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ORIGINAL RESEARCH REPORT

Social Integration and Sleep Disturbance: A Gene-Environment Interaction Study

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Objective: Low levels of perceived social integration, or loneliness, are associated with increased risk for a range of poor health outcomes. Sleep disturbance plays a central role in the evolutionary theory of loneliness, which provides a mechanistic account of how low levels of social integration may negatively impact health. No studies, however, have examined whether the association between social integration and sleep disturbance is consistent with a causal effect after accounting for genes that are common to both variables.

Method: Using twin data (N = 905 twin pairs) from the nationally-representative Midlife in the United States (MIDUS) survey, I evaluated a series of bivariate twin models exploring whether the phenotypic association between low social integration and sleep disturbance can be explained by shared genetics. In addition, the current study specified a series of quantitative models for studying gene x environment (G X E) interactions to determine whether the genetic and environmental influences on sleep disturbance differ as a function of social integration.

Results: The phenotypic association between social integration and sleep disturbance was fully accounted for by genes that are common between the two variables, suggesting that within-twin pair differences in social integration do not exert a causal influence on sleep disturbance. Social integration, however, moderated the non-shared environmental influence on sleep disturbances, with the greatest environmental influences observed at the lowest levels of social integration.

Conclusions: The results of this study suggest that an essential feature of the evolutionary model of loneliness may need refinement or elaboration. The moderation findings are discussed in terms of the fit with a stress-buffering model of social support in which environmental influences on sleep disturbance are strongest when social resources are low.

Keywords: Social integration; loneliness; sleep; sleep disturbance; behavior genetics; twins

Low levels of perceived social integration, or loneliness, are associated with increased risk for a range of poor health outcomes, including depression [1], elevated vascular resistance [2], poor sleep [3], and early death [4]. Despite the fact that epidemiological literature linking objective and perceived social integration with health is quite large, questions about causality remain (cf. [5, 6]). Is it the case that loneliness exerts a negative effect on health, or are these associations due to third variables, including genetic factors common to both loneliness and poor health?

Behavior genetic methods are ideal for answering this type of question [7–9]. Cotwin control studies, for example, can be used to determine whether twins who are discordant for phenotypic exposure (e.g., divorce) demonstrate differences in an outcome (e.g., depression) after shared genetic influences— that are common to both the exposure and outcome variables— are taken into account. A comparison of the genetic relatedness of monozygotic (MZ) twins, who share 100% of their genes and their rearing environment, and dizygotic (DZ) twins, who share 50% of their genes and 100% of their rearing environment, can be used to formalize a biometric model for examining the potential causal association between two variables.[1] In twin methodology, these differences between MZ and DZ twins are used in structural equation modeling to decompose the variance in a trait or phenotype into additive genetic effects (A), common environmental effects (C), and unique or nonshared environmental influences (E); together, this decomposition yields an "ACE" model that can be used to derive the heritability of a phenotype (i.e., the percentage of variance that is due to additive genetics (A), the environmental influences that are shared between

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twins in a family (C), and those that are unique to each twin (E, which also includes measurement error).

In a bivariate specification, this ACE model allows us to examine whether within-pair differences in a predictor variable—for example, loneliness—are associated with differences in an outcome of interest. Using twin data from the nationally-representative Midlife in the United States (MIDUS) study, for example, Fujiwara and Kawachi [6] found the associations among perceived social integration and perceived physical or mental health were *not* consistent with a direct causal influence from social integration to either of the (self-reported) outcomes. This finding suggests that reducing loneliness (or, improving social integration) would not lead to improvements in self-rated physical or mental health; conceptually, another way of understanding these findings would be to consider a hypothetical twin pair: Twin A's loneliness would predict Twin B's health just as well as Twin B's loneliness, and this type of effect is not consistent with a causal effect *from* loneliness *to* health. Using twin models to interrogate questions of causality has direct implications for intervention science. If treatment and other public health efforts attempt to alter loneliness in order to improve or promote health (cf. [10]), this work should proceed by targeting potential mechanisms of action that are consistent with a causal link from loneliness to an outcome of interest. In this respect, the twin models I report on in this paper are a useful tool for identifying these potentially causal links and, perhaps more importantly, may be used to determine that the association between loneliness or social integration and another variable is *inconsistent* with a direct causal effect.

