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Article

Genetic Influence on Social Support: A Twin Study

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Abstract

Social support is often considered an environmental factor affecting health, especially in aging populations. However, its genetic underpinnings suggest a more complex origin. This study investigates the heritability of social support through applying a threshold model on data of a large adult sample of twins ($N = 8019$) from the Netherlands Twin Register, collected between 2009 and 2011. The study employed the Duke – UNC Functional Social Support Questionnaire to assess social support quality. Our analysis revealed genetic contributions to social support, with heritability estimated at 37%, without a contribution of shared environment and no differences between men and women in heritability. The study's results underscore the complexity of social support as a trait influenced by genetic and environmental factors, challenging the notion that it is solely an environmental construct.

Keywords: Heritability; Twins; Netherlands Twin Register; Perceived social support

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Social support involves interactions with others, notably friends and family, creating an environment where individuals feel supported and appreciated (Taylor, 2011). It is often conceptualized as an environmental influence that mitigates the risk of physical and mental health conditions, especially in ageing populations (Plomin & Bergeman, 1991). Different societies exhibit varying levels of social support due to cultural values. For instance, collectivist cultures, like those in many Eastern societies, emphasize community and family ties, which often results in robust social support systems. In contrast, individualistic cultures, predominantly found in Western societies, encourage self-reliance, which might lead to less perceived social support (e.g., Tayler et al., 2007). As pointed out by Kendler (1997), however, viewing social support solely as an environmental measure may be incorrect. Kendler looked at perceived social support in a longitudinal study of female same-sex twin pairs, with ages ranging from 22 to 59 years from the Virginia Twin Registry. Heritability estimates ranged between 44% (relative support) and 75% (social integration) for six social support factors (i.e., friend support, relative support, friend problem, relative problem, confidants and social integration). A person's genotype thus seems to play a substantial role in creating and/or perceiving their social environment, possibly through genetically influenced traits such as cognition, temperament and personality.

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Other research generalizes these findings to men. Agrawal et al. (2002) studied the same six factors in a sample of 7506 male and female MZ and DZ twins and triplets with an average age of 36.6 years. While women had higher mean levels for most aspects of social support, there was no evidence for sex differences in the magnitude of genetic and environmental influences. In a more recent study, Coventry et al. (2021) looked at the Kessler perceived social support (KPSS) measure in 7059 male, female and opposite-sex twin pairs aged 18–95 years from the Australian Twin Registry. There was some evidence for different genetic mechanisms in males and females for support from friends and the average KPSS score of all subscales, but otherwise, this study confirmed there are few sex differences in the genetic architecture of indices of social support.

Wang et al. (2017) analyzed two indices of social support, namely support quality and support quantity, in 1215 male and female 18-year-old twin pairs who take part in the Twins Early Development Study (TEDS). Both measures were heritable, with estimates of 55% and 49% respectively. Wang et al. suggested that these findings point to gene-environment correlation, where individuals create and perceive their supportive environment based upon their genotypes. Schnittker (2008) analyzed the heritability of social support and other traits related to success and happiness in a sample from the National Survey of Midlife Development in the United States (MIDUS). The study included 3023 unrelated individuals, 2330 siblings and 1588 twins, aged 25–74 years. Genetic factors substantially influenced how individuals perceive and benefit from social support networks. Interestingly, there were quite large differences in heritability estimates, ranging from 26% and 22% for friend and family support to 52% for marital status and 59% for spouse support.

Bergeman (2001) investigated the genetic and environmental determinants of social support over time in a longitudinal study of identical and fraternal twins from the Swedish Adoption/Twin Study of Aging. The study, which assessed friend and family support over three time points, found that social support is moderately stable over time and significantly heritable, with genetic correlations ranging from 65% to 97%

Not all aspects of social support appear to be equally influenced by genetics. Vinkhuyzen et al. (2010) analyzed the size of social support networks and satisfaction with social support in 560 Dutch twins and their siblings (59% females) from 256 families registered with the Netherlands Twin Register (NTR), with an average age of 47.11 years. While the size of social support networks showed modest heritability, satisfaction with social support did not. This variation highlights the complex picture of different dimensions of social support and genetic factors.

