Running Head: TEMPORAL DYNAMICS OF GENE-ENVIRONMENT CORRELATION

How Nonshared Environmental Factors Come to Correlate with Heredity

Draft version 1, 01/01/2020 (not peer-reviewed). Please do not copy or cite without authors' permission.

Christopher R. Beam¹, Patrizia Pezzoli², Jane Mendle³, S. Alexandra Burt⁴, Michael Neale⁵, Steven Boker⁶, Pamela K. Keel⁷, & Kelly L. Klump⁴

¹University of Southern California

²Åbo Akademi University,

³Cornell University

⁴Michigan State University

⁵Virginia Commonwealth University

⁶University of Virginia

⁷Florida State University

Corresponding Author:

Christopher R. Beam

3620 McClintock Ave

Seeley G. Mudd, Room 501

Los Angeles, CA 90089

phone: +1 213-740-0726

email: beamc@usc.edu

How Nonshared Environmental Factors Come to Correlate with Heredity

Abstract

Conventional longitudinal behavioral genetic models estimate the relative contribution of genetic and environmental factors to stability and change of traits and behaviors. Longitudinal models rarely explain the processes that generate observed differences between genetically and socially related individuals. We propose that exchanges between people and their environments (i.e., phenotype-environment effects) can explain the emergence of observed differences over time. Such models, however, require violation of the independence assumption of standard behavioral genetic models, that is, uncorrelated genetic and environmental factors (Beam & Turkheimer, 2013; de Kort, Dolan, & Boomsma, 2012; Dolan, De Kort, Van Beijsterveldt, Bartels, & Boomsma, 2014). We review how specification of phenotype-environment effects contributes to understanding observed changes in genetic variability over time and longitudinal correlations among nonshared environmental factors. We then provide an example using 30 days of positive and negative affect scores from an all-female sample of twins. Results demonstrate that the phenotype-environment effects explain how heritability estimates fluctuate as well as how nonshared environmental factors persist over time. We discuss possible mechanisms underlying change in gene-environment correlation over time, the advantages and challenges of including gene-environment correlation in longitudinal twin models, and recommendations for future research.

Abstract words: 197

Keywords: developmental behavioral genetics; gene-environment interplay; affect; mood; longitudinal

How Nonshared Environmental Factors Come to Correlate with Heredity

In psychopathology research, developmental behavior genetic studies have the principal goal of specifying mechanisms through which some persons fare better in life than others. The great majority of longitudinal twin studies show that heritable factors account for stability of phenotypes, such as traits, behaviors, and emotions, whereas environmental factors account for change (Bartels et al., 2004; Bartels, Rietveld, Van Baal, & Boomsma, 2002; Briley et al., 2019; Bronfenbrenner & Ceci, 1994; Eaves, Long, & Heath, 1986). These studies are largely descriptive, as they often do not specify the processes that explain accrual of differences in phenotypic outcomes over time (for exceptions, see Dolan et al., 2014; Neale & McArdle, 2000; van den Berg & Boomsma, 2006). The limitation of these models are a consequence of the assumption that genetic and environmental factors are uncorrelated in the often-used additive model (Polderman et al., 2015). Since, in reality, genes and environments do correlate and interact with one another, developmental behavioral genetic models should incorporate this interdependence to better investigate the processes that contribute to variability in human complex traits.

This is not the first such call to address this limitation. In 1958, Anastasi commented, “as we proceed along the continuum of indirectness, the range of variation of possible outcomes of hereditary factors expands rapidly. At each step in the causal chain, there is fresh opportunity for interaction with other hereditary factors as well as with environmental factors” (Anastasi, 1958, p. 199). The conventional assumption that genetic and environmental factors are uncorrelated breaks an important link in the causal chain of Anastasi’s continuum of indirectness: how people interface with their environments. People receive, select, and evoke responses from their environments in systematic ways. Known as gene-environment correlation (r_{GE}), nonrandom exposure to environments based on

genetically influenced characteristics is part of what it means to be a person embedded within continuously changing social environments (Eaves, Krystyna, Martin, & Jinks, 1977; Plomin, DeFries, & Loehlin, 1977; Scarr & McCartney, 1983). This statistical phenomenon arises from various processes. Passive r_{GE} occurs when both genes and environments are provided to individuals (e.g., parents pass along genes for affective dysregulation and provide chaotic home environments). Active (or selective) r_{GE} occurs when individuals nonrandomly select environments syntonetic with their genetically influenced characteristics (e.g., persons with high risk of affective dysregulation select affectively dysregulated peers). Evocative r_{GE} occurs when environments nonrandomly reinforce genetically influenced characteristics (e.g., persons with high risk of affective dysregulation elicit greater interpersonal conflict from their environments) (Plomin et al., 1977). Gene-environment correlation, however, is conventionally not accounted for in developmental behavioral genetic (more generally, longitudinal twin) studies. A research priority, thus, is to modify longitudinal twin models to incorporate gene-environment correlative processes that represent real-time processes (Briley et al., 2019).

Available longitudinal twin models also miss an important feature of the causal chain between genes and environments: namely, persons. As argued by Scarr and McCartney, “some genotypes are more likely to receive and select certain environments than others” (1983, p. 426). Yet *genotypes* do not receive and select environments, people do (Turkheimer & Waldron, 2000). Numerous intermediate and bidirectional processes internal and external to people connect genetic and environmental predispositions with complex traits, including cognition, personality, and affect (Cole, 2009; Gottlieb, 2003). Intermediary pathways that connect genetic factors to environments could include but are not limited to people’s unique social environments, methylation activity affecting RNA transcription, and hormones. Genes contributing to people’s risk for affective dysregulation, in other

words, must be mediated by other processes, like changes in people's social environments, hormones, or other molecular processes. People, thus, are a critical node in the causal processes underlying gene-environment correlation.

Reciprocal Effects Models

Several efforts have been made to understand within-family diversification, or “sibling drift,” by incorporating gene-environment correlation in longitudinal twin models (e.g., Beam & Turkheimer, 2013; de Kort et al., 2012; Dolan et al., 2014; Neale & Cardon, 1992). Reciprocal effects models (REMs), in particular, have guided our thinking about change processes (Beam, Turkheimer, Dickens, & Davis, 2015; Beam & Turkheimer, 2013; Dickens, Turkheimer, & Beam, 2011). REMs are not novel (Bell, 1968; Scarr, 1992; Winship & Korenman, 1999) and summarize how small phenotypic advantages (e.g., calm demeanor) translate into superior abilities (e.g., affective stability). People initially are provided supportive environments (e.g., quiet versus chaotic household), which in turn predisposes them to seek out novel correlated environments (e.g., organized friends versus disorganized friends). Further reinforcement of a calm demeanor in these novel environments may then lead to the provision of additional support for affective stability (e.g., adults are more likely to mentor and model how to cope with added stress). Eventually, via iterative person-environment matching, phenotypes become increasingly correlated with environments over time. To the extent that phenotypes are genetically influenced, genetic influences will themselves become increasingly correlated with environments with time.

In previous work, we invoked Dickens and Flynn's (2001) version of the REM to explain how fleeting exogenous environmental experiences could explain time-limited rank order differences in cognitive ability between genetically-related individuals (Dickens et al., 2011). We subsequently

adapted REMs to explain how person-environment matching processes might cause genetically related individuals to drift apart over time (Beam & Turkheimer, 2013). Importantly, the degree of genetic relatedness between individuals influences the degree of similarity and differences of environments, which generates how different individuals become (i.e., less genetic relatedness between individuals engenders greater drifting apart over time). The general model is presented in Figure 1 as a multilevel model, in which total genetic effects are divided into genetic and environmental effects shared by twins in the same family (A^b and E^b , respectively) and genetic and environmental effects unshared by twins in the same family (A^w and E^w , respectively). At the within-level only, there is an autoregressive parameter (b_{PE}) projecting from persons' phenotypic scores at time t (P_t) to persons' unshared (unique) environment (E_{t+1}^w). Although similar to a modified genetic simplex model (Boomsma & Molenaar, 1987; Eaves et al., 1986) in which genetic and environmental factors unidirectionally influence phenotypes across repeated-measurements, autoregressive parameters projecting from phenotypes at time t to latent nonshared environmental factors at time $t+1$ (b_{PE}) model the influence people have on their future environments. The b_{PE} parameters necessarily generate within-family gene-environment correlation, that is, person-specific correlations between genotype and environments. Adding a single parameter generates different model expectations for monozygotic (MZ) twins and non-genetically identical siblings (e.g., dizygotic twins or siblings), and more accurately models how non-MZ siblings differentiate over time compared to MZ twins.