The current report extends this prior analysis in two ways. First, although Fujiwara and Kawachi [6] found no evidence for a causal link between perceived social integration and health, it is plausible that the epidemiological association exists via indirect effects, with loneliness exerting a causal influence an intermediate variable, which then exerts a causal effect on a health outcome of interest (i.e., the direct association between loneliness and health may not be causal, but loneliness may exert a causal effect on an intermediate variable that is causally related to a health outcome). From this perspective, sleep quality is an important candidate intermediate variable. Not only are sleep disturbances associated with a range of morbidities and risk for early death [11], but sleep plays an important role in the evolutionary theory of loneliness [12, 13]. The theory holds that over the course of evolutionary history being on the social periphery increased the likelihood of predation; loneliness functions in part as a social alarm system alerting people to their status within a group and the need to reconnect with others for safety. Although it is adaptive for lonely people to maintain vigilance for signs of environmental threat, over time this vigilance comes with a negative cost to one's health (cf. [14]).

Within this framework, sleep disturbances are an expectable form of hypervigilance, and many studies find that lonely people evidence considerable sleep difficulties, ranging from reports of daytime fatigue [3, 15] to objectively measured sleep fragmentation [16]. Importantly, recent genetically-informed studies reveal that the associations between sleep duration and both body mass and depressed mood are consistent with a causal influence from sleep to these outcomes of interest [17, 18]. Given the importance of sleep for understanding the evolutionary significance of the loneliness-health association, I examine the potential etiology of the association between perceived social integration and self-reported sleep disturbances using data from the MIDUS twin sample. The main goal of this paper is to investigate whether within-pair differences in social integration (i.e., when one twin reports being more socially integrated than his or her cotwin) are associated with sleep disturbances once genetic influences that are common to both variables are taken into account.

The main analytic strategy of this paper is to examine whether social integration is associated with sleep disturbance in a manner consistent with a causal explanation; however, another way to explore the association between these variables is to conceptualize social integration as an "environmental context" that can shape the genetic and environmental influences on sleep disturbance (cf. [19]). To understand social integration as an environmental context, I offer two competing hypotheses. First, consistent with a general diathesis-stress model, the genetic contributions to sleep disturbance may be strongest at low levels of self-reported social integration (i.e., high loneliness). In this case, low social integration would provide a context for revealing genetic liabilities to sleep disturbance. Alternatively, consistent with a stress-buffering model of social support (see [20, 21]), environmental influences on sleep disturbance may be strongest at the lowest levels of social integration. In this case, low levels of social integration would provide a context in which the environmental influences on sleep disturbance are the strongest; alternatively, a putatively positive environmental context (i.e., high social integration) would protect against stressful environmental influences on sleep disturbance.

Testing these competing ideas involves incorporating a statistical interaction into the standard biometric twin model to determine whether the genetic and environmental influences on sleep disturbance differ as a function of social integration. Biometric moderation analyses [22] are receiving increased attention in psychological science [18, 19, 23, 24, 25], and this approach allows researchers to study quantitative gene-environment interaction(s) in the context of gene-environment correlation (i.e., in situations where common genetics can explain part of the association between predictor and outcome variables). This approach holds promise for expanding the evolutionary theory of loneliness. If low levels of perceived social integration increase the genetic contribution to sleep disturbance, we observe another route through which loneliness, as an environmental exposure (highly heritable in-and-of itself, see [26]) may shape the genetic contributions to an important health-relevant variable like sleep.

The Present Study

Using the twin subsample from the MIDUS study, this paper investigated two primary research questions. First, consistent with a quasi-causal association (see [9]), I expected the non-shared environmental component of social integration to be significantly associated with sleep disturbances after accounting for genetic influences that are common to both low social integration and high levels of sleep disturbance. Second, in the context of this environmental main effect, I also explored the possibility that social integration moderates the genetic and environmental influences on sleep disturbance; regarding these moderation analyses, I did not have a strong a priori hypothesis. On one hand, consistent with a diathesis-stress model, the largest heritability in sleep disturbance may be observed among people who report low levels of social integration. On the other hand, consistent with a stress-buffering model, the environmental influences—the so-called *slings and arrows of life*—may exert their strongest influences on sleep disturbance when perceived social integration is low. Thus, the moderation analyses were largely exploratory, but they were informed by these competing ideas about how social integration may differentially shape the genetic and environmental influences on sleep disturbance.

