



An Interactionist Perspective on Genetic and Environmental Contributions to Personality

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Abstract

It is now well established that nature *and* nurture are both important contributors to variation in human personality. As a result, the field of personality behavior genetics is moving beyond simply estimating the magnitude of genetic and environmental influences on various personality constructs. Recent methodological advances provide for the study of how these different sources of influence interact in the development of personality. Specifically, newer *biometrical moderation* models allow for group-specific estimates of heritability and environmental influences on personality (a form of gene–environment interaction). In the current paper, we review selected recent research using these models. Furthermore, we explore how moderation might also be important in understanding links between specific genes and personality. Accounting for the contingencies between genes and environment will be an important catalyst for the molecular genetic study of personality, as unmoderated ‘main effect’ types of gene → personality associations have been elusive.

Is the etiology of personality genetic or environmental? The answer, to as great a certainty as scientifically possible, is a resounding ‘both’. It is clear that genes *and* environment shape personality, giving rise to the individual differences in how people think, feel, and behave. At this point, it is time to move beyond broad estimates of the relative influences of genes vs. environment and instead focus on the transaction between these sources of influence. The field of behavior genetics is reinventing itself through methodological advances that capture the contingencies inherent in the interplay between genes and environment. A better understanding of this interplay may be the best hope for the future of molecular genetic studies of personality, where finding the genes for personality may hinge on incorporating interactions between genotype and environmental events. In this paper, our goal is to review some of these recent advances for a broader audience of personality and social psychology researchers.

The variance in almost any psychological individual difference is at least partly attributable to genetic influences. The well-known heritability statistic, which represents the proportion of total variation in an observed

trait (or phenotype) attributable to genes, is around 50% across numerous measures of normal personality (Krueger & Johnson, forthcoming). The rest of the variance in personality is accounted for by unique environmental influences, those experiences that we do not share with, and thus make us different from, family members. The shared family environment – those environments that make us similar to other family members – seems to have little significant influence on the variation in personality. The finding of 50% heritability of personality is robust, and holds across diverse assessments, including (i) self-reported broad superfactors (e.g., the ‘Big 5’; Bouchard & Loehlin, 2001); (ii) self- and peer-ratings of personality (Riemann, Angleitner, & Strelau, 1997); and (iii) observational measures of personality (Borkenau, Riemann, Angleitner, & Spinath, 2001).

Given the evidence of substantial genetic influences on personality, there was much enthusiasm over the possibility of finding the ‘genes for personality’. The first molecular genetic studies of personality arrived in 1996 with much fanfare (Ebstein, 2006). It was hoped that by finding specific genotypes, it would be possible to elucidate how genes influence the development of personality, from cells to temperament to social behavior. Nevertheless, more than a decade later, despite many concerted gene searches, improvements in the techniques used, more power to detect specific genetic effects, and significant reductions in the costs of implementing these techniques, the field is plagued by an inability to replicate gene–personality associations across different studies. Somewhat comforting to molecular genetic personality researchers, the situation is not unique to research on personality. Researchers studying chronic and common disorders, including both behavioral and medical disorders, face similar difficulties (Buchanan, Weiss, & Fullerton, 2006; Davey Smith et al., 2005; Mayeux, 2005).

The inability to find the genes that code for personality with any certainty, when we know that genes are responsible for roughly 50% of the variation in personality, is frustrating, to say the least. How do we reconcile the robust genetic effects on personality as revealed by twin research with the difficulty linking specific measured genes with personality? A potential resolution might involve research into the genetics of personality acknowledging the importance of contextual variation – that is, contingencies between the person and his or her environment. We approach this argument from two angles. First, we review new research that challenges the notion of a single heritability value for the entire population of interest. The heritability of personality is not fixed across the population, but rather is dependent on other circumstances. Second, we highlight new work from the field of molecular genetics that has examined how the links between measured genes and psychopathology can vary as a function of the environment. This type of methodology, already well espoused in the fields of medicine and psychiatric genetics, has great potential for application to the study of personality genetics. In particular, this research

may elucidate how nature and nurture transact in the development of personality, and ultimately, it is better understanding of this transaction that will lead to identifying the specific DNA sequences involved in personality. We see great potential for personality and social psychologists, who already have a long tradition of appreciating situational variability in the understanding of personality, to adapt these methodologies and thereby bring an individual, interactionist perspective to the study of personality genetics (Mischel, 2004).

Biometrical Moderation Models: When the Heritability of Personality Is Not 50%

In biometrical modeling, researchers use data from genetically informative samples (e.g., twin and adoption studies) to decompose the total variation in a psychological characteristic into those effects due to (i) genes, (ii) shared environment, and (iii) nonshared environment. Genetic effects index the extent to which observed or 'phenotypic' variation in a trait arises from genetic differences among people. Shared environmental effects make people similar because they grew up in the same household, independent of genetic effects and nonshared environmental effects (e.g., sharing a neighborhood, socioeconomic status, or religious traditions with other family members might make people in the same family similar, beyond the similarity predicted by their shared genes). Nonshared environmental effects indicate the extent to which family members are different, despite sharing genetic material and growing up together, and might include traumatic events, different peer groups, or even being treated differently by one's parents, compared with siblings.

