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USING SECONDARY DATA TO TEST QUESTIONS ABOUT THE GENETIC BASIS OF BEHAVIOR

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Behavioral genetic studies over the past several decades have shown that most human behavior is genetically influenced (Turkheimer, 2000). In general, however, research on genetic factors that influence human behavior becomes more fruitful when investigators move beyond the issue of whether heredity plays a role. Our own work uses behavioral genetic methods to identify the genetically influenced mediators between self-esteem and social behavior. Innate, heritable influences are important in explaining the origins of self-esteem, accounting for approximately 40% of the variance in self-esteem (Neiss, Sedikides, & Stevenson, 2002). Nonetheless, there is probably no "self-esteem gene." Rather, the pathway from DNA to self-esteem involves multiple genes whose expression relates to multiple processes, which in turn are related to multiple behaviors. For example, self-esteem is an affective evaluation of the self and thus may overlap with affective style in general. So it might be the case that the genetic influence on self-esteem reflects positive or negative affective style rather than genetic factors on self-esteem per se. Existing studies often include a wide range of constructs and thus provide an excellent opportunity to investigate genetic links among multiple behaviors. As such, secondary data sets are a useful tool for behavioral genetic research. Perhaps even more pertinently, secondary data sets provide an excellent way

for researchers new to behavioural genetics to implement genetically informed methodologies in their own work.

A variety of methodologies can inform whether and how genetic factors influence behavior. Our own work focuses on quantitative genetic analyses of twin data. In this chapter, we present quantitative genetic work that moves beyond identifying the magnitude of genetic influence to provide insight to more substantive questions. Before turning to our work, we describe briefly how adoption and molecular genetic studies provide complementary information about genetic influences on behavior. We present more discussion on twin data using an illustrative study. The purpose of the illustrative study here is to provide nonbehavioral genetic researchers with ideas about how genetically informative secondary data sets could prove useful in their own endeavors. The bulk of our chapter integrates information about the use of secondary twin data sets with an actual application of the approach.

ADOPTION STUDY DATA

Twin data are crucial for investigating genetic influences on behavior but are less suited to identifying shared environmental influences. Data from studies of adopted children are very useful for identifying environmental influences on behavior that operate independently of genetic factors. Resemblances between adopted children and their adoptive parents and nonbiologically related adoptive siblings can arise only through shared environmental effects. Similarly, resemblance between adopted children and their biological parents can arise only through genetic transmission. Both of these assertions are based on the assumption that adoption placements are made at random, and selective placement will undermine this assumption.

Nevertheless, adoption data are a potent adjunct to twin data. The two types of studies are complementary in that the twin design has good power to detect genetic effects on behavior but has less power to detect shared environment effects. The studies of adopted children and their adoptive families are a powerful design to detect shared environment effects but are less suited to examine genetic effects, unless data are available on biological parents (and this is often lacking). In addition, combining information across both types of studies allows for better understanding of more complex gene–environment interplay, such as gene–environment correlations or gene × environment interactions. The strengths and weaknesses of these alternative behavior genetic designs are discussed in Plomin, DeFries, McClearn, and McGuffin (2001).

Twin studies are more prevalent than adoption studies. Consequently, there is less scope for the secondary analysis of existing data from adoption studies. The Colorado Adoption Project (CAP; Plomin, Fulker, Corley, &

DeFries, 1997), a long-running project, is available for secondary data analysis. Details of the CAP can be found at http://ibgwww.colorado.edu/cap/, and the data are available at the Henry A. Murray Research Archive at Harvard University (http://www.murray.harvard.edu/). This study of adoptive children, their biological and adoptive parents, and their siblings has been running for more than 30 years. The study is particularly well suited for research questions that require longitudinal data, as 442 families continue to participate, representing over 90% of the original number enrolled.

MOLECULAR GENETIC DATA

Quantitative genetic analysis of twin and adoption provide significant insights into genetic and environmental influences on behavior. Such data can be used not only to identify which behaviors have strong genetic effects (a prerequisite for molecular genetic studies) but also to examine clues as to the ways different personality characteristics, abilities, and behaviors share genetic and environmental influences. However, such studies do not identify the specific genes involved. For this, molecular genetic data are needed.