Method

Participants

Participants contributing to the current analyses were part of the Midlife in the United States (MIDUS) survey twin sample. The MIDUS survey is a nationally representative random-digit-dial sample of noninstitutionalized, English-speaking adults aged 25–74 in the United States; the first wave of the MIDUS survey included 7,108 participants (3,395 men) who were an average age of 46.40 years old (SD = 13 years) when the initial phone interview was conducted in 1995–1996. The twin sample consists of 921 pairs. As reported in detail elsewhere (e.g., [24]), zygosity was assessed via self-report using questions about eye and hair color, as well as the degree to which people were confused as to the twin's identity in childhood. This approach is valid and widely used [27], but 16 of the MIDUS twin pairs were deemed to have indeterminate zygosity and were excluded from the present analysis. The final sample included 905 pairs (1,810 total participants): 162 male monozygotic (MZ) pairs, 186 female MZ pairs, 124 male dizygotic (DZ) pairs, and 197 female DZ pairs, and 236 opposite sex DZ pairs. The average age of the sample was 44.7 years (SD = 12.12 years, range 25–74). All participants provided informed consent, and the MIDUS study was approved by the institutional review boards at each data collection site. The author's local institutional review board does not consider de-identified secondary data analysis to be human subjects research.

Measures

Social integration. Social integration was assessed as part of the MIDUS survey's self-administered questionnaire. Three items, scored on a 7-point Likert-type scale from "Strongly Agree" to "Strongly Disagree," were used to compute a composite index. The items tapping perceptions of social integration were as follows: "I don't feel I belong to anything I'd call a community," "I feel close to other people in my community," and, "My community is a source of comfort." The composite index was scaled such that high scores reflected a greater sense of social integration. The scale has adequate internal consistency (α = .73) and has demonstrated construct validity [28, 29].

Sleep disturbance. Sleep disturbance was assessed with a single item in the self-administered questionnaire: "During the past 30 days, how often have you experienced trouble getting to sleep or staying asleep?" The sleep disturbance item was scored on a 6-point Likert-type scale from "Almost every day" to "Not at all." For the present study, the items were reverse-scored with higher scores reflecting greater sleep disturbance. The mean sleep disturbance score was 2.34 (SD = 1.67, range 1–6), indicating that, on average, the participants in this study reported sleep disturbances slightly more one time in the past 30 days. Single item assessments are not the most valid measures of self-reported sleep disturbance; the most well-validated self-report measure in this area is the Pittsburgh Sleep Quality Index (PSQI; [30]). Although the original MIDUS Survey (used in this report) did not include the PSQI, the MIDUS Biomarker Project, completed roughly 10 years after the original MIDUS Survey, included the PSQI. The single item sleep disturbance measure (used in this report) from the MIDUS survey was correlated r = .37 (n = 968, $p < .001$) with the PSQI Global Sleep Quality, a measure of overall sleep quality in the prior month, in the Biomarker Project. This test-retest stability over a 10-year period suggests the sleep disturbance item used in this sample is reliable and correlated with the gold-standard assessment for self-reported sleep disturbance up to a decade later.

Data Analysis

All data and computer codes associated with this paper are available online at the Open Science Framework portal and can be accessed at the following hyperlink: osf.io/utqrz. I analyzed the data beginning first with a biometric structural equation model (using Mplus, [31]) that examined the potential quasi-causal association between social integration and sleep disturbance. The model is described in detail elsewhere (see [9]) but its essential feature involves making use of the twin methodology to decompose the genetic and environmental influences that are common between the two variables. Following standard conventions for these models, I first residualized the social integration and sleep variables for both age and sex, then standardized the residual variables for use in the biometric models. I estimated how much of the variance in each trait is due to additive genetic influences (A), common environmental influences (C), and unique environmental influences (E). This bivariate ACE specification is shown in **Figure 1**. The ACE variance components were standardized and the paths from the components to the phenotypes were estimated; the specification outlined in

Figure 1 decomposes the variance of each variable into the ACE components and examines the variance shared between the two variables. To examine the potential quasi-causal effect, I regressed the sleep disturbance item on the ACE components of social integration. The key parameter of interest in this analysis is the regression of the sleep disturbance item on the E component of social integration after accounting for genetic influences that are common to the two phenotypes.

The second set of analyses focused on the potential moderation of the genetic components of sleep disturbance as a function of social integration. This biometric moderation [23] involves extending the bivariate twin model to include an interaction term as illustrated in **Figure 2**. This extension allows the cross-paths and residual genetic and environmental influences on sleep disturbance to vary as a function of social integration. I examined goodness of fit using the root mean square error of approximation (RMSEA; [32]), where values below .05 are considered a close fit and values up to .08 represent reasonable approximations of the data. I also reported the comparative fit index (CFI; [33]), where values of .95–1.0 indicate a good fit, as well as the likelihood-ratio test (distributed as a χ^2 and calculated as the difference in the –2 log-likelihood values between the two models), which can be used to test differences between nested models that add or remove specific parameters.