Classically, behavior genetic studies of personality have focused on the magnitude of these genetic and environmental influences on personality. Twin studies, which compare correlations between monozygotic twins, who share 100% of their genes, and dizygotic twins, who share, on average, 50% of their genes, are consistent in demonstrating that 50% of the variation in most major 'normal' personality traits is due to genes (Bouchard & Loehlin, 2001). Adoption studies, which take advantage of the differences between biological and adopted family members, are rarer than twin studies. Like twin studies, adoption studies show little influence of the shared environment, but they also yield smaller estimates for genetic influence on personality and temperament when compared with twin studies, probably because twin studies can pick up non-additive genetic influences, or the ways in which specific combinations of multiple genes might be relevant to personality (for a more complete explanation of this phenomenon, see Krueger & Johnson, forthcoming).

Estimates of genetic and environmental influences on a trait or disorder have always been population estimates. Heritability (or the equivalent proportions for shared and unique environmental effects) is a concept that

applies to the entire population from which the sample is drawn. That is, when the heritability of extraversion is reported as 50%, we interpret this as meaning that 50% of the total variance in extraversion *in that sample of a specific population* is associated with genetic influences. It does not mean that a specific person's extraversion level is '50% genetic'; heritability cannot be applied to a single individual but instead refers to the differences among many individuals, specifically those from whom the data are collected. In other words, heritability is a statistic that applies to the variance of a set of observations, rather than to a single specific observation. Essentially, traditional approaches to modeling the genetic and environmental influences on personality average over any differences within the population being studied, thus resulting in an overall account of genetic and environmental influences on a personality construct.

Of course, the heritability of a phenotype is not set in stone. Estimates of heritability can change from one sample to another, although most heritability values for major personality traits are fairly consistent across different populations. Even within a sample, it is possible to estimate different heritability values for certain segments of the population – most commonly, this is done across gender and age groups. Finding that heritability is higher in men than women for a phenotype would tell us that, for men, genetic contributions are more important contributors to variation in the phenotype.

We can extend this basic premise and split a sample based on the presence or absence of an environmental variable. For instance, Heath, Eaves, and Martin (1998) divided a sample of female Australian twins into pairs concordant for a marriage-like partnership, concordant for no relationship, and discordant. The heritability of depression increased from 29% in married twins to 51% in unmarried twins over 31 years of age. Marriage, therefore, acted as a protective factor by reducing the genetic liability to depressive symptoms.

This idea, that a specific genotype will only lead to a certain phenotype under the right environmental circumstances (or that a genotype can be moderated by the environment), is an example of 'gene–environment interaction', one of several types of interplay between genes and environments. The notion of gene–environment interaction has long been inherent in the diathesis–stress model of psychopathology, in which a stressor is necessary for the expression of a genetic predisposition to mental illness. Indeed, many studies have emerged from the fields of psychopathology, psychiatric genetics, and medicine that endorse and empirically test for gene–environment interactions (see Rutter, Moffitt, & Caspi, 2006, for a review). One of the reasons for the growth of this research is the recent development of new quantitative models for gene–environment interactions (Purcell, 2002), also referred to as 'heritability–environment' interactions to distinguish them from interactions between measured genes and measured environments (Moffitt, Caspi, & Rutter, 2006). These biometric moderation

models, which can be used to model continuous variation in environmental variables, have the potential to critically alter how we think about the transactions between individuals and their environments in the development of personality. To date, this approach has been somewhat underutilized in the study of personality, an area where it offers many potential advantages.

Biometrical moderation models data obtained from specific individuals directly, instead of using sample-level summary statistics (e.g., variances and covariances). As a result, instead of averaging over the sample from which the data are drawn, estimates of genetic and environmental influences on personality can be estimated as functions of, or contingent on, other characteristics of the individual and his or her environment. Consider, as an example, the almost universal experience of the commute to and from work. As an indicator of countrywide commuting time, you could calculate an average rush-hour commute across every city in the USA. But this would gloss over important differences due to both regional variation (e.g., small cities vs. large cities) and individual variation (e.g., living close or far to work). This is less helpful than knowing the average rush hour commute in your own city, or, even better, knowing the average commute from your neighborhood to the location of your workplace. Similarly, these new behavior genetic models are able to bring heritability to a more specific level and estimate genetic and environmental influences on personality as a function of variations that can be measured for each specific individual.