The prime questions confronting behavior genetics concern the interplay between genetic and environmental influences (Rutter, Moffitt, & Caspi, 2006). The influences are not independent, and the action of one is highly contingent on the influences of the other. Gene expression is modified by experience, and the impact of life events is moderated by genetic differences between people. The methods for focusing on this joint action of genetic and environmental factors have been systematically reviewed elsewhere (Moffitt, Caspi, & Rutter, 2005). These methods are most insightful if they include molecular genetic data.

A crucial feature of molecular genetic studies of behavior is the need to demonstrate that the results are not sample specific and can be replicated on independent samples. This is necessary in the case of gene–environment interaction studies, in which often a wide range of potential genetic moderators is examined for large sets of environmental measures. Replication is also important. Studies to identify genes implicated in influencing behaviors are now using genome-wide association methods, where 500,000 genetic variants can be tested (e.g., Butcher, Davis, Craig, & Plomin, 2008). In these types of studies, multiple tests of significance may produce false positive result, and replication in an independent sample is highly desirable, if not essential.

Existing and open access databases are particularly valuable when it comes to replication, although there are obvious limitations such as whether the same phenotypic measures are available in the existing data set and whether the same genetic variants (polymorphisms) have been genotyped.

With these constraints in mind, it may be prudent to select some psychological measures for a specific study based on what is known to be available in the established archives.

One such archive that includes genotyping is the National Longitudinal Study of Adolescent Health (Add Health) study (details of which are given in Recommended Data Sets section). The Generation R Study conducted in Holland is also an open access database that includes measures of behavioral and cognitive development, such as maternal and paternal psychopathology, fetal and postnatal brain development, psychopathology and cognition, neuromotor development, and chronic pain (Jaddoe et al., 2007). Investigators enrolled 9,778 mothers, with more detailed information available on a subgroup of 1,232 women and their children. The biological determinants include parental anthropometrics and blood pressure; fetal and postnatal growth characteristics, endocrine and immunological factors; and important for the purposes of this chapter, genetic variants (polymorphisms). The data can be particularly informative, as they include environmental determinants (maternal and childhood diet, parental lifestyle habits including smoking, alcohol consumption, and housing conditions) and social determinants (parental education, employment status and household income, parental marital status, and ethnicity). The inclusion of both biological and social measures means that the data set is well suited for studies of gene–environment interplay. The study accepts requests for collaboration, which are vetted through the Generation R Study Management Team (see http://www.generationr.nl).

ILLUSTRATIVE STUDY

In our own research, we sought to identify behaviors that share genetic factors with self-esteem. Self-esteem correlates with several constructs, such as negative emotionality, depression, and neuroticism (Judge, Erez, Bono, & Thoresen, 2002; Neiss, Stevenson, Legrand, Iacono, & Sedikides, in press). We expected a portion of this correlation to arise from common heritable factors and sought to characterize those heritable factors using twin data. We turned to existing data to investigate the connection between the self and broad affectivity or personality.

ADVANTAGES OF SECONDARY DATA

It is no small undertaking to gather a large, genetically informed sample. Such a sample would include studies of twins, adoptive families, or molecular genetic studies that genotype the participants. Each type of study requires

large-scale and expensive recruitment efforts. As some of the existing twin registries have grown to several thousand twin pairs, the standard for twin studies now involves fairly large samples. Adoption studies best assess genetic effects by including both the biological and adoptive families, but that dictates a long-term effort to recruit the multiple informants. These challenges mean that, in most cases, the expense and effort are worthwhile only if a group of investigators wish to carry out an extensive study of participants and follow the participants longitudinally. Such studies usually occur under the aegis of a dedicated research center with considerable administrative support. Many of the larger existing twin registries offer opportunities for collaboration. This route also carries costs, such as substantial charges for data collection and the time involved for the vetting and approval of the research proposal by the associated investigators. For investigators looking for something more immediate and viable on a small scale, existing data sets are an appealing option. In our case, we opted to use the National Survey of Midlife Development in the United States (MIDUS).