Results

Perceived social integration was negatively associated with self-reported sleep disturbances (r = –.14, 95% CI [–.24, –.09]). The within-trait and cross-trait twin correlations for social integration and sleep disturbance are presented in **Table 1**. As shown, the substantially larger MZ than DZ within-trait, cross-twin correlations are consistent with a genetic contribution to the variance in both

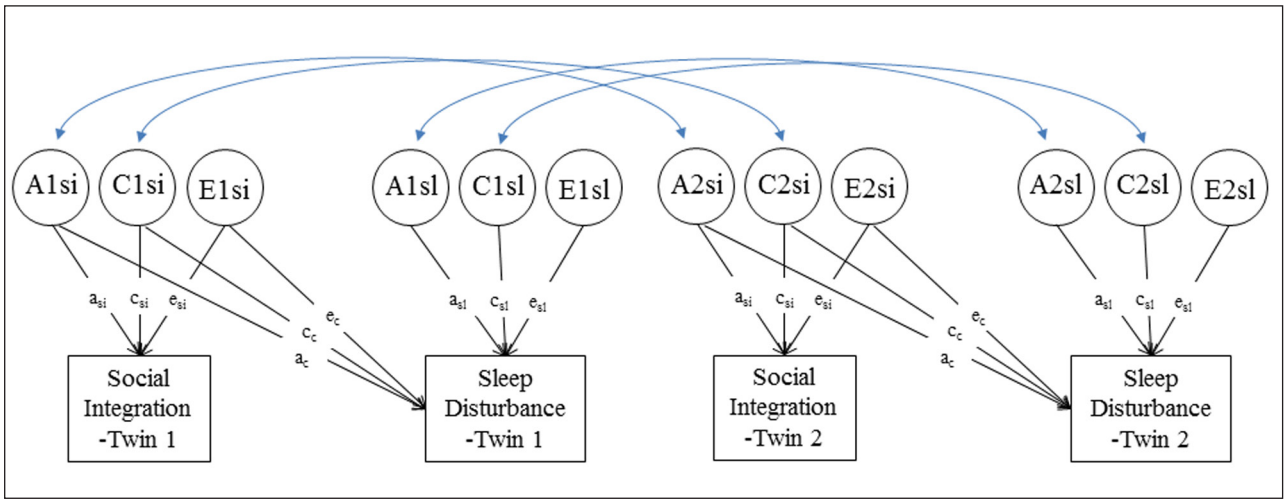

Figure 1: Structural equation model of social integration and sleep disturbance in adult twin pairs. A = common genetic variance; C = shared environmental variance; E = non-shared environmental variance. ACE components are standardized. Si = social integration; Sl = sleep disturbance. Within MZ twins, the A component correlation is fixed at 1.0; within DZ twins, this correlation is fixed at .5. The C component correlation is 1.0 in all twins, and the E component correlation is fixed to 0.

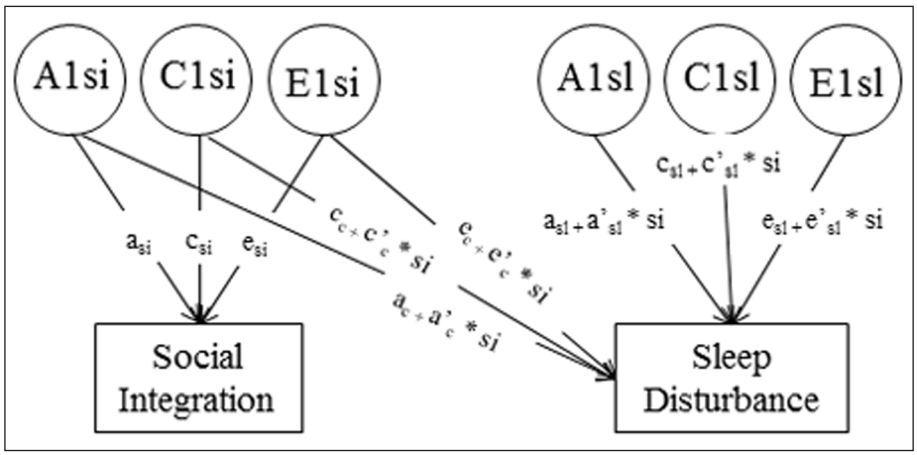

Figure 2: Biometric moderation model that incorporates an interaction term into the sleep disturbance variance components, as well as in the cross-regressions from the social integration variance components. Only one twin pair is shown. A = common genetic variance; C = shared environmental variance; E = non-shared environmental variance. Si = social integration; Sl = sleep disturbance.