A further advantage of biometrical moderation modeling is the ability to decompose the moderator variable into its genetic and environmental variance components and test for gene–environment interaction in the presence of gene–environment correlation (Purcell, 2002). A different type of gene–environment interplay (see Rutter et al., 2006), gene–environment correlation is the degree to which a genotype influences the likelihood of exposure to an environmental variable (Plomin, DeFries, & Loehlin, 1977).

It can be difficult to detect gene–environment interaction in the presence of gene–environment correlation. For example, a child who displays high levels of disruptive behavior may evoke unpleasant reactions from his or her parents, thus resulting in the development of a personality prone to mental disorder (i.e., high in negative affectivity and/or low in constraint; Krueger, 1999). In this circumstance, both gene–environment interaction and correlation concepts are relevant to understanding development. The child evoked unpleasant reactions (a correlation between the child and his environment), but then those reactions may also serve as an environment that moderates genetic effects (an interaction between the child and his environment).

Biometrical moderation models are able to directly estimate the genetic overlap between a phenotype and an environmental moderator variable (a gene–environment correlation) by calculating a genetic correlation, which ranges from -1 to $+1$ (similar types of correlations can be computed for shared and nonshared environmental influences). It is important to

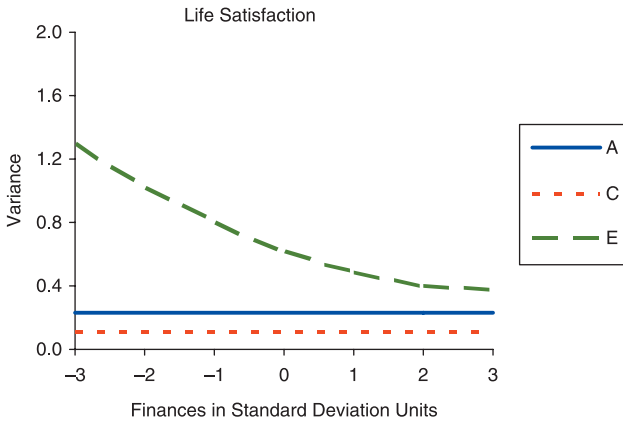


Figure 1 Genetic and environmental variance in life satisfaction as a function of finances. Reprinted from Johnson and Krueger (2006). Copyright 2006 by the American Psychological Association. Reprinted by permission.

note that this model can only be used when the environmental variable differs between twins (or the perception of the environmental stressor differs). If the environmental risk is obligatorily shared between twins (i.e., socioeconomic status or parents' marital status), it is necessary to use a moderation model in which the gene–environment correlation cannot be separated from the gene–environment interaction (Purcell, 2002). However, when each twin's value on the environmental variable differs, biometrical moderation can be used to determine whether the magnitude of genetic and environmental influences on a personality trait depends on an environmental moderator variable (gene–environment interaction), and the extent to which etiologic influences acting on the personality trait also exert influences on the environmental variable (gene–environment correlation).

We present an example of a biometrical moderation model in Figure 1, reprinted from Johnson and Krueger (2006). In this study, the authors were interested in how the proportion of variance in life satisfaction due to genetic (A), shared environmental (C), and nonshared environmental (E) effects varied as a function of income. The graph presents the unstandardized ACE components of variance in life satisfaction across the different levels of income. The moderation model shows that the influence of genes and shared environment on life satisfaction was constant across financial status, but the influence of unique environment decreased from low to high levels of income. Thus, at low levels of financial status, the variation in life satisfaction due to E was much higher. This suggests that greater financial resources may act as a protective factor against the shock of random events (which would be represented as a source of E variance).

Most of the research on moderation of genetic and environmental influences has utilized twin data. Adoption studies of biometrical moderation of personality have yet to appear, although interestingly, adoption studies of conduct disorder and aggressive behavior were the first to suggest that those with greater genetic predisposition are more vulnerable to pathogenic rearing environments (e.g., Cadoret, Yates, Troughton, Woodworth, & Stewart, 1995; Riggins-Caspers, Cadoret, Knutson, & Langbehn, 2003). In fact, the majority of recent work on biometrical moderation has focused on how aspects of the family environment may moderate genetic and environmental influences on personality. The family environment was long thought to be a key source of socialization and developmental influence (Bell, 1968). Although some have suggested that parents have little influence on their children's development (Harris, 1995, 1998), a reasonable conclusion based on all available evidence is that child personality and parental influence are related through 'bidirectional interactive processes' (Collins, Maccoby, Steinberg, Heatherington, & Bornstein, 2000; p. 222). Thus, when searching for an environmental variable that might allow for the expression of a genetic diathesis, many researchers have naturally turned to measures of the family environment. Instead of estimating genetic contributions to personality in terms of an overall heritability statistic that averages across diverse family circumstances, biometrical moderation models estimate the effect of genetic and environmental factors on individual differences in the presence of gene-environment interaction and correlation (see, e.g., Eaves & Erkanli, 2003; Johnson, forthcoming; Purcell, 2002).