Figure 1. P → E Model. Biometric components of phenotypic scores for twin i at time t , P_{it} , are estimated between- and within-families; A_t^b = between-family genetic effect at time t ; E_t^b = between-family (common) environmental effect at time t ; A_t^w = within-family genetic effect at time t ; E_t^w = within-family (nonshared) environmental effect at time t ; uA_t^b = unique between-family genetic effect at time t ; uE_t^b = unique between-family environmental effect at time t ; uA_t^w = unique within-family genetic effect at time t ; uE_t^w = unique within-family environmental effect at time t ; a_{ar} , c_{ar} , and e_{ar} = auto-regression coefficient between adjacent components; the between-family and within-family genetic loadings for the MZ twins are 1 and 0, respectively, to meet the assumption that MZ twins share 100% of their genes; the between-family and within-family genetic loadings for the DZ twins are both $\sqrt{.5}$ to meet the assumption that DZ twins share 50%, on average, of their segregating genes. The red line represents that the $P \rightarrow E$ parameter, b_{PE} , which was only estimated at the within-family level in the DZ group.

According to path tracing rules (Boker & McArdle, 2014), the $P \rightarrow E$ parameter necessarily induces accumulation of gene-environment correlation across time as well as correlations among nonshared environmental components (de Kort et al., 2012; Eaves et al., 1977). As an example, affect is

genetically and environmentally influenced (Montag et al., 2016), which has implications for how persons engage with their social environments. Two siblings – one more affectively labile than the other – are likely to select and evoke different environmental milieus. Compared to the less affectively labile sibling, the more labile sibling may be drawn to people who are more emotionally expressive and engage in more aggressive, argumentative, and baiting behaviors with others. As a result, the more affectively labile sibling may contribute to a social environment characterized by more conflict, potentially leading to greater lability over time. Although $P \rightarrow E$ models have not yet been applied to affect, we have demonstrated that small within-family phenotypic differences put genetically related siblings onto different cognitive (Beam et al., 2015) and personality (Beam et al., submitted) trajectories.

Longitudinal twin models that adhere to the independence assumption risk generating upwardly biased genetic variance estimates. When data generated under the assumption of correlated genetic and environmental factors are fit with conventional twin models, genetic variance estimates are inflated (Beam & Turkheimer, 2013). Conventional longitudinal twin models might erroneously conclude that heritability increases when, in fact, it does not. In other words, unmodeled r_{GE} leads to the well-known conclusion that genetic variance components are larger than they should be under the independence assumption (Purcell, 2002). The accumulation of unmodeled r_{GE} in the genetic variance components also might lead to downwardly biased longitudinal correlations among nonshared environmental components.

Longitudinal twin studies consistently report uncorrelated structures of nonshared environmental factors across time. One explanation of this finding is that, within families, twins are re-sorted randomly as time passes, meaning that there is no rank-order stability between twins over time (i.e., twin 1 and twin 2 reverse position from time 1 to time 2). Given the expectation that people are

nonrandomly exposed to environments for genetic and environmental reasons (Plomin et al., 1977; Scarr & McCartney, 1983), the conclusion that twins randomly swap positions over time makes little sense. It is unlikely, for example, that the shorter of two siblings suddenly would become the superior basketball player without ongoing selection and reinforcement of environments that improve basketball skills. Indeed, as life plods along, environmental influences stabilize, suggesting that twins' environments become canalized (Dickens et al., 2011). The modified genetic simplex model (or $P \rightarrow E$ model) in Figure 1 accommodates violations of the independence assumption, thereby permitting gene-environment correlation to accumulate over time. We believe that $P \rightarrow E$ models provide a better representation of actual longitudinal processes, given that genes and environments, in fact, correlate. $P \rightarrow E$ models have statistical consequences for model-estimated heritability and nonshared environmental variance and covariance estimates. Accounting for gene-environment correlation in longitudinal twin models can explain how environmental processes lead to increases in heritability, as well as misspecification of the longitudinal stability of nonshared environmental components.

One consequence of model estimated gene-environment correlation, however, is that the interpretation of nonshared environmental components changes (Beam et al., 2015; de Kort et al., 2012). In $P \rightarrow E$ models, each nonshared environmental component in longitudinal twin models consists of two components: a part that correlates with genotype (i.e., it differs due to genotypic differences) and a part that is uncorrelated with genotype (i.e., occasion-specific residuals). In the former, genetic factors indirectly influence nonshared environmental factors, by definition, and are therefore inherently confounded with genotype. Comparisons of the longitudinal structure of nonshared environmental components between models that accommodate r_{GE} and models that assume GE independence provide a straightforward empirical approach to determining whether accommodating r_{GE} alters the meaning of the nonshared environment. In one previous report, we have shown that differences in nonshared

environmental structures between models that accommodate r_{GE} and models that do not are greater in DZ groups than MZ groups, suggesting that accommodation of r_{GE} helps to explain why environmental factors might be more correlated over time (Beam et al., 2015).

Quality of Environments and Measurement Density

Two conditions affect estimation of within-family r_{GE} but have not yet been considered: the assumption that persons have a wide range of environments available to them and the intervals of time between measurements (e.g., days versus weeks versus years). First, as posited by Fuller and Thompson (1960), enriched environments allow individuals to utilize environments freely, which support genetic expression of traits (Bronfenbrenner & Ceci, 1994; Fischbein, 1978) and allow individuals to adapt differently from one another. In contrast, restricted environments minimize behavioral options, leading individuals to behave more similarly, irrespective of genotypic differences. Therefore, siblings who are less genetically related (e.g., fraternal twins, full siblings, half-siblings, and so forth), and who have the resources to select from a range of environmental support factors, are expected to become less similar to each other over time. Instead, genetically identical individuals are more likely to select similar environments and, in turn, to become more similar over time. Statistically, this would imply that heritability increases for the reason that within-pair MZ correlations are predicted to remain stable over time while non-MZ correlations are expected to decline. One implication of these expectations is that within-family gene-environment correlation ought to increase over time, as genetically dissimilar sibling pairs develop. As within-family gene-environment correlation can be tested statistically, these competing hypotheses can be evaluated systematically.

Second, intervals of time between measurements can affect estimates of within-family gene-environment correlation. As intervals of time between measurements increase, estimated

autocorrelation between measurement occasions will decrease, as long as the process is stationary and noncyclic. Because longitudinal twin studies are laborious and expensive, dense measurement schedules of phenotypes are rare, and the temporal dynamics of r_{GE} remain poorly understood. Shorter intervals between measurements, such as diurnal measurement schedules, could lead to greater estimates of the magnitude of the within-family gene-environment correlation compared to longer intervals between measurements, such as annual measurement schedules. Developmentally, however, shorter divisions of time might not allow enough time for persons to receive, select, and evoke environments critical enough to make a difference for certain phenotypes, especially in view of evidence that effects of twins' unique measured environments on behavior are small (Turkheimer & Waldron, 2000). Thus, to best understand how environments guide change in genetically influenced characteristics, intervals of measurement should be suitably matched to expected change in phenotypes of interest.

The Current Study

In the present study, we explored the temporal dynamics of r_{GE} using daily measurements of affect in a young all-female sample of twin pairs aged 16-25. Specifically, we investigated how nonrandom matching between these women and their environments accounts for pair differences in their affect over 30 days. Using a $P \rightarrow E$ model, we tested two hypotheses: (1) Heritability tends to be over-estimated for daily affect when gene-environment correlation is unmodeled; *and* (2) within-family gene-environment correlation will generate greater correlations among nonshared environmental factors over time. With respect to the latter hypothesis, we expected environmental factors more proximally situated in time to be more correlated than environmental factors more distally situated in time. Both hypotheses suggest that the extent to which people engage with their environments on a

daily basis should affect their nonrandom selection of environments based on unique genotypically influenced characteristics and cause people to gravitate toward more like environments from day-to-day.