	Within-Trait, Cross-Twin Correlations		Cross-Trait, Cross-Twin Correlations
Zygosity	**Social Integration**	**Sleep Disturbance**	**Social Integration-Sleep Disturbance[a]**
MZ	0.38	0.29	–0.12/–.16
DZ	0.15	0.04	–.18/–.09

Table 1: Within-trait and Cross-twin Correlations for the Social Integration and Sleep Disturbance Items in the MIDUS Sample.
Note: MZ = monozygotic (identical) twin pairs; DZ = dizygotic (fraternal) twin pairs. a = two correlations are presented from each twin pair. Twin 1's social integration with Twin 2's sleep disturbances, and Twin 1's sleep disturbance with Twin 2's social integration.

social integration and sleep disturbance; in addition, for both variables, the within-trait, cross-twin correlations for DZ twins is less than half that of MZ twins, suggesting little shared environmental influence on either phenotype. The cross-trait, cross-twin correlations, however, approximate the individual-level phenotypic correlation presented above, which suggests that the genetic influences on social integration may account for the association between social integration and sleep disturbance. This possibility was tested formally with the bivariate model displayed in **Figure 1**.

Model 1 (**Table 2**) includes the model parameters for the full bivariate specification estimating the ACE variance components for social integration and sleep disturbance, as well as regressions from each of the variance components in social integration to sleep disturbance. This model fit the data well (CFI = .96, RMSEA = .02). As shown, estimates for a common environmental influence (C) on both variables did not appear to be different from zero. In addition, cross-regressions from the common environment and the non-shared environment variance in social integration to sleep disturbance did not appear to be different from zero. Therefore, I tested a parsimonious specification (Model 2) by fixing these four parameters to zero. This specification did not significantly decrease the model fit ($\chi^2 = .30$, $\Delta df = 4$, $p = .99$). I confirmed that it was reasonable to set the common environment to zero in univariate biometric models for social integration and sleep disturbance. For each construct, altering the model from an ACE to an AE specification did not significantly degrade model fit.

A notable feature of Model 2 is that fixing the cross-regression from the non-shared environmental variance of social integration on sleep disturbance to zero did not result in a decrement in model fit. It is informative to consider these associations from a different perspective as well: What happens when the cross-regression from the genetic variance of social integration on sleep disturbance

Parameter	Model 1	Model 2	Model 3	Model 4
Variation in Social Integration				
Additive Genetic (A_{si})	.56 (.04)*	.56 (.04)*	.55 (.05)*	.55 (.04)*
Shared Environment (C_{si})	.00 (.24)	[0]	[0]	[0]
Non-shared Environment (E_{si})	.83 (.03)*	.83 (.02)*	.83 (.03)*	.83 (.03)*
Social Integration à Sleep				
A → Sleep (A_c)	–.30 (.06)*	–.28 (.04)*	–.33 (.07)*	–.29 (.05)*
Social Integration Interaction (A'_{si})			.08 (.07)	[0]
C → Sleep (C_c)	.00 (.16)	[0]	[0]	[0]
E → Sleep (E_c)	.02 (.04)	[0]	.05 (.05)	[0]
Social Integration Interaction (C'_{si})			-.01 (.04)	[0]
Unique Variation in Sleep				
Additive Genetic (A_{sl})	.36 (.08)*	.38 (.07)*	.29 (.13)*	.37 (.07)*
Social Integration Interaction (A'_{sl})			.13 (.13)	[0]
Shared Environment (C_{sl})	.00 (.14)	[0]	[0]	[0]
Non-shared environmental effect (E_{sl})	.89 (.03)*	.88 (.03)*	.87 (.03)*	.87 (.03)*
Social Integration Interaction (E'_{sl})			–.09 (.03)*	–.08 (.02)*