Several instances of this new methodological approach to behavior genetic modeling of personality have now appeared in the literature. As noted, family environment has been a popular choice of moderator. In one study, parental bonding, family functioning, and non-assaultive traumatic events affected genetic and environmental influences on emotional instability (similar to neuroticism), often by enhancing the impact of non-shared environmental factors (Jang, Dick, Wolf, Livesley, & Paris, 2005), whereas another study found that religious upbringing reduced the impact of genetic factors on disinhibitory personality characteristics (Boomsma, de Geus, van Baal, & Koopmans, 1999). Despite this growing evidence of the importance of biometrical moderation, there may also be instances when influences on a personality construct are *not* moderated by an environmental variable. For instance, Kendler, Aggen, Jacobson, and Neale (2003) reported that family dysfunction did not significantly moderate genetic and environmental effects on neuroticism.¹

We illustrate one application of this model using data from the Minnesota Twin Family Study. Our goal for this study was to show how adolescents' perceptions of their relationships with their parents affected the relative importance of genetic and environmental effects on positive and negative emotionality (Krueger, South, Johnson, & Iacono, forthcoming). Using

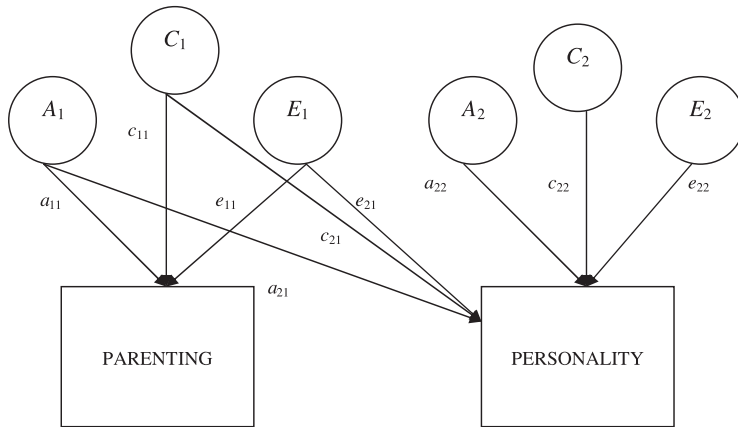


Figure 2 Path diagram of a standard bivariate decomposition model for parent–adolescent relationship (PARENTING) and adolescent personality (PERSONALITY). For simplicity, only one half of the twin pair is shown. The variance in PARENTING and PERSONALITY is parsed into that which is due to additive genetic effects (A_1 , A_2), shared environmental effects (C_1 , C_2), and nonshared environmental effects (E_1 , E_2). Paths, which are squared to estimate the proportion of variance accounted for, are represented by lowercase letters followed by two numerals (e.g., a_{11}).

measures of perceived relationship with parents (regard and conflict) and Multidimensional Personality Questionnaire (Tellegen & Waller, forthcoming) data collected from more than 2000 17-year-old twins, we compared two models: (i) An unmoderated model, in which the genetic and environmental influences on personality were estimated as constants, without regard to the level of conflict or regard in the parent–adolescent relationship; and (ii) A moderation model, which tested for gene–environment interaction in the presence of gene–environment correlation. The models were fit to raw data using the Mx (Neale, Boker, Xie, & Maes, 2003) statistical program. If the moderation model provided a better fit to the data, it would suggest that aspects of the parent–adolescent relationship contribute to the expression of genetic and environmental aspects of personality traits.

Figure 2 presents the path diagram for the unmoderated biometric model. This model is equivalent to a standard bivariate (Cholesky) decomposition model, in which the variances and covariances of the observed variables are decomposed into the proportion of variance associated with genetic (a^2), shared environmental (c^2) and nonshared environmental (e^2) components that are shared between the phenotypes and unique to one of them. The bivariate decomposition model estimates a total of 11 parameters: three a parameters, three c parameters, three e parameters, and two means. The total phenotypic variance in the downstream variable, Personality in Figure 1, is computed by square and adding all paths leading to it ($a_{21}^2 + a_{22}^2 + c_{21}^2 + c_{22}^2 + e_{21}^2 + e_{22}^2$).