A strength of the MIDUS data is that they include a large population-based sample, allowing researchers to contrast phenotypic and genetically informed analyses. Researchers often discuss the potential genetic confound in correlational studies of parenting effects, but few consider shared genetic factors as a potential confound in phenotypic models. Specifically, the apparent causal ordering of the relation between the self and affectivity may be different in phenotypic versus genetic analyses. Given that information on the representativeness of twin samples is rarely available directly, another strength of the MIDUS design is that researchers can verify whether phenotypic relations are similar across the twin and population samples. Researchers also used the large, separate sample of no twin participants to test measurement models for implementation in subsequent behavioral genetic analyses (Neiss et al., 2005).

DISADVANTAGES OF SECONDARY DATA

In dealing with the MIDUS study, we faced challenges common to the use of secondary data. One challenge was finding appropriate measurement scales for our purposes. The original investigators did not directly assess self-esteem, leading us to compile a self-esteem measure from items that assessed personal acceptance and satisfaction with the self.

We intended to look also at broad negative and positive affectivity, conceptualized as general dispositional tendencies to experience either positive or negative mood. Here, we were confronted with another challenge.

Although MIDUS included measures of both positive and negative affect, these did not correspond to the widely accepted Positive Affect and Negative Affect Scales (PANAS; Watson, Clark, & Tillage, 1988). It is important to note that the PANAS is based on the premise that positive and negative affect are relatively independent. Positive and negative affect are, however, inversely correlated in the MIDUS sample (Mroczek & Kolarz, 1998). Hence, we had to cope with a discrepancy between a widely accepted theory about the structure of affect (positive and negative affect are independent) and the empirical findings in the MIDUS sample. This discrepancy could not be reconciled satisfactorily because of the measurement issue. In the end, we chose to focus primarily on negative affectivity. In other words, the use of secondary data required that we modify goals in light of measurement constraints.

However, not all measurement issues are disadvantages. When we combed through the MIDUS variables to construct a scale of mastery or locus of control, we discovered that the survey also assessed primary and secondary control strategies, allowing us to extend our original focus to the broader idea of the executive self. The *executive self* is a broad term that includes such constructs as control beliefs, control strategies, and self-regulation (Baumeister, 1998; Sedikides & Gregg, 2003). The MIDUS survey included items that tap into people's beliefs that they can control many aspects of their lives (*mastery*), possess strategies to change the external world to fit with their own needs (*primary control*), and possess strategies to protect the self in negative situations (*secondary control*). Few studies have assessed directly the executive self, so our operationalization provided a unique addition to the literature.

Accuracy of zygosity determination is one potential issue with twin studies, as self-reported zygosity may be incorrect. The MIDUS investigators included a zygosity questionnaire to assess physical resemblance and attempted to obtain DNA samples from the twin participants to verify zygosity. However, not all existing data sets may have verified the genetic relatedness of sibling pairs and some pairs may be misclassified.

PHENOTYPIC STUDY OVERVIEW

We took advantage of the MIDUS survey by investigating the relations among these three constructs with both (a) phenotypic (i.e., observed) analyses in the population sample (Study 1) and (b) behavioral genetic analyses in the twin sample (Study 3). We also included a short-term longitudinal study to strengthen the phenotypic analyses (Study 2). By using multiple methodologies, we were able to gain a richer understanding of how executive self,

self-esteem, and negative affectivity interrelate. The use of secondary data facilitated this in-depth approach, and in the remainder of this chapter, we describe the analyses drawn from the MIDUS survey.

We examined first the phenotypic relations among these three constructs. In particular, we considered the idea that both the executive self and self-esteem serve as protective factors against psychological distress (Metalsky, Joiner, Hardin, & Abramson, 1993; Pyszczynski, Greenberg, Solomon, Arndt, & Schimel, 2004). We tested two alternative phenotypic models: one in which self-esteem mediates the link between executive self and negative affectivity, and another in which the executive self mediates the link between self-esteem and negative affectivity. The mediational models allowed us to evaluate whether the influence of the self system on negative affectivity operates primarily through one self-aspect (executive self vs. self-esteem). In addition, this study allowed us to validate our composite scales and test the relations among our constructs in a sample independent from that to be used for the behavioral genetic analyses.