Table 2: Unstandardized Parameter Estimates (and Standard Errors) from Biometric Models of Social Integration and Sleep Disturbance.
Note. Model 1 is the full bivariate specification. Model 2 is the reduced bivariate specification (fixing the common environment estimates of both variables, as well as the environmental cross regressions, to zero). Model 3 introduces interaction terms, and Model 4 is a reduced specification that includes only the non-zero estimates from Model 3. * $p < .05$

is fixed to zero and the cross regression from the non-shared environmental variance is freely estimated? When the common genetic path is omitted from the model, the effect of non-shared environment variance in social integration on sleep disturbance is different from zero (B = –.13, *SE* = .03, 95% [CI –.18, –.07]), which is consistent with findings from research that is not genetically informed. However, fixing the genetic influences (shared between social integration and sleep disturbance) to zero resulted in a large decrement in model fit ($\chi^2 = 23.8$, $\Delta df = 1$, $p < .0001$). This pattern of results suggests that within-twin differences in social integration do not exert a causal influence on sleep disturbance. Instead, evidence from the MIDUS sample suggests that common genetics cannot be excluded from the model; the negative phenotypic association between perceived social integration and perceived sleep disturbance is best explained by genes that are common to both variables.

The next series of analyses explored the possibility that perceived social integration moderates the genetic and environmental influences on sleep disturbance. These models involve adding an interaction term to the AE variance estimates in the sleep disturbance variable (see **Figure 2**), as well as to the cross-regression from social integration to sleep disturbance. Model 3 (**Table 2**) displays the 10 parameter estimates from this moderation model. Although Model 2 fixed the cross-regression from the non-shared variance in social integration to sleep disturbance to zero, I estimated this main effect in order to also estimate the interaction on this cross-regression in Model 3; conceptually, this would allow for a potentially causal influence from social integration to sleep disturbance to operate at specific levels of social integration. However, as shown in **Table 2** (Model 3), neither the main effect nor the interaction effects were significant from the non-shared variance in social integration to sleep disturbance. Among the three other interaction effects, social integration moderated only the unique non-shared environmental variance of sleep disturbance. To ensure these results were not spurious, I re-estimated the model by fixing the non-significant estimates to zero, and the resulting estimates are displayed in the Model 4. The key parameter of interest in Model 4 is the negative interaction (E'_{sl}) between the non-shared variance in sleep disturbance and social integration, providing evidence that social integration moderates the unique environmental influences in sleep disturbance.

The results of this analysis (Model 4) are displayed in **Figure 3**. At low levels of social integration, non-shared environmental contribution to sleep disturbance is highest, whereas the influence of genetics on sleep disturbance increases steadily as social integration increases. For example, among people who report the lowest levels of social integration (i.e., those two *SD*s below the mean on this composite), 83% of the variance in sleep disturbance is due to non-shared environment variance, whereas among those who report the highest levels of social integration (i.e., those two *SD*s above the mean on this composite), 70% of the variance in sleep disturbance is due to non-shared environmental influence.