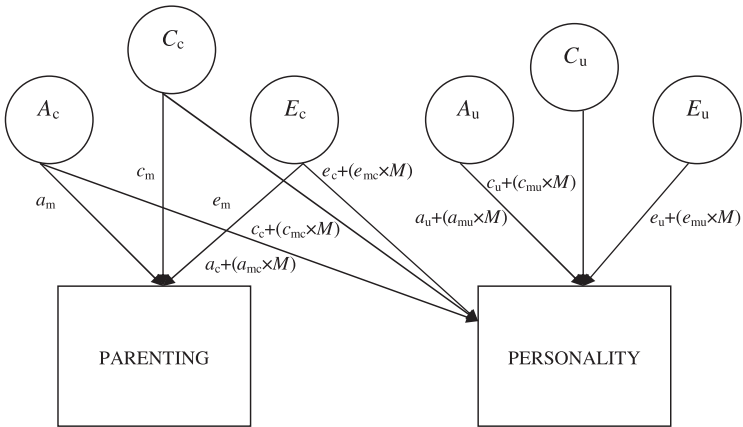


Figure 3 Path diagram of a biometrical moderation model with parent–adolescent relationship (PARENTING) moderating the genetic and environmental influences on adolescent personality (PERSONALITY). Each of the paths impacting PERSONALITY is now a linear function that combines an overall coefficient separate from the moderator variable (e.g., a_c) with the product of a coefficient that indexes the moderation of PERSONALITY by PARENTING (a_{mc}) multiplied by the level of the moderator (M).

The moderation model is presented as a path diagram in Figure 3. Again, similar to the standard bivariate model, there are two sets of paths contributing genetic and environmental influences: those common to personality and the moderator ('parenting' on the figure) and those unique to personality. The paths from the moderator (M) variable to the dependent variable are now linear functions of the form [e.g., $a_c + (a_{mc} \times M)$], where a_c is the parameter for genetic influence on the variable, a_{mc} is a regression coefficient, and M is the level of the moderator variable. This results in a total of 17 estimated parameters: the three a parameters plus two M regression weights for the shared and unique a parameters (a_m , a_c , a_u , and a_{mc} , a_{mu}), three c parameters plus two M regression weights for the shared and unique c parameters, three e parameters and two M regression weights for the shared and unique e parameters, and two means. The type of moderator model used for the current analyses is notable for its ability to decompose the covariance between the moderator (parenting) and the downstream phenotype (personality) into its a , c , and e components, making it possible to examine whether the genetic and environmental correlations between parenting and personality also vary as functions of parenting.

Using biometrical moderation models, we found significant moderation for Positive and Negative Emotionality, such that adolescent's perceived relationships with their parents acted to both enhance and diminish genetic and environmental effects (Krueger et al., forthcoming). These findings have important implications for the heritability of personality and

for the interplay between genes and environment in personality development. Notably, the heritability of personality differs as a function of the adolescent's relationship with their parents, which challenges the notion that parents do not have much impact on offspring personality characteristics (Harris, 1998). Parents do not typically have a direct impact via the shared environment, but this is just one way in which parents might have an impact on offspring, beyond their provision of genetic endowments. Our findings point to another way in which parents matter, specifically, in the way genetic effects are enhanced or dampened depending on contextual factors in the family.

Of course, it is possible that these types of moderating effects might also work in the opposite direction, with personality moderating the etiology of various outcomes. Returning to the example from our recent work, we reversed the direction of the effect to look at the moderating effects of adolescent personality on parent–adolescent relationship (South, Krueger, Johnson, & Iacono, forthcoming). We found significant moderation of both positive and negative qualities of the parent–adolescent relationship, such that the etiology of relationship quality varied as functions of the adolescent's levels of personality. In particular, high levels of positive emotionality enhanced the genetic effects on parental regard; when combined with results of Krueger et al. (forthcoming), in which high levels of parental regard also enhanced the genetic effects on positive emotionality, we start to see a bidirectional feedback loop whereby adolescents with positive emotional dispositions elicit parental regard, a situation that allows for the enhanced expression of genetic effects on positive emotionality.

In summary, there is now growing evidence that genetic and environmental influences on personality will differ depending on other circumstances in the person's life. This type of moderation modeling is still in its infancy, but offers the potential for important advances in our understanding of the etiology and development of personality. Most of this work has focused on aspects of the family environment, suggesting that family influences are more important in understanding personality development than some have argued (Harris, 1995, 1998). Our research did confirm one aspect of Harris's argument – at the average population level, the shared environment has little effect on making children in the same family more similar than they would be based on their shared genetic endowments. However, in families with extreme levels of conflict in the parent–adolescent relationship, there is a moderate effect of the shared environment. A reasonable interpretation of this finding is that the shared environment does act to make children in the same family more similar on levels of negative emotionality, but only when parent relationship is notable for high levels of conflict. In general, families seem to influence how and when genetic influences on personality are expressed. There is no reason to suspect that other 'environmental' measures would not also moderate genetic influences on personality. For instance, we recently found that marital relationship

quality moderated the genetic and environmental influences on the internalizing spectrum of personality and psychopathology (i.e., depression, anxiety, panic, and the personality trait of neuroticism; South & Krueger, forthcoming). As experience with this type of modeling grows, there is the potential to more richly contextualize what we know about the heritability of personality, as the well-known 50% is qualified according to individual-specific demographic, family, and relationship characteristics.