In our theory-based construction of composite variables, we combined scales in ways that may not have been foreseen by the original investigators. Preliminary analyses bolstered the case for our constructed measures (Neiss et al., 2005). We then tested the phenotypic relations through a series of hierarchical regression analyses. Specifically, we tested the mediational status of executive self versus self-esteem. Both executive self ($\beta = -.34$, $p < .001$) and self-esteem ($\beta = -.53$, $p < .001$) were related to negative affectivity: People reporting weaker executive self or lower self-esteem also reported higher negative affectivity. Whereas the relation between self-esteem and negative affectivity declined minimally with the addition of executive self, the relation between executive self and negative affectivity was lowered substantially once self-esteem was included in the model. Thus, lowered self-esteem accounted for the majority of the influence of the self system on negative affectivity.

Nevertheless, given that the analyses used nonstandard measures, it is possible that our results were contingent on the specific measures used. We note that we did in fact replicate the phenotypic analyses in another sample using more standard scales (Neiss et al., 2005; Study 2). The use of secondary data encouraged us to pursue multiple methodologies. Although secondary data might require compromises in measurement, replications using smaller-scale studies based on convenience samples can provide important lines of converging evidence. Such a strategy is a compelling scholarly practice that can help build a cumulative science of social and personality psychology. Moreover, behavioral genetic methodologies can provide additional insight into the understanding of psychological mechanisms. We next turned to the behavioral genetic analyses.

TWIN STUDY

A multivariate behavioral genetic approach allowed us to address more complex questions about the relations among executive self, self-esteem, and negative affectivity. Do the three constructs share common genetic antecedents or are genetic influences unique to each? Do environmental effects reflect a common influence on executive self, self-esteem, and negative affectivity, or are environmental effects more specific to each? Such questions help clarify the etiological underpinnings of the constructs.

Behavioral genetic studies seek to identify genetic and environmental sources of variance. Genetic effects include all influences with an origin in genetic differences between people. Environmental sources include shared environmental effects that act to make siblings more alike, and nonshared environmental effects that create differences between siblings. Multivariate behavioral genetic analyses go beyond apportioning the variance of a specific behavior into genetic and environmental components, by identifying the sources of covariance between multiple phenotypes. That is, the covariation between two or more characteristics may be due to common genetic influences or common environmental influences affecting multiple phenotypes. For example, a common genetic factor may influence the executive self, self-esteem, and negative affectivity all together, or each may show a unique and separable genetic influence.

Identifying the source of covariation between phenotypes contributes to the understanding of underlying causal processes. Indeed, we were particularly interested in common genetic etiology as an indicator of an underlying common temperamental "core." Other researchers have suggested that many related personality traits are in fact measures of the same underlying core construct (Judge et al., 2002). For example, Judge et al. (2002) found that self-esteem, locus of control, self-efficacy, and neuroticism were all markers of a higher order construct, which they viewed as broad Neuroticism. It may be that innate, heritable differences account for much of the overlap between the self system and negative affectivity. Furthermore, if this genetically influenced temperamental core is left out of psychological models, researchers may imbue phenotypic correlations (including those found in our own phenotypic analyses) with a misleading causal interpretation.

Our multivariate behavior genetic design apportioned the covariance between executive self, self-esteem, and negative affectivity into genetic and environmental components. We sought to identify both common origins of the different self-aspects and negative affectivity as well as points of uniqueness, where genetic and environmental factors affect primarily one phenotype.

Method

We used the twin sample from the MIDUS survey ($N = 1,914$ individuals). The design allowed multiple twin pairs from the same family to participate; we limited our sample to only one pair per family. Our selection process yielded 878 twin pairs: 344 identical, or monozygotic (MZ), twin pairs (160 female pairs, 184 male pairs), and 534 fraternal, or dizygotic (DZ), twin pairs (189 female pairs, 115 male pairs, 230 mixed-sex pairs). More detail on the sample and methods can be found elsewhere (Neiss et al., 2005).