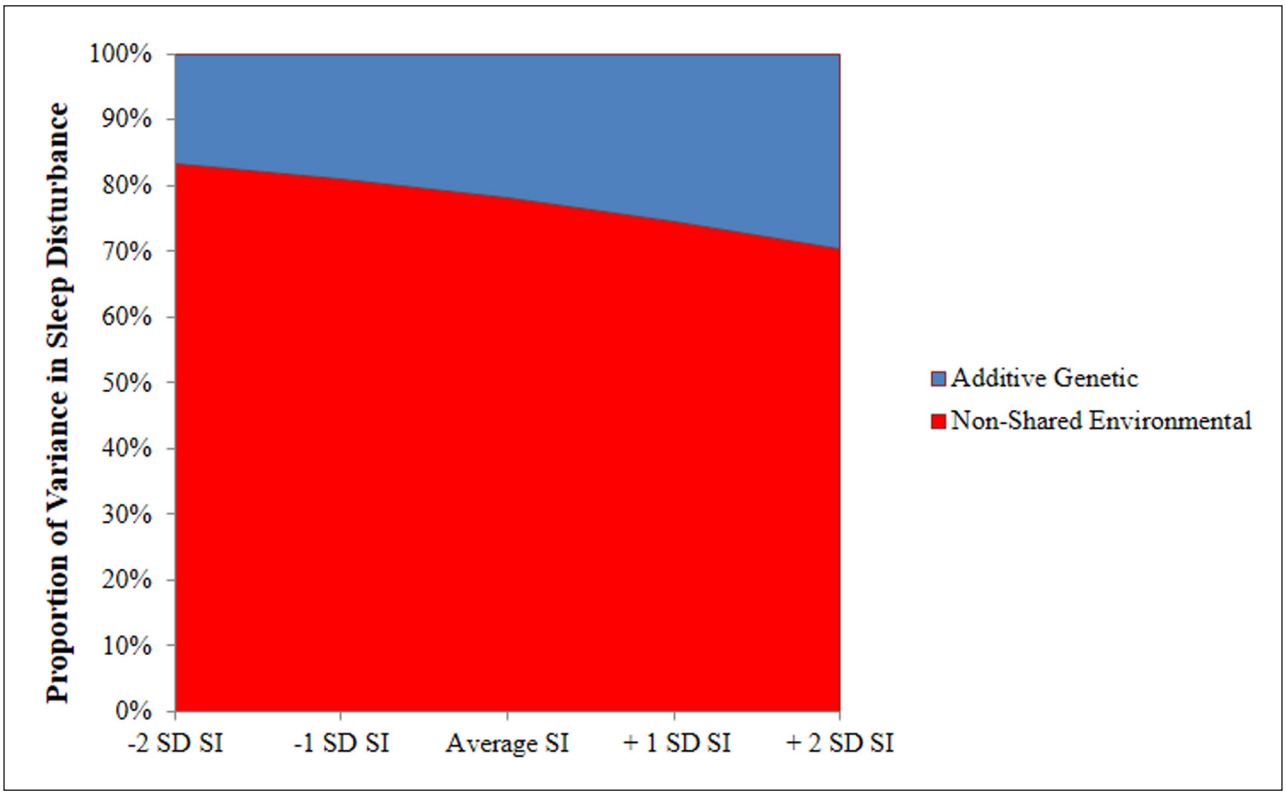

Figure 3: Proportion of variance in sleep disturbance due to genetic and non-shared environmental influences as a function of social integration (SI). SD = standard deviation. (Figure estimates derived from the parameters reported in Model 4, Table 2.)

Discussion

The results of this study suggest that an essential feature of the evolutionary model of loneliness may need refinement or elaboration. Contrary to my primary hypothesis and the hypervigilance formulation, which holds that low levels of social integration lead to sleep disturbances (for people who are frequently monitoring their social standing), I found no evidence for a quasi-causal effect linking the two constructs. Instead, genes common to both variables explain the phenotypic association between social integration and sleep disturbance. These findings are consistent with a prior twin analysis from the MIDUS data, which found that the association between social integration and perceived overall (self-rated) health was due to genetic influences common to both variables [6].

Both social integration and sleep disturbance are complex traits that likely involve contributions from hundreds of different genes. Although these analyses do not identify the specific genes that are shared by the two traits, recent molecular studies suggest that variability in the polymorphic region of the serotonin transporter gene (*5-HTTLPR*) plays an important role in shaping emotional responses to stress [34] and is related to both loneliness and a variety of sleep disturbances [28, 35]. For example, relative to non-caregivers, caregivers of a spouse or parent with dementia who also carried a short copy of the serotonin transporter gene self-reported significantly worse sleep [36], and adolescents carrying the short allele of *5-HTTLPR* who also reported low maternal support were at increased risk of developing loneliness [37]. Although the serotonin transporter gene may account for some of the shared genetics in social integration and loneliness, many other genes will play a role in this association as well; for this reason, this topic would greatly benefit from further research.

In a series of biometric moderation analyses, I examined whether the genetic or environmental influences on sleep disturbance differed as a function of social integration. Effectively, the analyses constituted studying a potential quantitative G X E interaction in the context of a gene-environment correlation (that accounts for genetic influences that are common to both variables). Although I had no a priori hypotheses for these analyses, I was motivated to explore two competing possibilities: a diathesis-stress model (in which low levels of social integration were associated with the largest genetic influences on sleep disturbance) and a stress-buffering model (in which low levels of social integration were associated with the greatest environmental influences on sleep disturbance). The moderation analyses revealed that social integration interacted with the non-shared environmental influences on sleep disturbance but was largely unassociated with the genetic influences (either those common to social integration or unique to sleep disturbance). Thus, the results are most consistent with a stress-buffering model of social support. At the lowest levels of social integration (i.e., highest levels of loneliness), non-shared environmental influences on sleep disturbance were the greatest, accounting for up to 83% of the variance in sleep disturbance (calculated from the unstandardized regression coefficients in Model 4, **Table 2**). Prior reports demonstrate a large non-shared environmental influence on sleep duration [18], and the current results are consistent with this finding, on average, and further suggest that as social integration decreases, the influence of non-shared environmental factors grows.