Molecular Genetics: Measured Gene × Measured Environment Interactions

By this point, it is well acknowledged that personality is a complex phenotype multiply determined by environmental and genetic influences. The field of molecular personality genetics, like other fields of genetic inquiry (e.g., psychopathology), has moved away from a Mendelian, one-gene/one-trait model of causation to a polygenic model that better captures the complexity of the phenotype. Yet, even with the acceptance that each personality construct is most likely attributable to multiple genes, each accounting for a relatively small portion of the variance, researchers have still been unable to produce consistently reliable links between specific genes and specific personality traits. We argue that, just as twin, family, and adoption studies have progressed via new methodologies, the field of molecular genetics will move forward by accounting for the complex contingencies between genes and environment.

Human genetic information resides on strands of DNA present on the 23 pairs of chromosomes (one set of chromosomes inherited from the mother, one set from the father). Genes are specific sequences of DNA that encode for products (proteins and RNA), and different variants of a gene are called alleles. People carry two copies of each gene (one from each parent); thus, they can be categorized as homozygous (identical alleles) or heterozygous (different alleles). Researchers have now generally accepted a polygenic conceptualization of personality, such that many genes, each having a small effect, contribute to personality, a quantitative trait that has a continuous range and is more or less normally distributed throughout the population (cf., McCrae & Costa, 2003). The location of a gene on a chromosome is called a locus, thus the search for genes influencing a continuously distributed trait is called quantitative trait loci (QTL) analysis. In QTL analysis, researchers determine how much of the variance in a given personality trait is accounted for by the genetic markers. Most molecular genetic studies of personality have used association analyses, in which the association between a polymorphism or variant of the allele and the personality trait is measured.

Following the sequencing of the human genome, there was great excitement at the prospect of the imminent discovery of the specific genes that contribute to population variation in individual differences (Plomin

& Crabbe, 2000). It was believed that we were only years away from the identification of specific genes for personality that would help to elucidate personality development from genome through adulthood. Despite advances in molecular genetics, including improvements in techniques to detect genetic variation and mutation, the initial optimism for discovery has been replaced by a guarded realism that the process will be a marathon, not a sprint. Researchers have certainly been industrious in the sheer number of different genes and personality traits that have been investigated, particularly in the dopaminergic and serotonergic systems, and several excellent reviews have appeared in the last few years (Ebstein et al., 2002; Ebstein, 2006; Noblett & Coccaro, 2005; Reif & Lesch, 2003; Savitz & Ramesar, 2004; Van Gestel & Van Broeckhoven, 2003). Unfortunately, these association studies have not been consistently replicated (Munafò et al., 2003). For instance, recent meta-analyses have failed to confirm two of the earliest, and, it was thought, strongest personality–gene associations: DRD4-7R (a base pair repeat coding for the dopamine neurotransmitter) and self-reported Novelty Seeking (Kluger, Siegfried, & Ebstein, 2002; Schinka, Busch, & Robichaux-Keene, 2004), and the 5-HTTLPR (serotonin transporter) short allele and Neuroticism/Harm Avoidance (Schinka, Letsch, & Crawford, 2002; Sen, Burmeister, & Ghosh, 2004).

There are many reasons for the failure to replicate molecular genetic association studies of personality, and most can be traced back to the difficulty with studying a polygenetic phenotype. Savitz and Ramesar (2004) provide an illustrative review of the many inherent difficulties in genetic association studies. A major obstacle in QTL analysis often is small sample size, which limits the ability to detect significant QTL gene effects. Adding more complexity to the picture is the heterogeneity among outcome measures. Researchers have used different inventories of the same putative personality construct, but research clearly shows that these measures cannot easily be substituted for each other. For instance, neuroticism, a trait-like tendency toward negative affectivity, and Harm Avoidance, a dimension of behavioral inhibition, worry and pessimism as defined by the Temperament and Character Inventory (Cloninger, Svrakic, & Przybeck, 1993), are significantly positively correlated (De Fruyt, Van De Wiele, & Van Heeringen, 2000). However, neuroticism (as measured by the NEO-PI-R; Costa & McCrae, 1992) but not Harm Avoidance has been linked to the serotonin transporter polymorphism (Schinka et al., 2002; Sen et al., 2004). Other difficulties with QTL analysis include small effect sizes, different sex ratios across studies, and publication bias in favor of studies that report a gene–personality link. Finally, there are ethnic differences in allele frequency, which can result in nonsignificant associations. For instance, one replication study using a Japanese sample found a low prevalence (6%) of individuals homozygous for the long variant of the serotonin transporter gene, thus reducing the power to detect statistically significant differences (Kumakiri et al., 1999).