Results

The phenotypic relations among executive self, self-esteem, and negative affectivity replicated those observed in the nontwin population sample, with self-esteem mediating the relation between executive self and negative affectivity. Next, we used behavioral genetic analyses to identify genetic and environmental connections among the three constructs.

This type of classic twin study relies on the comparison of similarity between MZ twins and DZ twins. MZ twins share all genes that vary between individuals, whereas DZ twins share, on average, half of those genes. The analyses rely on the assumption that DZ twins are treated as similarly to one another as are MZ twins (*equal environment assumption*). Therefore, greater resemblance among MZ twins as compared with DZ twins provides evidence for heritable influences. In our study, the MZ twins resembled each other to a greater degree than did DZ twins, providing cursory evidence of a genetic effect on each of variables. Univariate structural equation modeling confirmed this impression. Genetic influences explained a substantial portion of the differences between individuals in executive self (41%), self-esteem (45%), and negative affect (38%). Shared environmental influences were minimal (0%–4%). Nonshared environmental influences explained the majority of variance in executive self (59%), self-esteem (55%), and negative affect (57%). Thus, environmental influences that make siblings different from one another explained the majority of variance in all three constructs, although this estimate includes measurement error as well.

Our interest, however, lay in identifying the genetic and environmental architecture that underlies the relations among executive self, self-esteem, and negative affect. The logic behind univariate analyses extends to multivariate analyses. Greater MZ as compared with DZ cross-correlations (i.e., the correlation between one twin's score on a variable with the other twin's score on a second variable) implicate common genetic influences. Conversely, if the cross-correlation is similar across MZ and DZ twins, there is evidence for common shared environmental effects. In fact, we found that

the MZ cross-correlations were larger than the DZ cross-correlations for our constructs.

We used a Cholesky decomposition to model the genetic and environmental factors underlying the relations among executive self, self-esteem, and negative affectivity. Figure 8.1 illustrates the model for just one member of a twin pair and provides standardized path estimates. The first set of genetic and environmental factors are common to all three variables (a1, c1, e1). The second set of factors underlies only executive self and negative affectivity (a2, c2, e2). The third set of factors represents genetic and environmental influence unique to negative affectivity (a3, c3, e3). Summing all squared path estimates to each construct from a particular source of effects (genetic, shared environment or nonshared environment) provides the total portion of variability ascribed to that source.

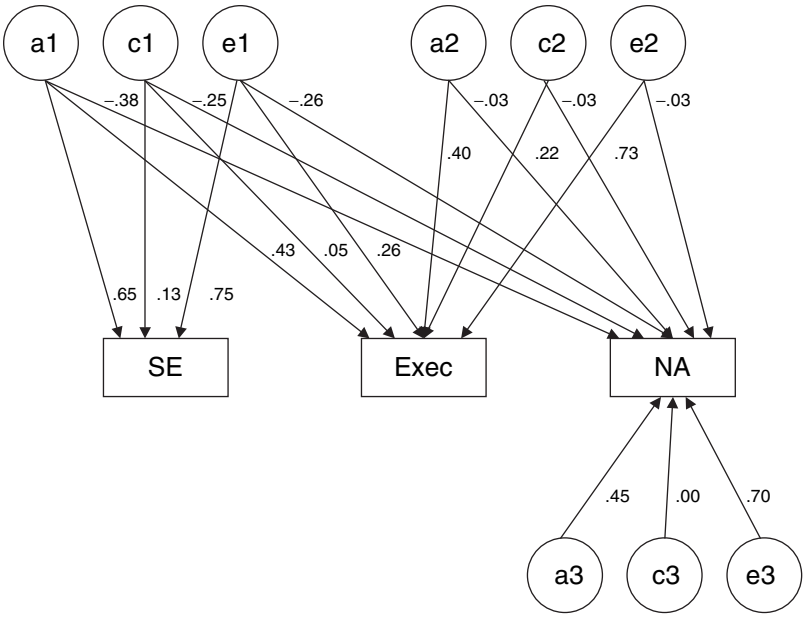

Figure 8.1. Cholesky model of genetic and environmental factors underlying self-esteem (SE), executive self (Exec), and negative affectivity (NA). The Cholesky decomposition models additive genetic factors (a), shared environmental factors (c), and nonshared environmental factors (e). From "Executive Self, Self-Esteem, and Negative Affectivity: Relations at the Phenotypic and Genotypic Level," by M. B. Neiss, J. Stevenson, C. Sedikides, M. Kumashiro, E. J. Finkel, and C. E. Rusbult, 2005, *Journal of Personality and Social Psychology, 89,* p. 602. Copyright 2005 by the American Psychological Association.