As the sample consists of only young women, hormonal changes across the menstrual cycle also may account for differences in daily affect. Although affect change across the menstrual cycle is not the focus of the current study, cyclic fluctuations in the levels of two ovarian steroid hormones in the female body, estrogen and progesterone, may correlate with affect. Whereas estrogen is the predominant hormone produced in the first, proliferative half of the cycle (follicular phase), progesterone predominates in the secretory half of the cycle (luteal phase) following ovulation, although estrogen also remains somewhat elevated (Poromaa & Gingnell, 2014). The cyclical fluctuation of neuroendocrine levels has psychological consequences (Farage, Osborn, & MacLean, 2008), including producing variation in affect (Romans, Clarkson, Einstein, Petrovic, & Stewart, 2012). The luteal phase, for example, may engender a high-risk phase for increased negative and depressed affect as a result of higher progesterone levels (Bäckström et al., 2011; Halbreich et al., 2012).

Data collected over the menstrual cycle raises two issues pertinent to the current study. First, the cyclic nature of estrogen and progesterone means that the correlation between persons and environments is non-stationary and varies in an oscillatory manner. Second, estrogen and progesterone direct genomic actions (e.g., gene transcription) and moderate genetic influences underlying behavioral phenotypes, like binge eating, independent of genetic influences underlying ovarian hormones (Klump et al., 2015). Estrogen and progesterone, in other words, may influence affect through changes in gene expression that could mimic (or be identical to) the expected pattern hypothesized via person-environment matching. To the extent that ovarian hormones act upon genetic components, they

constitute an additional “environmental” source of variance in the $P \rightarrow E$ system, as our model cannot distinguish between environmental factors that vary between or within twin pairs.

Method

Participants

Participants were 441 individual same-sex female twins (age range 16-25 years) who participated in the Twin Study of Hormones and Behavior across the Menstrual Cycle (HBMC) project (Klump et al., 2013; Klump et al., 2014) within the Michigan State University Twin Registry (MSUTR; Burt & Klump, 2013; Klump & Burt, 2006). There are 265 families in the current study, of which there were 176 (66.42%) complete pairs (MZ = 105, DZ = 71) and 89 (33.58%) incomplete pairs (MZ = 40, DZ = 49). Study inclusion/exclusion criteria were: 1) menarche before the age of 15; 2) regular menstrual cycles every 22-32 days for the past 6 months; 3) no hormonal contraceptive use within the past 3 months; 4) no psychotropic or steroid medications within the past 4 weeks; 5) no pregnancy or lactation within the past 6 months; and 6) no history of genetic or medical conditions known to influence hormone functioning or appetite/weight. Although twins could have provided up to 45 days of affect data, data coverage beyond 30 days was low. Only the first 30 days of affect data were used. The mean number of days of data contributed was 27.31 ($SD = 2.76$) with a minimum of 17 days and a maximum of 30 days (75.28% of the sample had one complete cycle within the 30 days). Monozygotic twins contributed 0.72 days greater than dizygotic twins ($t = 2.64$, $df = 439$, $p = .009$). Sample demographics are provided in Table S1. Twins, on average, were in late adolescence ($M = 17.62$, $SD = 1.75$) and born to college educated parents (modal category was bachelor’s degree for both twins’ mother and father) who combined make greater than \$60,000 per year (59.80%). The ethnic

composition of the sample was White (84.09%), African American (10.69%), Asian (0.24%), American Indian/Alaskan Native (0.48%), and mixed ethnicity (4.51%),

Procedures

All study measures and procedures were approved by the Michigan State University Institutional Review Board (IRB) and the University of Southern California IRB (UP-19-00623). Questionnaires were completed each evening (after 5:00 PM) using an online data system or pre-printed scantrons.

Measures

Negative and Positive Affect. The Positive and Negative Affect Schedule (PANAS; Watson, Clark, & Tellegen, 1988) was used to assess daily levels of positive and negative affect. The positive affect scale includes 10 items that assess a range of positive emotions (e.g., interested, excited, alert, inspired), while the negative affect scale consists of 10 items that assess a range of negative emotions (e.g., distress, nervousness, irritability, fear). The degree to which each emotion was experienced on each day of data collection was rated on a 5-point scale, ranging from 1 = *very slightly/not at all* to 5 = *extremely*. The positive and negative affect scales have exhibited excellent internal consistency. McDonald's omega ranged from .85-.90 for the 10 positive affect items over the 25 days ($M = .89$) and .80-.85 ($M = .83$) for the 10 negative affect items. Daily positive and negative items were summed and used in the current study.

Time Scale. Selecting a time metric common to all twins was restricted to aligning twins by a common day in the menstrual cycle. Twins PANAS scores were sorted so that all twins scores on Day 1 were the first day of the follicular phase (the day following the final day of bleeding in twins' previous menstrual cycle). Menstrual cycle phase was coded using daily reports and daily hormone values from

saliva samples. The first day of bleeding served as the graph anchor, and phase days were coded based on this anchor, hormone levels, and the overall length of each cycle (Klump et al., 2015).

Data Analysis

We first examined plots of the absolute pair mean differences of positive and negative affect in MZ, DZ, and unrelated pairs across the 30 days. Unrelated pairs were constructed as follows: each twin was assigned a random number generated from the normal distribution, then sorted from highest to lowest. New pair numbers then were assigned to twins. Mean positive and negative affect difference scores for MZ, DZ, and unrelated pair groups were constructed by calculating the mean of the absolute difference between twin pairs and randomly paired individuals.

Next, we estimated univariate MZ and DZ twin correlations of positive and negative affect and plotted heritability and environmental estimates based on these twin correlations across the 30 days. Traditional univariate twin modeling assumptions were made in estimating heritability and environmental estimates. Additive genetic (A) components are the cumulative effect of all shared genes between twins and estimated by virtue of the fact that monozygotic (MZ) twins share approximately 100% of their genes and dizygotic (DZ) twins share 50% of their genes, on average. Shared environmental (C) components are the cumulative effect of any environment that makes twins reared in the same family more similar to one another and estimated under the assumption that shared environmental influences affect twins similarly regardless of genetic relatedness. Nonshared environmental (E) components are any environmental factor that makes twins different from one another, including measurement error. Conventional twin models make further assumptions that A, C and E components are uncorrelated with one another, that they do not interact with one another, and that genetic relatedness is the product of parents' random mating strategies. To illustrate how the

heritability of positive and negative affect fluctuates across days, we estimated the proportion of variability in positive and negative affect attributable to heritability (h^2), shared environments (c^2), and nonshared environments (e^2).

Longitudinal structural models were then fit to the data using a multilevel structural equation modeling approach (ML-SEM; McArdle & Prescott, 2005). We structured the data so that days were wide-formatted, whereas the twin pairs remained in long format and nested within each family. We estimated a genetic simplex model (baseline model) and compared this model to a $P \rightarrow E$ model (research model). In the *genetic simplex model*, twins' affect scores on each day were decomposed into random variance components (subscript 1 for twin 1 and subscript 2 for twin 2):

$$P_{ft,1} = b_{0t} + w_{ab} A_{ft}^b + E_{ft}^b + w_{aw} A_{ft,1}^w + E_{ft,1}^w, \text{ and}$$

$$P_{ft,2} = b_{0t} + w_{ab} A_{ft}^b + E_{ft}^b + w_{aw} A_{ft,2}^w + E_{ft,2}^w.$$

The phenotypic scores, P , of twin 1 and twin 2 in family, f , at day, t , are decomposed into between-family and within-family genetic and environmental factors. All biometric variables (A and E), have a mean of zero so that the expectation of the phenotypic mean $E[P]_{ft,i}$ equals the intercept, b_{0t} . At the between-family level, phenotypic scores are decomposed into a genetic factor (A^b) and a common environmental factor (E^b) shared by both twins. At the within-family level, twins' scores are decomposed into a genetic factor unique to twins raised in the same family (A^w) and a nonshared environmental factor unique to twins raised in the same family (E^w). The total genetic effect, A , for each twin is equal to:

$$A_{ft,1} = w_{ab} A_{ft}^b + w_{aw} A_{ft,1}^w, \text{ and}$$

$$A_{ft,2} = w_{ab} A_{ft}^b + w_{aw} A_{ft,2}^w.$$

The variances of the A^b and A^w factors are constrained to be equal. The weights, w , are fixed values that indicate the proportion of genetic information shared by each twin pair. In MZ pairs, w_{ab} equals 1 and w_{aw} equals 0 to satisfy the assumption that identical twins share all of their genes. In DZ pairs, w_{ab} equals 0.5 and w_{aw} equals 0.5 to satisfy the assumption that fraternal pairs of twins share only half of their segregating genes, on average; the other half varies between them. The weights of the genetic factors between- and within-families were scaled so that $w_{ab}^2 + w_{aw}^2 = 1$, with the expectation that A^b and A^w are uncorrelated, $E[A_{ft}^b, A_{ft,i}^w] = 0$.