Several of these methodological limitations will most likely be dealt with through technological advances and a reduction in cost of molecular genetic research, which will allow, in particular, for greater sample size. However, we suggest an additional methodological feature that may be particularly fruitful in the search for personality genes – using measured genes *and* measured environments jointly. As noted before, gene–environment interaction is a term for the fact that people with different genotypes will respond differently to the same environment. This type of research has been used by Caspi et al. in a series of studies examining developmental psychopathology. In a birth cohort of men from New Zealand, Caspi et al. (2002) found a genotype by environment interaction between variations in the *monamine oxidase A (MAOA)* gene (a gene coding for MAOA, a substance that metabolizes major neurotransmitters) and childhood maltreatment on antisocial behavior in adulthood. Childhood maltreatment was a risk factor for antisocial behavior but only for men with the genetic polymorphism coding for low MAOA activity. Several studies have now attempted to replicate this finding, and a recent meta-analysis confirmed a stronger relationship between maltreatment and mental health problems in boys who have the genotype conferring low MAOA activity (Kim-Cohen et al., 2006). Similarly, Caspi et al. (2003) showed that variation in the serotonin transporter (*5-HTT*) gene predicted whether or not people developed depression and suicidality in response to stressful life events. Finally, Caspi et al. (2005) found that adolescent cannabis use was a significant risk factor for psychotic symptoms and schizophreniform disorder in adulthood, but only for those carrying the valine allele of the *COMT* gene. In every one of these examples, the presence of the underlying diathesis (allele at the QTL) led to the expression of pathology only in the presence of a specific stressor.

Thus far, this technique has not been widely used in the study of personality. However, two intriguing studies from Finland provide evidence for the potential of this methodology. In the first study, Keltikangas-Jarvinen, Raikkonen, Ekelund, and Peltonen (2004) found an interaction between the *DRD4* polymorphism and early childhood rearing environment in the prediction of the personality trait of novelty seeking (as assessed by the Temperament and Character Inventory; Cloninger et al., 1993). There was an association between high scores on novelty seeking and the 2- or 5-repeat *DRD4* alleles but only in the presence of a negative childhood family environment. In a second study from the same research group, Lahti et al. (2005) examined whether exposure to parental alcohol use during childhood moderated the relationship between the dopamine *DRD4* receptor gene polymorphism and novelty seeking in adulthood. They found a strong association between the 2- or 5-repeat alleles of the *DRD4* gene and high novelty-seeking scores, but only for those participants whose father reported more frequency alcohol consumption or drunkenness.

These two studies illustrate perhaps the most important reason for conducting this type of moderation study. Finding that certain environmental variables, like parental alcoholism, moderate a gene–personality trait association offers a potential explanation for the decidedly mixed results in the molecular genetic literature. In particular, the seminal association between DRD4 polymorphisms and novelty seeking is not consistently replicable (Kluger et al., 2002; Schinka et al., 2004). As we noted above, the traditional heritability statistic of personality glosses over any potential differences in aspects of the individual's environment that do not exert a direct main effect on personality (e.g., family, peer, or marital relationships). Similarly, until the recent work noted above (Keltikangas-Jarvinen et al., 2004; Lahti et al., 2005), the numerous studies of DRD4 and novelty seeking have heretofore summed across any potential differences between subjects in relationship to environmental measures. It is reasonable to assume that, just as the magnitude of genetic influences on personality vary as a function of environment, the manifestation of a specific DNA sequence as a specific phenotype may also depend on the presence of a specific environment. Thus, providing for contingencies between measured genes and measured environments in the association with personality may result in more reliable and consistent linkages between genes and personality traits.

Certainly, gene–environment interaction is not a panacea that will solve all of the problems that have faced molecular geneticists. As outlined by Rutter et al. (2006), the pitfalls that have plagued the search for 'genes for' personality and psychiatric disorders may also hamper gene–environment interaction, including small sample sizes, inconsistent assessment and heterogeneity of the phenotype, environmental stressor, and gene, publication bias, ethnic variations in alleles, and issues of multiple significance testing. However, incorporating the interaction between measured genes and measured environments into the study of personality acknowledges the importance of this type of gene–environment interplay (for other types, see Rutter et al., 2006).

Moffitt, Caspi, and Rutter (2005, 2006) outline a series of steps for investigating measured gene–environment interaction for psychopathology, which can be widely adapted for the study of personality. First, they recommend looking to heritability–environment interaction models (i.e., biometric moderation models) for sources of potential measured gene–measured environment interactions. Given that these types of models have only recently been applied to personality traits, there is still much work to be done here. They also recommend that researchers start by identifying possible environmental pathogens largely because 'the heterogeneity in response to environmental hazards constitutes the key background evidence base' (Rutter et al., 2006, 251). An environmental risk factor should predict the disorder, but not for everyone in the population (or else it would be a main effect, not an interaction). The

environmental variable and the phenotype of interest should also show evidence of environmental mediation, such that the overlap between the two is due to similar environmental influences, not genetic overlap. If the overlap between the phenotype and the environmental moderator was genetic, this would be evidence of gene–environment correlation, which, so far, has not affected any measured gene–measured environment interactions. The need for a sample with wide-ranging variation in the environmental stressor of interest necessarily means gene–environment interaction should be studied in large, population-based epidemiological cohorts. Another possibility is to work with populations known to have been exposed to the environmental stressor of interest (Moffitt et al., 2005).