In this contribution, we seek to enhance the understanding of the heritability of social support by focusing on a large adult twin sample from the Netherlands. Given that prior research on the heritability of social support has predominantly been centered in the U.S., our study seeks to broaden this perspective by focusing on a large adult sample from the Netherlands. While not the first study of its kind in this region, our research employs a significantly larger sample size than previous Dutch studies (Vinkhuyzen et al., 2010), enhancing the statistical power of our findings. This is particularly relevant given the stark differences in welfare policies, such as those related to work-life balance and social security, which are more robust in European countries, especially the Scandinavian countries and the Netherlands but others as well, compared to the U.S. (e.g., Alesina & Glaeser, 2006). Exploring these genetic influences within such a distinct framework can provide deeper insights into the environmental interactions that shape social support.

Methods

Participants and Protocol

Participants were registered with the Netherlands Twin Register (NTR; Ligthart et al. 2019). Adolescent and young adult twins and their parents were initially recruited into the NTR through city Dutch council registrations, followed by recruitments via the NTR website and newsletters as well as publicity in the media. The present study is based on data from the eighth wave of survey data collection that were collected between 2009 and 2011 (Geels et al., 2013). After obtaining approval from the Medical Ethics Committee of the VU University Medical Center Amsterdam, all NTR participants aged 18 years and older with a known valid address were invited to complete survey 8 ($N = 47{,}122$). They first received a written invitation with a unique login name and password and a link to a webpage with a web-based version of the survey. If they did not access the web-based survey in the 6 weeks after the invitation, a hard-copy of the survey was sent. Between 3–9 months after the paper versions of the survey were sent out, nonresponders received a reminder by post or email. Several groups of nonresponders were contacted by phone. This resulted in completion of the survey by 16,891 individuals. A final effort to increase response rates early in 2012 consisted of three extra mailings with the option to fill out a shorter version of the survey either on paper or online. This led to 3436 additional responders (total $N = 20{,}236$). However, the shorter survey 8.1 did not contain the items on social support, hence for the current article we analyze the data from the first longer version of survey 8 with phenotype information on social support, including 8019 twins with no more than two missing items for the phenotype (see below). Twin zygosity was determined from DNA polymorphisms for 61% of all same-sex twin pairs and from harmonized longitudinal survey information for the others. Zygosity was missing for 124 twins who had only completed surveys that did not contain questions on zygosity. The correspondence between zygosity based on survey items and on DNA is 97% (Willemsen et al., 2005; Lighthart et al., 2019). The average age of the twins was 32.8 years ($SD = 14.2$).

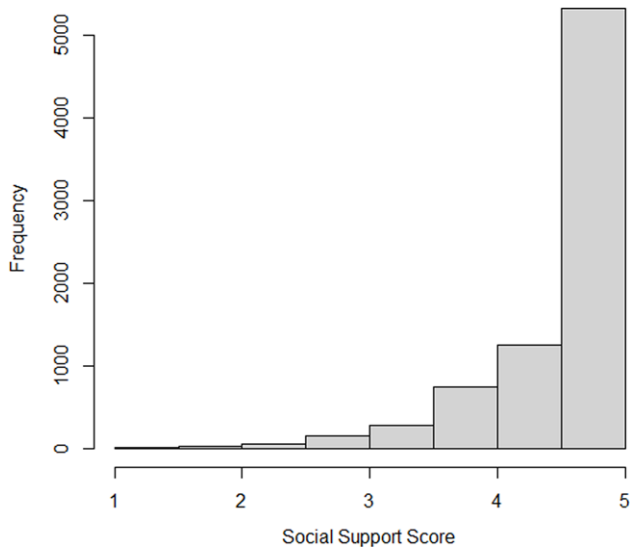

Figure 1. Distribution of the mean social support scores.

The Phenotype

The Duke – UNC Functional Social Support Questionnaire (FSSQ) asks people 'To what extent do people around you give you help and support when needed?' (Broadhead et al., 1988). The FSSQ consists of 8 items ('I have people who care what happens in my life'; 'I get love and affection'; 'I have the chance to talk to someone about problems at work or my home situation'; 'I have the chance to talk to someone I trust about my personal problems'; 'I have the chance to talk to someone about money matters'; 'I'm invited to go out or do things with others'; 'People give me valuable advice about important things in life'; 'I get help when I'm sick in bed') that are scored on a 5-point scale, from 'much less than I would like' to 'as much as I would like'. The reliability of the scale was good with a Cronbach's alpha of .89. The FSSQ allows for two specific dimensions of support: confident support and affective support. We performed a principal component analysis (PCA) on the eight social support items to explore their dimensionality. The PCA identified several components with varying degrees of contribution to the total variance, evidenced by their eigenvalues. The first component had an eigenvalue of 4.656, indicating a strong underlying factor that accounted for 58.2% of the total variance. All other components had eigenvalues below 1 and did not contribute to more than 9% of the variance. Additionally, the scree plot gave clear support for one factor. Given this result, we chose to analyze the average score of all social support items, allowing for a maximum of two missing items. Notably, nearly 40% of participants had an average score of 5 (the highest possible score), leading to a highly skewed distribution of the data, as is displayed in Figure 1. We therefore dichotomized the social support score