The ordering of variables affects the interpretation of a Cholesky model (Loehlin, 1996). The mediational results informed the order chosen: We placed executive self second, to investigate whether genetic and environmental influences explain any modest direct relation between executive self and negative affectivity after accounting for the genetic and environmental influences that also impact self-esteem. The model fit the data well, as evidenced by a nonsignificant chi-square, χ^2 (24, N = 572) = 29.34, p < .21, a low (.03) root-mean-square error of approximation (RMSEA), and negative Akaike's information criterion (AIC, –18.66).

The genetic factor common to all three variables showed large to moderate genetic loadings (i.e., .43, .65, and –.38 for executive self, self-esteem, and negative affectivity, respectively). The negative loading to negative affectivity reflected the direction of the phenotypic relations: Genetic influences that contributed to higher executive self or self-esteem led to lower negative affectivity. Although the genetic factor on executive self and negative affectivity (second factor) showed a moderate loading to executive self (.40), it had a very low loading on negative affectivity (–.03). In other words, this factor represented genetic effects that were essentially unique to executive self; genetic links between executive self and negative affectivity were carried primarily by the common genetic factor influencing all three variables. Negative affectivity showed moderate unique genetic influence (.45). Overall, the common genetic factor accounted for a large proportion of the genetic influence on executive self and negative affectivity: 53% percent of the genetic variance in executive self and 41% of the genetic variance in negative affectivity. Because of the constraints of the model, genetic influence on self-esteem was modeled entirely through the common factor.

Common shared environmental influences (c1 paths) influenced both self-esteem and negative affect, whereas shared environmental influences on executive self were separable and unique to executive self. However, these results must be interpreted with caution, as shared environmental estimates were small and statistically insignificant. We could drop all six shared environmental paths without reducing significantly model fit, χ^2 (30, N = 572) = 29.88, p < .47 (AIC = –30.12; RMSEA = .02). In addition, the change in chi-square between the full model and one with no shared environmental influence was not significant, which led us to conclude that shared environmental effects do not explain individual differences in or covariation between executive self, self-esteem, and negative affect.

Each common nonshared environmental factor showed stronger loadings to one particular construct: the first, to self-esteem; the second, to executive self. In addition, nonshared environmental influences on negative affectivity

stemmed primarily from the third, specific factor. In other words, nonshared environmental effects were primarily unique to each variable. Any modest overlap stemmed from the common factor underlying all three. These estimates include measurement error.

The multivariate analyses yielded modest links between just executive self and negative affectivity. Therefore, we tested one final model in which we dropped all shared environment paths (as described above) and the remaining direct genetic and nonshared environmental paths between executive self and negative affect (a2 and e2 paths to NA). This reduced model fit well, χ^2 (32, $N = 572$) = 32.52, $p < .44$ (AIC = −31.48; RMSEA = .02). Of note, this model suggests that executive self does not display any genetic or environmental link with negative affect over and above those effects shared with self-esteem.

CONCLUSION

Our aim was to investigate the overlap between aspects of the self system (executive self and self-esteem) and negative affectivity. Using a secondary data set allowed us to compare phenotypic analyses and behavioral genetic analyses involving large samples and complicated study design (twin methodology). Capitalizing on both sets of results, we concluded that self-esteem explained much of the relation between executive self and negative affectivity. The behavioral genetic analyses added the information that the overlap stemmed primarily from common genetic influences. Nonetheless, the behavioral genetic methodology allowed us also to specify distinctions between the self system and negative affectivity, as illustrated by specific genetic and nonshared environmental influences.