Another important methodological concern is the need to proceed with a hypothesis regarding the biological pathways that operate in the interplay between genotype and environment. It must be accepted that an environmental pathogen interacts with genes to produce the behavioral phenotype through the action of neurobehavioral pathways (Moffitt et al., 2005; Rutter et al., 2006). One of the ultimate promises of gene–environment interaction is the potential to explicate causal mechanisms in the development of personality and psychopathology. Thus, having a hypothesis about these developmental pathways is an essential rebuttal to those who would argue that gene–environment interaction is simply one way of ‘data mining’ for significant results. In one of the few direct examples of this work with personality, Meyer-Lindenberg et al. (2006) examined the link between a common variable number tandem repeat polymorphism of the *MAOA* gene (associated with antisocial behavior among men who experienced childhood maltreatment in a measured gene–measured environment interaction described above; Caspi et al., 2002) and brain structures involved in emotional control using a multimodal imaging approach. When affectively salient social stimuli (angry and fearful faces) were presented to carriers of the *MAOA-L* polymorphism (3 or 5 repeats), participants exhibited significant structural and functional changes in brain circuitry related to affect regulation, emotional memory, and impulsivity. The authors argue that the risk imparted by the *MAOA-L* allele contributes to the impulsive-aggression dimension of the larger construct of antisocial and violent behavior. Ultimately, of course, as with any study that demonstrates evidence of a gene–environment interaction, the results must be replicated in other samples; in particular, meta-analyses have been particularly useful with studies of the main effects of genes, and will likely prove advantageous with regard to gene–environment interaction.

Summary

Recent methodological developments in the field of behavior genetics have the potential to significantly alter how we conceptualize the heritability of personality. Instead of estimating genetic and environmental influences

that average across important contextual differences among the members of the population being studied, new biometrical moderation models provide a way of determining individual-specific estimates that incorporate specific measures of the person's world. In this way, these models offer the potential for better explicating the transaction between genes and environment. Moderation may also offer an important avenue of investigation for molecular genetic studies of personality, which have been plagued by replicability problems. By incorporating contingencies between genes and environment, both behavior genetics and molecular genetics will move forward to a better understanding of the effects of specific environments on the personality traits of individuals with varied genotypes.

A focus on person–environment interaction in the field of personality genetics has been noticeably lacking until now, a surprising gap considering that personality psychologists have long stressed the importance of the interplay between person and situation variables (Funder, forthcoming). It is easy to envision the addition of genotype collection to already existing personality research paradigms and pursuing work exposing individuals with different genotypes to various experimental situations. This type of methodology has the potential to elucidate the developmental context of personality. For instance, is the finding of peer socialization of aggressive behavior (cf., Cohen & Prinstein, 2006) contingent on the presence of a specific allele? Alternatively, this research could clarify the role of genotype in behavioral expression. Consider the substantial literature examining how people with high levels of narcissism react to failure by derogating others (Morf & Rhodewalt, 2001). A variation on this study design could examine whether this reaction depends on the presence of a certain gene polymorphism – for instance the *MAOA* gene, which has been linked to aggressive and violent behavior (Caspi et al., 2002). Given the rich history of personality and social psychology paradigms from which to draw, it is certain that there are many possible avenues to explore in the study of gene–environment interaction and personality.

Short Biographies

Susan C. South, PhD, is a Postdoctoral Fellow on a National Institute of Mental Health training grant in 'Neurobehavioral Aspects of Personality and Psychopathology' in the Department of Psychology at the University of Minnesota, Twin Cities. Dr. South obtained her PhD from the University of Virginia and completed her clinical internship at the Charleston Consortium/Medical University of South Carolina. Dr. South's research interests involve understanding the interplay between normal and maladaptive personality, psychopathology, and interpersonal relationships. She is the recipient of a National Research Service Award from the National Institute of Mental Health and a Dissertation Award from the Society for a Science of Clinical Psychology.

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Endnotes

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¹ Kendler et al. (2003) studied how genetic and environmental effects on neuroticism changed based on levels of family dysfunction, and although their results were in the direction of greater genetic effects on neuroticism at higher levels of family dysfunction, this effect was not statistically significant. However, their biometrical modeling did not directly model a possible correlation between neuroticism and family dysfunction. This may be a limitation of their study that might have impacted their ability to pick up significant moderating effects, given that their findings suggest such effects are present in their data, albeit at nonsignificant levels.

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