In order to present the $P \rightarrow E$ model, we begin by presenting the conventional genetic simplex model (Eaves et al., 1986). Between- and within-family genetic and environmental factors are correlated via first-order autoregressions ($t > 1$) as follows:

$$\begin{aligned} A_{ft}^b &= a_{ARt, t-1} A_{ft-1}^b + uA_{ft}^b, \text{ and} \\ E_{ft}^b &= c_{ARt, t-1} E_{ft-1}^b + uE_{ft}^b, \text{ and} \\ A_{ft,i}^w &= a_{ARt, t-1} A_{ft-1,i}^w + uA_{ft,i}^w, \text{ and} \\ E_{ft,i}^w &= e_{ARt, t-1} E_{ft-1,i}^w + uE_{ft,i}^w. \end{aligned}$$

The autoregressive coefficients ($a_{ARt, t-1}$, $c_{ARt, t-1}$, and $e_{ARt, t-1}$) of the genetic and environmental variables and their corresponding disturbances (uA_{ft}^b , uE_{ft}^b , $uA_{ft,i}^w$, and $uE_{ft,i}^w$) were freely estimated. The first-order autoregressive processes between the genetic and environmental factors meet the independence assumption in conventional twin modelings. Graphically, this model is identical to Figure 1 *without* the bold red pathways projecting from the phenotypic scores to the nonshared environmental variables. Pre-analysis demonstrated that the longitudinal genetic and shared

environmental structures could each be reduced to a single common factor, so in all of our models the $a_{ARt,t-1}$ and $c_{ARt,t-1}$ were not estimated.

In the $P \rightarrow E$ model, the autoregressive correlations of the E^w components are re-specified as regressions of $E_{ft,i}^w$ at day $t > 1$ on the phenotype at day $t-1$:

$$E_{ft,i}^w = b_{PEt,t-1} P_{t-1}^w + u E_{ft,i}^w.$$

The nonshared environmental variables, $E_{ft,i}^w$ at day $t > 1$, are regressed on the phenotype at day $t-1$. The autoregressive coefficients ($b_{PEt,t-1}$) and disturbances ($u E_{ft,i}^w$) were freely estimated. By path tracing rules, in the DZ group the $b_{PEt,t-1}$ parameters necessarily transmit effects of the within-family genetic factor ($A_{ft-1,i}^w * b_{PEt,t-1}$) and the nonshared environmental factor ($E_{ft-1,i}^w * b_{PEt,t-1}$) at day $t-1$ via the phenotype at day $t-1$. As there is no within-family genetic variation, A^w variables are fixed to zero in the MZ group. This means that $b_{PEt,t-1}$ effects are equal to the autoregressive effects of the nonshared environment, $e_{ARt,t-1}$. The baseline model assumes that $b_{PEt,t-1}$ effects are different in the MZ group than the DZ group. In the DZ group, significant $b_{PEt,t-1}$ effects support the hypothesis that pair differences in affect on previous days systematically expose twins to unique environments on subsequent days, which causes unique environments to become correlated with genetic factors and unique environments on previous days. In the MZ group, significant $b_{PEt,t-1}$ effects suggest that unique environments at day t correlate with unique environments at $t-1$. The baseline model was compared to a restricted model that constrains all $b_{PEt,t-1}$ parameters to be equal between MZ and DZ twins. If the more restricted model fits equal as well as the baseline model, this means that $b_{PEt,t-1}$ parameters

cannot be distinguished from the $e_{ARt,t-1}$. Under this more parsimonious model, the null hypothesis is that environmental effects over time are equivalent to person-environment effects over time.

The $P \rightarrow E$ parameter, $b_{PEt,t-1}$, has three consequences in the DZ group. First, it necessarily induces accumulating within-family r_{GE} . Second, $b_{PEt,t-1}$ parameters change the meaning of the nonshared environmental effects when $t > 1$ for the reason that the parameters correlate $E_{ft,i}^w$ with $A_{ft-1,i}^w$ (Dolan et al., 2014). Third, $b_{PEt,t-1}$ parameters increase the stability of nonshared environment over days as twins are matched to environments well suited to their phenotype.

Since b_{PE} parameters necessarily change the meaning of the nonshared environment at all days but the first day via indirect correlations between genetic and environmental components (Beam et al., 2015), we empirically test the longitudinal structure of the nonshared environment by statistically comparing model implied nonshared environmental variances and covariances in the DZ group against the MZ group.

Models were fit in *Mplus* 8.2 (Muthén & Muthén, 1998-2017) using Full Information Maximum Likelihood (FIML) estimation with robust standard errors to handle missing data, violations of multivariate normality, and modest sample sizes. Missing data were assumed to be missing at random (Enders, 2010). Model comparisons were made with the Satorra-Bentler scaled chi-square difference test (S-B χ^2), which corrects the chi-square distributed test statistic in cases of multivariate normality assumption violations (Satorra & Bentler, 2001). Model fit also was evaluated using the Akaike Information Criterion (AIC) and the Bayesian Information Criterion (BIC) (Burnham & Anderson, 2004). We also employed the Sample Size Adjusted Bayesian Information Criterion (SSABIC), which adjusts the sample size penalty of the BIC to provide better model fit performance than the BIC when sample sizes are small or there are a large number of parameters (Sclove, 1987;

Tofighi & Enders, 2007). Models with lower AIC, BIC, and SSABIC values indicate better model fit, because these indices take into account the trade-off between model parsimony and model complexity.

Results

Figure 2 presents the means and standard deviations of positive and negative affect across the 30 days. There was relatively little fluctuation in the affect means, with greater variance in positive affect than negative affect.

Figure 2. Means and standard deviations (error bars) of positive affect and negative across all days.

Figure 3 presents the twin correlations for positive affect and negative affect on each day with LOESS smoothing lines overlaid to illustrate trends in twin similarity over days. Beginning at Day 1, MZ and DZ twin correlations for positive affect (top panel) gradually diverge until about day 10, remain constant from day 11 through day 18, diverge again from day 18 through about day 28, and then converge the final two days. For negative affect, twin correlations generally converge from day 1 through day 11, then diverge until about day 28, after which the correlations tend to converge with DZ twins more similar than MZ twins in the final days. Within-pair differences in person-environment match, the basis for generating within-family gene-environment correlation, are expected to account for divergence of MZ and DZ twin correlations.

Figure 3. Daily twin correlations of positive and negative affect scores. Smoothing lines (in blue) are overlaid to illustrate general trends in twin similarity for each phenotype.

The above twin correlations were used to estimate the daily heritability and environment estimates, which are depicted in Figure 4. Both MZ and DZ correlations demonstrated variability in twin similarity in positive affect scores over the 30 days. Heritability estimates (red lines) tended to increase until about day 14, were variable from day 15 through day 19, increased dramatically from day 19 through day 25, and then declined. Shared environmental estimates were generally around zero (or negative), although on days where heritability declined, shared environmental estimates tended to increase above zero (e.g., days 6, 14, 29, and 30). Nonshared environmental estimates over days were stable.

Figure 4. Heritability and environment estimates of positive affect (left) and negative affect (right) by day. h^2 = heritability, or the proportion of total variance in daily affect scores attributed to genetic variance; c^2 = shared environment, or the proportion of total variance in daily affect scores attributed to shared environmental variance; e^2 = nonshared environment, or the proportion of total variance in daily affect scores attributed to nonshared (unique) environmental variance. All estimates are based on univariate ACE models.

Twin correlations for negative affect also tended to vary across days, suggesting variability in genetic and environmental estimates. Heritability estimates generally declined from day 1 through day

12, increased through day 25 and then slightly declined. Shared environmental estimates tended to increase across days where heritability declined and declined on days when heritability increased. Nonshared environmental estimates slightly increased for the first 15 days and slightly declined for the last 15 days. As rises in heritability suggest that DZ twin similarity diverges from MZ twin similarity, we next tested whether r_{GE} accounts for daily fluctuations in heritability, particularly across days where heritability of positive and negative affect increases.

Person → Environment Model Results

Model fitting results (Table 1) indicate that the $P \rightarrow E$ model provided better fit to the data than a model that equates $P \rightarrow E$ and nonshared environmental parameters for both positive affect (LRT = 90.72, $df = 29$, $p < .001$) and negative affect (LRT = 55.83, $df = 29$, $p < .003$). Further, AIC and SSABIC values were lower for models that distinguish $P \rightarrow E$ parameters than models that do not, further indicating better fit to the data. That is, person-environment matching parameters (b_{PE}) significantly improved model fit for both positive affect and negative affect.