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Table 1. Estimates for tetrachoric twin correlations and 95% confidence interval

Type	*r*	Confidence interval	*N* complete pairs	Average age (range); *SD*	*N* twins	Maximum score social support (%)
MZF	.414	0.329, 0.493	1096	34.8 (17–90); 14.9	2866	41.28
DZF	.206	0.067, 0.340	484	32.3 (18–86); 13.4	1496	40.84
MZM	.266	0.104, 0.417	369	34.2 (17–82); 15.0	1071	37.91
DZM	.183	−0.052, 0.402	184	32.4 (18–81); 14.4	656	38.87
DOS	.130	−0.018, 0.273	462	29.8 (18–78); 12.7	1806	38.65
All MZ	.379	0.304, 0.451	1465	34.6 (17–90); 14.9	3937	39.59
All DZ	.172	0.079, 0.262	1130	31.0 (18–86); 13.3	3958	39.25

Note: MZF, monozygotic female pairs; DZF, dizygotic female pairs; MZM, monozygotic male pairs; DZM, dizygotic male pairs; DOS, dizygotic opposite sex pairs; MZ, monozygotic; DZ, dizygotic.

Table 2. Estimates for variance components and 95% confidence interval from ACE and AE models

Component	Full model estimate (CI)	Reduced model estimate (CI)
Additive genetic variance (A)	0.415 (0.403, 0.649)	0.3733 (0.303, 0.440)
Common environmental variance (C)	−0.036 (-0.235, -0.036)	–
Unique environmental variance (E)	0.621 (0.621, 0.656)	0.6257 (0.558, 0.695)

into two categories, with participants who had a lower average than 5 assigned a zero and all others a 1.

Statistical Analysis

Genetic analysis of the data employed a threshold model (Falconer & Mackay, 1996) in which a dichotomous variable is seen as the expression of an underlying continuous risk distribution called 'liability'. The threshold, which is estimated from the data, divides the sample into 'affected' and 'unaffected' subjects. Tetrachoric twin correlations were estimated to quantify the resemblance for liability in MZ and DZ twins, allowing for differences in correlation for men and women and for twins of opposite sex. The contributions of genetic and environmental factors to individual differences to liability can be inferred from the different level of genetic relatedness of MZ and DZ twins (e.g., see Posthuma et al., 2003). We decomposed the variance of the liability scale into variance due to additive genetic (A) influences, due to shared environment (C) and due to nonshared environment (E). The shared or common environment (C) is defined as those environmental influences that are similar for MZ and DZ twins; thus, the shared environmental factors correlate 1.0 in both types of twins. Nonshared environmental influences are uncorrelated and also absorb uncorrelated error. Model fitting was performed with raw-data maximum likelihood in Mx (Neale et al., 2006), including all data from complete and incomplete twin pairs. Fixed effects were included for sex, age (standardized) and age (standardized) squared. A saturated model was specified first, and then constraints and an ACE and an AE model were tested by likelihood-ratio tests. When comparing nested models, a change in the -2 log-likelihood between models is distributed as a chi-square with degrees of freedom (*df*) equal to the differences in df between the models. A significant difference ($p < .05$) when relaxing a constraint means that this constraint cannot be relaxed. We computed likelihood-based 95% confidence intervals (Neale & Miller, 1997).

Results

A fully saturated model, allowing for different estimates of thresholds in men and women, regressions of age (standardized) and age (standardized) squared on thresholds and five different twin correlations, gave -2LL = 10513.58 (*df* = 7886). Table 1 presents the estimates for the five twin correlations and their 95% confidence intervals, the average age and the age range in the sample, and also shows the percentage of twins with the maximum score on social support. The correlations suggested an AE model for females, and an ACE model for males. However, constraining the two MZ (males and females) and three DZ correlations (same-sex males and females and opposite sex pairs) to be equal gave a -2LL = 10516.89 (*df* = 7889). The chi-squared test statistic (3 *df*) thus is 3.31, indicating that MZ and all DZ correlations did not differ between men and women.

