years	
Missing	11.84.3
Major depressive disorder or dysthymia within past year	
Yes	12.2
No	87.8

Table 2

Summary Statistics for Family Support, Friend Support, and Psychological Distress

Variable	<i>N</i>	Min to Max	<i>M</i>	<i>SD</i>
Family support	1646	-2.02 to 0.63	0.00	0.15
Friend support	1646	-2.16 to 0.97	0.00	0.64
Psychological distress	1654	-0.19 to 0.59	0.00	0.15

Note. Table 1 presents means (*M*), standard deviations (*SD*), and ranges for family support, friend support, and psychological distress for the entire sample. These summary statistics reflect correction for positive skewness using log transformation (for psychological distress) and adjustment for the effects of twins' age, sex, marital status, and frequency of contact with co-twins for each variable.

Table 3

Parameter Estimates, 95% Confidence Intervals, and Fit Statistics from the Full and Best-Fitting Models

		Variable 1: Family support	Variable 2: Friend support	Variable 3: Lower psychological distress			
Full Model Latent	Factor	Path	Estimate (CI)	Path	Estimate (CI)	Path	Estimate (CI)
Variance explained by family support:							
A1	a11	.58 (.38, .68)	a21	.11 (-.20, .31)	a31	.16 (-.15, .38)	
C1	c11	.16 (-.40, .40)	e21	.21 (-.44, .44)	e31	.20 (-.50, .50)	
E1	e11	.80 (.74, .86)		.28 (.19, .38)		.12 (.04, .21)	
Variance explained by friend support:							
A2	a22	.33 (-.49, .49)	a32	.34 (-.64, .64)			
C2	c22	.10 (-.37, .37)	e32	.16 (-.45, .45)			
E2	e22	.86 (.81, .91)		.01 (-.06, .09)			
Residual variance in psychological distress:							
A3	a33			a33	.41 (-.59, .59)		
C3	c33			e33	.00 (-.45, .45)		
E3	e33				.79 (.73, .84)		
Reduced Model Latent							
Factor	Path	Estimate (CI)	Path	Estimate (CI)	Path	Estimate (CI)	
Variance explained by family support:							
A1	a11	.57 (.47, .64)	a21	-	a31	.21 (.08, .33)	
C1	c11	-	e21	-	e31	-	
E1	e11	.82 (.77, .88)	e21	.38 (.32, .43)	e31	.11 (.04, .19)	
Variance explained by friend support:							
A2	a22	.28 (.19, .37)	a32	.57 (.48, .64)			
C2	c22	-	e32	-			
E2	e22	.88 (.84, .91)	e32	-			
Variance explained by family support:							
A3	a33	-	a33	-			

	Variable 1: Family support	Variable 2: Friend support	Variable 3: Lower psychological distress
C3	c33	-	-
E3	e33	.79 (.73, .84)	

Note. Latent factors and paths correspond to Figure 1. Each path name has three components: a lower case letter, followed by two subscripted numbers. The lower case letter and first subscripted number refer to a specific latent factor: A, C or E. The second subscripted number refers to the specific manifest variable (identified by its' order in the model) that is linked to the latent factor via the path. For example, path a21 links latent factor A1 to the second variable in the model A1. CI = 95% Confidence Intervals. For the most parsimonious model, dashes (-) indicate parameters that could be dropped without resulting in a significant increase in the χ^2 value.