Table 1. *Model fitting results*

Positive Affect Models	LL	df	ΔLL	df	p	AIC	BIC	SSABIC
1. $P \Rightarrow E$ Model	-34470.97	871	-	-	-	69179.93	69666.53	69288.88
2. $P \Rightarrow E = E$ Model	-34561.69	900	91	29	0.000	69303.37	69671.39	69385.77
Negative Affect Models	LL	df	ΔLL	Δdf	p	AIC	BIC	SSABIC
1. $P \Rightarrow E$ Model	-31147.25	871	-	-	-	62532.51	63019.10	62641.45
2. $P \Rightarrow E = E$ Model	-31203.08	900	55.83	29	0.002	62586.16	62954.18	62668.56

Notes. Model 1 is the $P \rightarrow E$ model, which is the less restricted model that distinguishes between person-environment match via b_{PE} parameters and nonshared environmental effects over days. Model 2 restricts b_{PE} effects to be equal to nonshared environmental effects. LL = log likelihood value; ΔLL = likelihood ratio value; Δdf = differences in in degrees of freedom between models 1 and 2; AIC =

Akaike Information Criterion; BIC = Bayesian Information Criterion; SSABIC = Sample Size Adjusted Bayesian Information Criterion.

Figure 5 presents the line plots of model estimated within-family r_{GE} for positive affect and negative affect from the $P \rightarrow E$ models. Within-family r_{GE} was small and tended to fluctuate from day 1 to day 15. From day 15 through day 25, r_{GE} increased but began to decline again from day 26 through day 30. By comparison, within-family r_{GE} did not vary significantly from zero when the same models were fit to data where days were randomly ordered within twins (lines labeled PA Random Days and NA Random Days, respectively).

Figure 5. Model estimated within-family gene-environment correlation (r_{GE}) over 30 days for positive affect (PA) and negative affect (NA). r_{GE} was re-estimated in $P \rightarrow E$ models where days were randomly ordered within twins to illustrate that r_{GE} systematically changes across the 30 days.

The $P \rightarrow E$ parameters affected heritability of daily affect scores attributed to genetic effects alone, that is, excluding r_{GE} generated via b_{PE} paths (Figure 6). Heritability estimates under the independence assumption (blue lines) for positive affect and for negative affect are compared to

heritability estimates under accommodation of r_{GE} (red lines). For both positive and negative affect, estimating $P \rightarrow E$ effects in the DZ group reduced heritability estimates by approximately 3% across days, on average, with reductions as great as 7-8%. Heritability estimates, thus, were attenuated when r_{GE} was modeled.

Figure 6. Heritability estimates of positive affect (top) and negative affect (bottom) from $P \rightarrow E$ model (red) and genetic simplex model (blue) across the 30 days.

Finally, $P \rightarrow E$ effects that accommodate r_{GE} also affected the longitudinal correlations between nonshared environmental components across the 30 days. Figure 7 presents the nonshared environmental correlations in the MZ group (left side) and the DZ group (right side) for positive affect (top plots) and negative affect (bottom plots). As a reminder, longitudinal correlations between nonshared environmental components in the MZ group do not include r_{GE} (there are no within-family genetic effects) whereas in the DZ group r_{GE} is accommodated. In the MZ group, longitudinal nonshared environmental correlations persist up to 5 days, declining from a moderate correlation of .40-.50 between adjacent days (e.g., day 1 and day 2) to essentially zero 5 days later (e.g., between day

1 and day 6). Nonshared environmental correlations decayed more rapidly when accommodating r_{GE} by about 1-1.5 days earlier, but are systematically correlated across days, although the correlations are small. Differences in longitudinal correlations estimated with and without accommodation of r_{GE} are similar, suggesting that the interpretation of nonshared environmental components may have been affected minimally by allowing genetic and environmental components to correlate. Differences in lag-1 correlations were the largest (range: .00 – .20) while correlations among components with greater lags never exceeded .10.

Figure 7. Longitudinal correlations among nonshared environmental correlations across 30 days for positive affect (PA) and negative affect (NA). MZ and DZ correlations are taken from $P \rightarrow E$ models.

Discussion

Plomin et al. (1977) recognized that “environmental and genetic threads in the fabric of behavior are so tightly interwoven that they are indistinguishable” (p. 309). The diurnal twin data presented here and elsewhere (Beam et al., 2015; Dolan et al., 2014) supports the idea that genetic and environmental influences covary across days to support differentiation in psychological traits and abilities over time. As matching between people and their environments ebbs and flows, so does r_{GE} ,

addressing one process through which environments might come to be correlated with outcomes and genotype (Plomin, 1986).

Modeling approaches for accommodating and testing gene-environment correlation (Beam & Turkheimer, 2013; de Kort et al., 2012; Dolan, Huijskens, Minică, Neale, & Boomsma, 2019; Moscati, Verhulst, McKee, Silberg, & Eaves, 2018) are finally catching up to discussions over how genetic and environmental influences reciprocally influence one another (Anastasi, 1958; Briley et al., 2019; Eaves et al., 1977; Wachs, 1983). The reciprocal effects modeling approach taken in the current study places the person at the center of change processes that drive observed phenotypic differences in positive and negative affect. People are not passive recipients of their genotype and environments, as is implied in conventional twin models through specification of unidirectional pathways from genetic and environmental variance components to phenotypic outcomes. In this way, phenotypic stability does not only depend just on the degree of genetic and environmental relatedness but also on the consistency of similarity and differences of people's environmental systems (Lickliter & Harshaw, 2010; West & King, 1987). Siblings, for example, could increasingly differ if they are exposed to different learning activities and environments (e.g., one child is read to daily while the other is not) yet converge if their environments are highly similar (e.g., whatever one child gets, so does the other). By including person-environment effects in the current model that quantify the strength of the relation between twins' affective outcomes and unique environments, we have shown real time selection and evocation of environments that contribute to daily differences in twins' affect.

Person-environment effects that induce within-family r_{GE} have implications for heritability estimates and longitudinal correlations of nonshared environments. In the present study, we found lower heritability estimates when allowing indirect relation between twins' unique genotype and their unique environments, compared to models in which independence between genotype and environment

was assumed. Adaptation to one's unique environmental context, thus, might account for why affect scores appeared to be highly heritability at first glance. Lower heritability estimates when genotype-environment correlation is modeled are a well-known statistical consequence due to gene-environment correlation inflating genetic variance (Briley et al., 2019; Purcell, 2002) and possibly heritability, at least under the assumption of constant genetic variance across a range of environments.

We found support for the hypothesis that genetic influences on affect come to be correlated with environments because of the correlation between people's phenotypes and subsequent environmental influences contributing to their phenotypes (Gottlieb, 2003). Female twins in the sample may not have been selecting and reacting to environments randomly; rather, they were selecting some environments and reacting to others based on the suitability of those environments, with the ultimate purpose of stabilizing their positive and negative affect.

Nonshared environments are expected to correlate across days, as people's environmental systems are not randomly distributed over time although they tend to decay over time (Burt, Khlar, & Klump, 2015). The content of environmental systems is worthy of comment. As nonshared environmental components in twin models comprise *any* nongenetic feature that contributes to within pair differences (including measurement error), identification of specific environmental factors that correlate with twins' affect scores is beyond the scope of this study. In this way, environmental systems may comprise twins' different interpretations of their shared relationships (e.g., parents) or neighborhoods, their unique peer networks, hormone levels (e.g., estrogen, progesterone, cortisol), and even molecular environments like differences in DNA methylation and RNA transcription. Twins who prefer quiet solitude compared to their cotwins, for example, probably will avoid loud crowded venues no matter the situation, but especially if they are perceived as engendering stress that might increase negative affect or lower positive affect. Similarly, twins who experience higher levels of progesterone

and estrogen compared to their cotwins may be more responsive to social stress, which in turn affects their choice of environment as well as their mood. As Scarr (1992) put it, environments are “largely the construction of individual family members in the ways they evoke responses from others, actively select or ignore opportunities, and construct their own experiences” (p.14). Construction of and reaction to experiences, broadly construed, should correlate with genotype, as genotype is responsive to environmental experiences (Kendler & Baker, 2007). Modeled gene-environment correlation, thus, showed that twins’ total unique environments are temporally linked for longer than expected under models that assume genetic and environmental covariation.