In this model the estimates for the regression of age (standardized) and age (standardized squared) were .002 and .011, respectively. The test of significance for the age regressions were nonsignificant (−2LL = 10518.517, *df* = 7891). Thresholds in men and women were estimated at .32 and .24, respectively. The test if thresholds are the same in males and females also gave a nonsignificant difference in likelihood (−2LL = 10521.382 with *df* = 7892).

For this last model Table 1 also presents the correlations in all MZ and all DZ twins. The estimate of .38 for MZ pairs is almost twice the correlation in DZ pairs (0.17), suggesting a modest heritability and no or very little influence of shared environment.

Fitting an ACE model to the data confirmed this, with heritability estimated at 41%. The ACE model (including one constraint on total variance) gave −2LL = 10521.382 (*df* = 7892). Omitting the influence of common environment was clearly permitted with a minimal difference in goodness of fit (−2LL = 10521.514, *df* = 7893). Heritability in the AE model was estimated at 37% (see also Table 2).

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Discussion

Our study highlights the contribution of genetic factors in shaping individual differences in social support. The contribution is modest, with heritability estimated at 37%, but too large to label social support as an environmental trait. Labeling traits as 'environmental' ignores that they are often not randomly distributed within a population but reflect heritable individual differences (Plomin & Bergeman, 1991; Vinkhuyzen et al., 2010). Social support is often labeled as an environmental measure and viewing it as such may have perhaps unintended consequences. People in aging populations, for example, face changes and challenges with loss of social contracts because of retirement, loss of loved ones, and health issues leading to decreased mobility and independence. Social support, which can include emotional, instrumental and informational assistance from others may mitigate these challenges and strong social support systems can help to buffer the negative effects of aging-related changes and contribute to better physical and mental health outcomes. Governments recognize the importance of investing in social support and advice to build social networks early in life, but may not always appreciate that differences between people in their social support networks may be influenced by genetic liabilities.

Our findings support the genetic basis of social support and align with other studies across different populations, including the US, Sweden and the UK, which also demonstrated significant genetic contributions, with figures ranging widely but consistently indicating a notable genetic component (e.g., Kendler, 1997; Bergeman et al., 2001; Wang et al., 2017). These studies, as well as our own findings, reinforce the concept that social support encompasses both genetic and environmental factors. As these findings are based on data from twins, one could wonder if twins experience more social support because of a close bond between some of them, or that MZ twins experience more social support (from each other) than DZ twins. However, previous research found no evidence to support these claims. For example, Willemsen et al. (2021) carried out a within-family analysis to test if there are mean differences between twins and (non-twin) singletons, that is, they compared twins to their siblings across a large number of traits, including the two subscales of the Duke – UNC Functional Social Support Questionnaire, and found no differences between twins and siblings. We also tested whether the prevalence of reported social support differed between MZ and DZ twins using a generalized estimating equation (GEE) to account for clustering. The analysis revealed no difference in the distribution of social support between MZ and DZ twins ($\beta = .035$, $SE = .048$, $p = .461$), indicating that both MZ and DZ twins report social support at comparable rates.

It should be noted that the significant genetic contribution does not, however, diminish the role of nongenetic factors. Unique environmental factors were found to account for a substantial portion of the variance (63%), underscoring the dual impact of genetic predispositions and unique environmental experiences on social support networks.

There is a multitude of different instruments to assess social support, and differences in heritability across studies may therefore not simply be interpreted as evidence reflecting differences in welfare state. These variations may point to the sensitivity of heritability estimates to the specific methods and instruments used in their assessment. Future research should critically evaluate the design and application of these instruments to ensure that they accurately capture the nuances of social support as it is experienced in different social and cultural contexts. Additionally, the variability in heritability estimates across different types of social support may suggest that genetic influences are modulated by varying environmental contexts and social structures. This indicates a complex interaction between genetics and environment, which can differ significantly depending on the nature of the social systems and types of support involved. Future research should focus on disentangling the specific environmental conditions that amplify or mitigate genetic influences on social support. Studies could explore how cultural differences impact the expression of genetic predispositions toward social support or investigate the role of specific life events, such as victimization, migration or significant personal losses, in shaping these dynamics. Furthermore, longitudinal studies that track changes in social support across different life stages could provide deeper insights into how the interplay between genes and environment evolves over time.

In conclusion, our study underscores the importance of considering both genetic and environmental influences when studying social support systems. This result is a valuable addition to existing discussions of how factors, such as social support, shape individual differences in behavior and have crucial implications for understanding the complex nature between genetic and environmental influences on complex traits.

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