The main idea behind the stress-buffering hypothesis [20] is that during periods of acute stress, social resources come online to alter the perception or experience of stress and thus attenuate the corresponding physiological and psychological responses to these events. Results of the current study suggest that when perceived social integration is low (i.e., when loneliness is high), non-shared environmental influences account for the largest amount of variance in sleep disturbances. These environmental influences are not shared within the family and may include, for example, differential exposure by twins to work or relationship stress, discrimination, academic rejections, or a host of other environmental experiences that may be related to sleep disturbance. When social integration is low, these non-shared experiences exert their strongest impact on sleep disturbance. In contrast, I find no substantial evidence in support of the diathesis-stress model in which we would expect the greatest genetic influences on sleep disturbances at low levels of social integration.

Although it is true— and perhaps somewhat perplexing at face value— that the largest genetic influences on sleep disturbance risk are observed at high levels of social integration, it is important to note that the 29% heritability observed at high levels of social integration are consistent with the heritability of low sleep duration in general (see [18]). I interpret the results to suggest that as social integration decreases (or, as loneliness increases) we observe a greater influence of the unique environmental influences on sleep disturbance. In considering this process overall, it is also important to note the moderation effect appears fairly small—a 13% increase in environmental variance across the entire spectrum of social integration. It will be incumbent upon future research to ultimately determine if a change in this amount is meaningful, and one way of doing so is to examine other moderators of sleep disturbance and to compare or benchmark the differential genetic and environmental influences across these potentially distinct moderators.

The findings from this study should be interpreted in light of several limitations. First, a single item tapping sleep disturbance is inadequate for making firm conclusions about the loneliness-sleep association more generally. As noted in the Method, however, the single item measure of sleep disturbance used here was significantly associated with the PSQI Global Sleep Quality score up to 10 years later, suggesting that the single item tapping sleep problems is sensitive to variability in self-reported sleep problems. A related point is that both measures used in this study rely exclusively on self-report, which may confound the nature of the genetic association. For example, it is possible that the common genetic influences on both traits reflect common method variance and genetic influences on the tendency to report low levels of social integration and high sleep disturbance. Genetically-informed studies that include objective measures of both traits will help clarify this. Second, this report relied on data from

a single wave of the MIDUS study; it is possible that, as exposure to loneliness accumulates in time, a prospective association between these traits would be consistent with a quasi-causal influence. Prospective analyses will add much to this literature in time. In addition, it is quite possible that the potentially causal ordering of the association between social integration and sleep flows from sleep to social integration (and not as studied here, from social integration to sleep). I chose the current analyses based on extant theory about loneliness and health (see [13]), but other genetically-informed designs have included sleep as the predictor variable of interest (e.g., [19]). Finally, although this study includes 905 twin pairs, the sample size is relatively small for testing complex biometric models, especially in cases where common environmental influence may be present and for the examination of statistical interactions. Examining these effects in larger twin samples would contribute to this growing body of knowledge.

Conclusion

Sleep and sleep disturbances play an important role in the evolutionary theory of loneliness [13], but is loneliness a causal agent of ill health or a marker of risk more generally? The theory dictates that the lonely are hypervigilant about their social standing; this hypervigilance can extend to sleep difficulties, and these difficulties represent an important route through which loneliness may affect health. Using data from the MIDUS twin sample, this paper examined whether within-pair differences in social integration were associated with sleep disturbances after accounting for shared genetic influences on both traits. The phenotypic association between social integration and sleep disturbance is best explained by genes that are common to both variables, and the observed results were not consistent with a quasi-causal effect from low social integration to greater sleep disturbances. Despite the absence of this direct effect, social integration moderated the non-shared environmental influences on sleep disturbance, with the greatest non-shared environment variance observed at the lowest levels of sleep disturbance. I interpreted these effects as being consistent with and providing evidence for a stress-buffering model of social integration rather than a diathesis-stress model in which low social integration would potentiate the genetic influences on sleep disturbance.

Competing Interests

The author declares that they have no competing interests.

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Acronym

MIDUS = Midlife in the United States Survey.

Notes

[1] This effect is often referred to as *quasi-causal* because causality cannot be determined without experimentation (see Turkheimer & Harden, 2014). The presence of a meaningful association between the two variables is consistent with a causal process, but this cannot be determined with certainty. However, if the association of interest is eliminated after accounting for genes that are common to both variables, we can determine with a high degree of certainty that the putative effect of X on Y is inconsistent with a direct causal effect.

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