Notably, r_{GE} estimates fluctuated systematically over time, particularly between days 15 and 30 – the latter “half” of the menstrual cycle. Although we could not identify specific factors in twins’ lives that determined the increase in r_{GE} underlying positive and negative affect, we can only speculate about the reasons why. Stress vulnerability to daily hassles, because of hormonal factors, social environmental factors, or both, might be greater in latter days of the cycle. Previous findings suggest that the luteal phase – and particularly the late luteal period – may represent a period of intensified daily hassles compared to the follicular phase (Kiesner, Mendle, Eisenlohr-Moul, & Pastore, 2016). Women may be more prone to select environments for stress management, as environmental factors such as perceived stress and social support might exacerbate cycle-related changes in affect (Romans et al., 2012). Accordingly, environmental context has been identified as an important contributor to daily mood ratings (Stone, Marco, Cruise, Cox, & Neale, 1996). A successful match between persons and environments might be especially relevant during high stress vulnerability phases relative to low stress vulnerability phases.

Environmental components in the within-family r_{GE} estimates likely consist of the correlation between genotype and hormones. Estrogen and progesterone trigger changes in gene expression (Cole,

2009; Östlund, Keller, & Hurd, 2003), and genetic factors account for individual physiological and behavioral responses to estrogen and progesterone levels (Klump, Burt, McGue, & Iacono, 2007; Wall et al., 2014). Within-pair differences in estrogen and progesterone levels during the luteal phase might moderate (or mediate) within-pair genetic effects on differences in affect, consistent with study results of binge eating in the same sample (Klump, Fowler, Mayhall, Sisk, Culbert, & Burt, 2018). Indirect and bidirectional associations among hormones, genotype, and environment, in other words, are more likely than direct genetic effects on affect, similar to any other human complex trait (Anastasi, 1958; Gottlieb, 2003). Future research in longitudinal twin modeling would benefit from specifying measured environmental factors, like internal (e.g., hormones) and external (e.g., peer relationships) factors, in addition to nonspecific environmental factors, as previously proposed (Wachs, 1983). $P \rightarrow E$ models that include intermediate variables in the causal chain, however, need to be developed.

Although accommodating r_{GE} in longitudinal behavioral genetic models has the advantage of explicating how environments come to be correlated with psychological traits and heredity, $P \rightarrow E$ parameters change the meaning of nonshared environmental components (Beam et al., 2015; Dolan et al., 2014). Our empirical test compared nonshared environmental components with and without r_{GE} and suggested that including $P \rightarrow E$ may do so only minimally. In fact, while the theoretical meaning of the nonshared environment does change by virtue of genetic components indirectly predicting environmental components, the model-estimated nonshared environment correlations did not differ appreciably, suggesting overall similarity in the interpretation of the nonshared environment. While twin studies do not clarify specific environmental factors that contribute to any phenotype (Wachs, 1983), the implication that differences in environmental exposure matter for maintaining stability of affect seem to be preserved when genetic and environmental components are allowed to correlate.

Accommodating r_{GE} in longitudinal twin models is an explicit demonstration of how mutual exchange between people and their environments might cause highly heritable traits to increase over time, as originally proposed by Dickens and Flynn (2001). Meta-analyses of longitudinal findings have drawn on Dickens and Flynn's version of the reciprocal effects model to understand age trends in genetic and environmental variance components, but only indirectly (Briley & Tucker-Drob, 2013; Briley & Tucker-Drob, 2014; Tucker-Drob & Briley, 2014). These studies must assume the same independence assumption and so describe that twin correlations decrease with age in DZ twins compared to MZ twins (see also McCartney, Harris, & Bernieri, 1990), but never address the developmental systems that explain how DZ twins diverge in similarity over time.

The temporal dynamics of phenotype-environment matching might differ across traits and abilities. For traits that tend to be highly stable over time, such as cognitive ability and personality, within-family gene-environment correlation is expected to rise precipitously and to level off when persons are more or less canalized into their environments. Thus, for stable traits, the interval of time between measurements might not matter much, as environments that support these traits are unlikely to change with time. Instead, for phenotypes that fluctuate with time, such as affect, perceived stress, and psychiatric symptoms, within-family gene-environment correlation should ebb and flow because of state dependence. Persons prone to depression are not continuously depressed nor do persons prone to seeing their world as stressful always feel stressed. As a result, within-family gene-environment correlation estimates will be temporally dynamic for state-dependent traits, meaning they might increase during some periods and decrease during others. Within-family gene-environment correlation for state-dependent traits, on the other hand, will require shorter divisions of time that can capture traits and characteristics that vary more frequently. Indeed, in studies with measurements separated by years, person-environment effects that generate within-family gene-environment correlation were not found

for depressive symptoms (Beam et al., 2016), but were found for cognitive ability (Beam et al., 2015; de Kort et al., 2014) and personality (Beam et al., under review). This is the first study to test gene-environment correlation over days.

Limitations & Future Directions

The most notable limitation in the current study is that processes other than r_{GE} (e.g., gene-environment interaction, hormones) might account for stability of pair differences in affect over the 30 days of the menstrual cycle studied here. Along this very theme, a second limitation is that other biological processes that factor into pair differences remains unaccounted for in the current study. Molecular environments like RNA transcription, protein transcription, and hormonal influences on genetic expression have a great deal to do with phenotypic expression (Cole, 2009). A third limitation of the current study is the assumption that all twins experienced functionally equivalent environments across the 30 days. As with most, if not all, quantitative genetic studies, conclusions about the roles of specific environments cannot be made (Wachs, 1983). In other words, it remains unclear whether one twin experienced a more extreme environment (e.g., trauma exposure) compared to her co-twin. A final limitation is that the $P \rightarrow E$ model assumes that the autocorrelation structure between measurement occasions are stationary and that the process under scrutiny is noncyclic. The time metric used in the current study, the menstrual cycle, however is nonstationary and cyclic. The $P \rightarrow E$ parameterization, thus, may oversimplify the person-environment matching process hypothesized to occur over time in these data. As there are no other diurnal twin studies with as many repeated measurements as in the MSUTR, this study offers a rare glimpse into person-environment processes that account for differences in daily affect scores.

There are a number of directions for future research that would benefit longitudinal behavioral genetic models, both of which are oriented toward understanding *how* heritability increases with time

and nonshared environments become correlated. First, diurnal twin studies with time scales that are both stationary and noncyclic (e.g., daily affect scores measured over days in advance of at least one twin who experiences a significant stressful event, like taking the a medical exam, the bar exam, or the graduate record examination) should be a priority, as this study design would satisfy the $P \rightarrow E$ model assumptions. Second, the inclusion of measured genotypic differences, like polygenic scores, would permit tests of whether nonshared environmental differences correlate with differences in measured causal variants. Work in this area is underway (Dolan et al., 2014). A third direction involves cohort sequential designs in longitudinal twin studies. This approach would help clarify when $P \rightarrow E$ effects matter most across different developmental periods. Certain periods of development might be more critical for person-environment matching than others (e.g., looking for a first job versus a lateral career move in midlife). The fourth direction we hope to see in future studies is the integration of experimental designs with behavioral genetic approaches, like the one take by Burt, Plaisance, and Hambrick (2019). Randomly assigning twins within pairs to different environmental exposures may shed insight into the ways in which twins' construction and reaction to initial random environmental exposure influences change trajectories and gene-environment correlation. Random assignment to different environments may induce twins to differentiate within brief windows of time because of within-family gene-environment correlative processes. Although $P \rightarrow E$ effect sizes tend to be small (see also Dolan et al., 2014), effects can have meaningful consequences when repeated consistently over time (Funder & Ozer, 2019). Experimental twin designs might offer the best and most feasible approach for advancing knowledge on the ways in which twins gradually drift apart over time.