The use of secondary data sets permits researchers to use behavioral genetic methods without undergoing the arduous process of actually having to collect genetically informative data. Although behavior genetic methodology can be used to answer theoretically driven questions about psychological phenomena, relatively few psychologists include this method in their toolbox. One obstacle is the difficulty in collecting relevant data—a difficulty that can be overcome by turning to secondary data sets.

RECOMMENDED DATA SETS

Developing and maintaining a large twin registry is expensive and time consuming. The high administrative burden means that investigators must invest substantial funds into collecting and maintaining the data. Thus, it is

relatively rare to find genetically informative data that are readily available to other researchers. We note that many twin registries do in fact allow researchers to propose secondary data analyses, collaborate with project directors or principal investigators, or pay for data collection. These are all valuable ways to access genetically informed data sets without setting up independent registries. We encourage researchers to pursue these routes as well. In keeping with the spirit of this book, however, we describe here several archived data sets that are available to researchers. This availability is especially laudable, as the large time and monetary investment in obtaining genetically informative data often encourages proprietary proclivities.

- *National Survey of Midlife Development in the United States (MIDUS)*. Our own research drew from the MIDUS data set, available from Interuniversity Consortium for Political and Social Research (ICPSR; http://www.icpsr.umich.edu). The MIDUS represents an interdisciplinary collaboration to examine the patterns, predictors, and consequences of midlife development in the areas of physical health, psychological well-being, and social responsibility. Respondents provided extensive information on their physical and mental health. Participants also answered questions about their work histories and work-related demands. In addition, they provided information about childhood experiences, such as presence or absence of parents, familial environments, and quality of relationships with siblings and parents. Psychological well-being measures included feelings of accomplishment, desire to learn, sense of control over one's life, broad interests, and hopes for the future. The data include respondents ages 25 to 74 recruited from the general population in a random-digit dialing procedure ($N = 4,244$), siblings of the general population respondents ($N = 950$), and a twin sample ($N = 1,914$). The first data wave was collected in 1995 to 1996 (Brim et al., 2007), and the second in 2004 to 2006 (Ryff et al., 2006).
- *Swedish Adoption/Twin Study on Aging (SATSA)*. Also available from ICPSR are data from SATSA (Pedersen, 1993). SATSA was designed to study the environmental and genetic factors contributing to individual differences in aging. SATSA includes four data waves (sample sizes vary by questionnaire and year, with $N = 1,736$ at 1984). The sample includes twins who were separated at an early age and raised apart as well as a control sample of twins raised together. Respondents answered questions about their personality, attitudes, health status, the way

they were raised, work environment, alcohol consumption, and dietary and smoking habits. A subsample of 150 pairs of twins raised apart and 150 pairs of twins raised together participated in four waves of in-person testing, which included a health examination; interviews; and tests on functional capacity, cognitive abilities, and memory. Identical twins raised apart provide a unique resource for identifying specific nonshared environmental effects.

- *National Longitudinal Study of Adolescent Health (Add Health).* This study (Harris et al., 2003) surveyed adolescents about health-related behaviors and their outcomes in young adulthood. In-school questionnaires were followed up by in-home interviews approximately 1, 2, and 6 years later. The study assessed adolescent health and sexual behavior, problem behavior, self-efficacy, and feelings. Participants answered questions concerning characteristics of their peer groups, schools, familial relations, familial structure, and communities. Adolescents nominated a social network, members of whom are included in the data set, allowing researchers access to rich detail about peer networks. The study involved 3,139 sibling pairs of varying degrees of genetic relatedness. Specifically, the pairs include identical and fraternal twins, full siblings, half siblings, and unrelated siblings. As such, the sample provides a unique resource for modeling genetic and environmental influences across multiple types of sibling pairs, not just twins. Access to variables concerning genetic relatedness and the molecular genetic data requires completion of a restricted-use data contract (see http://www.cpc.unc.edu/projects/addhealth/data). The application process involves a fee.

FOR FURTHER READING

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This review summarizes research on personality structure and development, with a section devoted to behavioral genetic approaches to studying personality. This section provides examples of how behavioral genetic approaches can lead to generative lines of research and illuminate the etiology of personality.

Rutter, M. (2002). Nature, nurture, and development: From evangelism through science toward policy and practice. *Child Development*, *73*, 1–21.

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