References

- Anastasi, A. (1958). Heredity, environment, and the question “how?” *Psychological Review*, 65(4), 197–208.
- Bäckström, T., Haage, D., Löfgren, M., Johansson, I. M., Strömberg, J., Nyberg, S., ... Bengtsson, S. K. (2011). Paradoxical effects of GABA-A modulators may explain sex steroid induced negative mood symptoms in some persons. *Neuroscience*, 191, 46–54.
<http://doi.org/10.1016/j.neuroscience.2011.03.061>
- Bartels, M., Rietveld, M. J. H., Van Baal, G. C. M., & Boomsma, D. I. (2002). Genetic and environmental influences on the development of intelligence. *Behavior Genetics*, 32(4), 237–49.
- Bartels, M., van den Oord, E. J. C. G., Hudziak, J. J., Rietveld, M. J. H., van Beijsterveldt, C. E. M., & Boomsma, D. I. (2004). Genetic and environmental mechanisms underlying stability and change in problem behaviors at ages 3, 7, 10, and 12. *Developmental Psychology*, 40(5), 852–867.
<http://doi.org/10.1037/0012-1649.40.5.852>
- Beam, C. R., Emery, R. E., Reynolds, C. A., Gatz, M., Turkheimer, E., & Pedersen, N. L. (2016). Widowhood and the Stability of Late Life Depressive Symptomatology in the Swedish Adoption Twin Study of Aging. *Behavior Genetics*, 46(1), 100–113. <http://doi.org/10.1007/s10519-015-9733-7>
- Beam, C.R., Sharp, E.S., Reynolds, C.A., & Pedersen, N.L. Social dynamics of personality development in late adulthood. *Manuscript submitted*.
- Beam, C. R., & Turkheimer, E. (2013). Phenotype-environment correlations in longitudinal twin models. *Development and Psychopathology*, 25(1), 7–16.
<http://doi.org/10.1017/S0954579412000867>
- Beam, C. R., Turkheimer, E., Dickens, W. T., & Davis, D. W. (2015). Twin differentiation of cognitive

- ability through phenotype to environment transmission: The Louisville Twin Study. *Behavior Genetics*, 45(6), 622–634. <http://doi.org/10.1007/s10519-015-9756-0>
- Bell, R. Q. (1968). Effects in studies of socialization. *Psychological Review*, 75(2), 81–95.
- Boker, S. M., & McArdle, J. J. (2014). Path analysis and path diagrams. *Wiley StatsRef: Statistics Reference Online*. Retrieved from <https://onlinelibrary.wiley.com/doi/10.1002/9781118445112.stat06517>
- Boomsma, D. I., & Molenaar, P. C. M. (1987). The genetic analysis of repeated measures. I. Simplex models. *Behavior Genetics*, 17(2), 111–123.
- Briley, D. A., Livengood, J., Derringer, J., Tucker-Drob, E. M., Fraley, R. C., & Roberts, B. W. (2019). Interpreting Behavior Genetic Models: Seven Developmental Processes to Understand. *Behavior Genetics*, 49(2), 196–210. <http://doi.org/10.1007/s10519-018-9939-6>
- Briley, D. A., & Tucker-Drob, E. M. (2013). Explaining the Increasing Heritability of Cognitive Ability Across Development: A Meta-Analysis of Longitudinal Twin and Adoption Studies. *Psychological Science*, 24(9), 1704–1713. <http://doi.org/10.1177/0956797613478618>
- Briley, D. A., & Tucker-Drob, E. M. (2014). Genetic and environmental continuity in personality development: A meta-analysis. *Psychological Bulletin*, 140(5), 1303–1331.
- Bronfenbrenner, U., & Ceci, S. J. (1994). Nature-nurture reconceptualized in developmental perspective: A bioecological model. *Psychological Review*, 101(4), 568–586. <http://doi.org/10.1037/0033-295X.101.4.568>
- Burnham, K. P., & Anderson, D. R. (2004). Multimodel inference: Understanding AIC and BIC in model selection. *Sociological Methods & Research*, 33(2), 261–304. <http://doi.org/10.1177/0049124104268644>
- Burt, S. A., Klahr, A. M., & Klump, K. L. (2015). Do non-shared environmental influences persist over

time? An examination of days and minutes. *Behavior genetics*, 45(1), 24-34.

<https://doi.org/10.1007/s10519-014-9682-6>

Burt, S. A., & Klump, K. L. (2013). The Michigan State University Twin Registry (MSUTR): An update. *Twin Research and Human Genetics*, 16(1), 344–350. <http://doi.org/10.1017/thg.2012.87>

Burt, S. A., Plaisance, K. S., & Hambrick, D. Z. (2019). Understanding “what could be”: A call for “experimental behavioral genetics.” *Behavior Genetics*, 49(2), 235–243.

<http://doi.org/10.1007/s10519-018-9918-y>

Cole, S. W. (2009). Social regulation of human gene expression. *Current Directions in Psychological Science*, 18(3), 132–137.

de Kort, J. M., Dolan, C. V., & Boomsma, D. I. (2012). Accommodation of genotype-environment covariance in a longitudinal twin design. *Netherlands Journal of Psychology*, 67(3), 81–90.

de Kort, J. M., Dolan, C. V., Kan, K.-J., van Beijsterveldt, C. E. M., Bartels, M., & Boomsma, D. I. (2014). Can GE-covariance originating in phenotype to environment transmission account for the Flynn Effect? *Journal of Intelligence*, 2(3), 82–105. <http://doi.org/10.3390/jintelligence2030082>

Dickens, W. T., & Flynn, J. R. (2001). Heritability estimates versus large environmental effects: The IQ paradox resolved. *Psychological Review*, 108(2), 346–369.

Dickens, W. T., Turkheimer, E., & Beam, C. R. (2011). The social dynamics of the expression of genes for cognitive ability. In K. S. Kendler, S. R. Jaffee, & D. Romer (Eds.), *The Dynamic Genome and Mental Health: The Role of Genes and Environments in Youth Development*.

Dolan, C. V., De Kort, J. M., Van Beijsterveldt, T. C. E. M., Bartels, M., & Boomsma, D. I. (2014). GE covariance through phenotype to environment transmission: An assessment in longitudinal twin data and application to childhood anxiety. *Behavior Genetics*, 44(3), 240–253.

<http://doi.org/10.1007/s10519-014-9659-5>

- Dolan, C. V, Huijskens, R. C. A., Minică, C. C., Neale, M. C., & Boomsma, D. I. (2019). Incorporating polygenic scores in the twin model to estimate genotype-environment covariance: exploration of statistical power. *bioRxiv*, 1–32. Retrieved from doi: <http://dx.doi.org/10.1101/702738>
- Eaves, L. J., Krystyna, L., Martin, N. G., & Jinks, J. L. (1977). A progressive approach to non-additivity and genotype-environmental covariance in the analysis of human differences. *British Journal of Mathematical and Statistical Psychology*, 30, 1–42.
- Eaves, L. J., Long, J., & Heath, A. C. (1986). A theory of developmental change in quantitative phenotypes applied to cognitive development. *Behavior Genetics*, 16(1), 143–62.
- Enders, C. K. (2010). *Applied missing data analysis*. New York, NY: The Guilford Press.
- Farage, M. A., Osborn, T. W., & MacLean, A. B. (2008). Cognitive, sensory, and emotional changes associated with the menstrual cycle: A review. *Archives of Gynecology and Obstetrics*, 278(4), 299–307. <http://doi.org/10.1007/s00404-008-0708-2>
- Fischbein, S. (1978). Heredity-environment interaction in the development of twins. *International Journal of Behavioral Development*, 1(4), 313–322. <http://doi.org/10.1177/016502547800100402>
- Fuller, J. L., & Thompson, W. R. (1960). *Behavior Genetics*. New York: John Wiley & Sons, Inc.
- Funder, D. C., & Ozer, D. J. (2019). Evaluating effect size in psychological research: Sense and nonsense. *Advances in Methods and Practices in Psychological Science*, 2(2), 156–168. <https://doi.org/10.1177/2515245919847202>
- Gottlieb, G. (2003). On making behavioral genetics truly developmental. *Human Development*, 46(6), 337–355. <http://doi.org/10.1159/000073306>
- Halbreich, U., Freeman, E. W., Rapkin, A. J., Cohen, L. S., Grubb, G. S., Bergeron, R., ... Constantine, G. D. (2012). Continuous oral levonorgestrel/ethinyl estradiol for treating premenstrual dysphoric disorder. *Contraception*, 85(1), 19–27. <http://doi.org/10.1016/j.contraception.2011.05.008>

- Kendler, K. S., & Baker, J. H. (2007). Genetic influences on measures of the environment: A systematic review. *Psychological Medicine*, 37, 615–626.
<http://doi.org/10.1017/S0033291706009524>
- Kiesner, J., Mendle, J., Eisenlohr-Moul, T. A., & Pastore, M. (2016). Cyclical symptom change across the menstrual cycle: Attributional, affective, and physical symptoms. *Clinical Psychological Science*, 4(5), 882-894. <https://doi.org/10.1177/2167702616635031>
- Klump, K. L., & Burt, S. A. (2006). The Michigan State University Twin Registry (MSUTR): Genetic, environmental and neurobiological influences on behavior across development. *Twin Research and Human Genetics*, 9(6), 971–977. <http://doi.org/10.1375/183242706779462868>
- Klump, K. L., Burt, S. A., McGue, M., & Iacono, W. G. (2007). Changes in genetic and environmental influences on disordered eating across adolescence: A longitudinal twin study. *Archives of general psychiatry*, 64(12), 1409-1415. doi:10.1001/archpsyc.64.12.1409
- Klump, K. L., Fowler, N., Mayhall, L., Sisk, C. L., Culbert, K. M., & Burt, S. A. (2018). Estrogen moderates genetic influences on binge eating during puberty: Disruption of normative processes?. *Journal of Abnormal Psychology*, 127(5), 458-470. <https://doi.org/10.1037/abn0000352>
- Klump, K. L., Hildebrandt, B., O'Connor, S. M., Keel, P. K., Neale, M., Sisk, C. L., ... Burt, S. A. (2015). Changes in genetic risk for emotional eating across the menstrual cycle: A longitudinal study. *Psychological Medicine*, 1–11. <http://doi.org/10.1017/S0033291715001221>
- Klump, K. L., Keel, P. K., Racine, S. E., Burt, A. A., Neale, M., Sisk, C. L., ... Hu, J. Y. (2013). The interactive effects of estrogen and progesterone on changes in emotional eating across the menstrual cycle. *Journal of Abnormal Psychology*, 122(1), 131–137.
<http://doi.org/10.1037/a0029524>
- Klump, K. L., Racine, S. E., Hildebrandt, B., Burt, S. A., Neale, M., Sisk, C. L., ... Keel, P. K. (2014).

Influences of ovarian hormones on dysregulated eating: A comparison of associations in women with versus women without binge episodes. *Clinical Psychological Science*, 2(5), 545-559.

<https://doi.org/10.1177/2167702614521794>

Lickliter, R., & Harshaw, C. (2010). Canalization and malleability reconsidered: The developmental basis of phenotypic stability and variability. In K. E. Hood, C. T. Halpern, G. Greenberg, & R. M. Lerner (Eds.), *Handbook of developmental science, behavior, and genetics* (pp. 491–525). West Sussex: Wiley-Blackwell.

McArdle, J. J., & Prescott, C. A. (2005). Mixed-effects variance components models for biometric family analyses. *Behavior Genetics*, 35(5), 631–652. <http://doi.org/10.1007/s10519-005-2868-1>

McCartney, K., Harris, M. J., & Bernieri, F. (1990). Growing up and growing apart: A developmental meta-analysis of twin studies. *Psychological Bulletin*, 107(2), 226–237.

Montag, C., Hahn, E., Reuter, M., Spinath, F. M., Davis, K., & Panksepp, J. (2016). The role of nature and nurture for individual differences in primary emotional systems: Evidence from a twin study. *PLoS ONE*, 11(3), 1–15. <http://doi.org/10.1371/journal.pone.0151405>

Moscato, A., Verhulst, B., McKee, K., Silberg, J., & Eaves, L. (2018). Cross-lagged analysis of interplay between differential traits in sibling pairs: Validation and application to parenting behavior and ADHD symptomatology. *Behavior Genetics*, 48(1), 22–33.
<http://doi.org/10.1007/s10519-017-9882-y>

Muthén, L. K., & Muthén, B. O. (1998-2017). *Mplus user's guide*. Los Angeles, CA: Muthén & Muthén.

Neale, M. C., & Cardon, L. R. (1992). *Methodology for genetic studies of twins and families*. Springer: New York, NY.

Neale, M. C., & McArdle, J. J. (2000). Structured latent growth curves for twin data. *Twin Research*

and *Human Genetics*, 3(3), 165-177.

Östlund, H., Keller, E., & Hurd, Y. L. (2003). Estrogen receptor gene expression in relation to neuropsychiatric disorders. *Annals of the New York Academy of Sciences*, 1007, 54–63.

Polderman, T. J., Benyamin, B., De Leeuw, C. A., Sullivan, P. F., Van Bochoven, A., Visscher, P. M., & Posthuma, D. (2015). Meta-analysis of the heritability of human traits based on fifty years of twin studies. *Nature genetics*, 47(7), 702-709.

Plomin, R. (1986). Multivariate analysis and developmental behavioral genetics: Developmental change as well as continuity. *Behavior Genetics*, 16(1), 25–43.

Plomin, R., DeFries, J. C., & Loehlin, J. C. (1977). Genotype-environment interaction and correlation in the analysis of human behavior. *Psychological Bulletin*, 84(2), 309–322.

<http://doi.org/10.1037/0033-2909.84.2.309>

Poromaa, I. S., & Gingnell, M. (2014). Menstrual cycle influence on cognitive function and emotion processing from a reproductive perspective. *Frontiers in Neuroscience*, 8(Nov), 1–16.

<http://doi.org/10.3389/fnins.2014.00380>

Purcell, S. (2002). Variance components models for gene-environment interaction in twin analysis.

Twin Research, 5(6), 554–571. <http://doi.org/10.1375/twin.5.6.554>

Romans, S., Clarkson, R., Einstein, G., Petrovic, M., & Stewart, D. (2012). Mood and the menstrual cycle: A review of prospective data studies. *Gender Medicine*, 9(5), 361–384.

<http://doi.org/10.1016/j.genm.2012.07.003>

Satorra, A., & Bentler, P. M. (2001). A scaled difference chi-square test statistic for moment structure analysis. *Psychometrika*, 66(4), 507–519.

Scarr, S. (1992). Developmental theories for the 1990s: Development and individual differences. *Child Development*, 63(1), 1–19.

- Scarr, S., & McCartney, K. (1983). How people make their own environments: A theory of genotype-environment effects. *Child Development*, 54, 424–435.
- Sclove, S. L. (1987). Application of model-selection criteria to some problems in multivariate analysis. *Psychometrika*, 52(3), 333–343.
- Stone, A. A., Marco, C. A., Cruise, C. E., Cox, D. S., & Neale, J. M. (1996). Are stress-induced immunological changes mediated by mood? A closer look at how both desirable and undesirable daily events influence sIgA antibody. *International Journal of Behavioral Medicine*, 3(1), 1–13. http://doi.org/10.1207/s15327558ijbm0301_1
- Tofighi, D., & Enders, C. K. (2007). Identifying the correct number of classes in growth mixture models. In G. R. Hancock & K. M. Samuelsen (Eds.), *Advances in latent variable mixture models* (pp. 317–341). Charlotte, NC: Information Age Publishing.
- Tucker-Drob, E. M., & Briley, D. A. (2014). Continuity of genetic and environmental influences on cognition across the life span: a meta-analysis of longitudinal twin and adoption studies. *Psychological Bulletin*, 140(4), 949–79. <http://doi.org/10.1037/a0035893>
- Turkheimer, E., & Waldron, M. (2000). Nonshared environment: A theoretical, methodological, and quantitative review. *Psychological Bulletin*, 126(1), 78–108. <http://doi.org/10.1037/0033-2909.126.1.78>
- van den Berg, S. M., Beem, L., & Boomsma, D. I. (2006). Fitting genetic models using Markov Chain Monte Carlo algorithms with BUGS. *Twin Research and Human Genetics*, 9(3), 334–342.
- Wachs, T. D. (1983). The use and abuse of environment in behavior-genetic research. *Child Development*, 54(2), 396–407.
- Wall, E. H., Hewitt, S. C., Case, L. K., Lin, C. Y., Korach, K. S., & Teuscher, C. (2014). The role of genetics in estrogen responses: A critical piece of an intricate puzzle. *FASEB Journal*, 28(12),

5042–5054. <http://doi.org/10.1096/fj.14-260307>

Watson, D., Clark, L. A., & Tellegen, A. (1988). Development and Validation of Brief Measures of Positive and Negative Affect: The PANAS Scales. *Journal of Personality and Social Psychology*, 54(6), 1063–1070.

West, M. J., & King, A. P. (1987). Settling nature and nurture into an ontogenetic niche. *Developmental Psychobiology*, 20(5), 549–562. <http://doi.org/10.1002/dev.420200508>

Winship, C., & Korenman, S. (1999). Economic success and the evolution of schooling and mental ability. In S. Mayer & P. E. Peterson (Eds.), *Earning and learning: How schools matter* (pp. 49–78). Washington DC: Brookings