A Behavioral Genetic Analysis of Callous-Unemotional Traits and Big Five Personality in Adolescence

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Abstract

Callous-unemotional (CU) traits, such as lacking empathy and emotional insensitivity, predict the onset, severity and persistence of antisocial behavior. CU traits are heritable, and genetic influences on CU traits contribute to antisocial behavior. This study examines genetic overlap between CU traits and general domains of personality. We measured CU traits using the Inventory of Callous and Unemotional Traits (ICU) and Big Five personality using the Big Five Inventory (BFI) in a sample of adolescent twins from the Texas Twin Project. Genetic influences on the Big Five personality dimensions could account for the entirety of genetic influences on CU traits. Item Response Theory results indicate that the ICU is better at detecting clinically relevant personality variation at lower extremes of personality trait continua, particularly low agreeableness and low conscientiousness. The proximate biological mechanisms that mediate genetic liabilities for CU traits remain an open question. The results of the current study suggest that understanding the development of normal personality may inform an understanding of the genetic underpinnings of callous and unemotional behavior.

Summary

Callous-unemotional (CU) traits include lack of empathy, lack of remorse and dampened emotions. Having high levels of CU traits is a risk factor for severe antisocial behavior. We find that genetic influences on normal personality traits, particularly conscientiousness and agreeableness, explain all of the genetic influence on CU traits

Keywords

callous-unemotional traits; big five; personality; behavioral genetics; item response theory

Callous-unemotional (CU) traits, including lack of empathy, lack of sensitivity and dampened affect, concurrently and prospectively predict a number of antisocial outcomes, including aggression (Dolan & Rennie, 2006; Frick, Cornell, Barry, Bodin & Dane, 2003; Marsee, Silverthorn & Frick, 2005), conduct problems, (Burke, Loeber & Lahey, 2007;

Enebrink, Anderson & Langstrom, 2005; Frick, Cornell, Barry, Bodin & Dane, 2003), delinquency (Marsee, Silverthorn & Frick, 2005; Lexcen, Vincent & Grisso, 2004), externalizing behavior (Oxford, Cavell & Hughes, 2003), sex offending (Caputo, Frick & Brodsky, 1999; Lawing, Frick & Cruise, 2010) and violent behavior (Dadds, Whiting, & Hawes, 2006; Edens, Skeem, Cruise & Cauffman, 2001). CU traits are frequently conceptualized as a downward extension of interpersonal and affective facets of psychopathy (Frick & Ellis, 1999; Viding, Blair, Moffitt & Plomin, 2005) and are thought to underlie a particularly virulent form of antisocial behavior that is severe and persistent across development (Frick & White, 2008; Frick & Viding, 2009; White & Frick, 2010). Based on this evidence, CU traits were recently incorporated into the *DSM*-5 clinical diagnosis of Conduct Disorder as a "limited prosocial emotions" specifier designed to capture youth with a "callous and unemotional interpersonal style" (American Psychiatric Association, 2013).

Behavior genetic research has revealed a number of noteworthy findings on CU traits and psychopathic personality. In particular, high levels of CU traits specify a form of childhood conduct disorder that is highly heritable (Viding, Jones, Frick, Moffitt, & Plomin, 2008). A common genetic factor underlies psychopathic personality and antisocial behavior (Larsson, Tuvblad, Rijsdijk, Andershed, Grann & Lichenstein, 2007), and genetic influences drive the stability of a psychopathic factor, as well as a lower-order CU factor, from mid-to-late adolescence (Forsman, Lichtenstein, Andershed, Larsson, 2008). Although previous research on CU traits has largely focused on the prediction of clinical behavior problems, there has been relatively little work on the extent to which genetic liabilities for CU traits overlap with those for other commonly studied psychological traits. Dimensional models of psychopathology suggest that CU traits and common domains of normal-range personality reflect the same underlying genetic bases (Kruegar & Piasecki, 2002; Krueger & Tackett, 2003; Krueger, Watson & Barlow, 2005; Miller, Lynam, Widiger & Leukefeld, 2001). Thus, in contrast to taxonomic models of psychopathy, dimensional models would predict that individuals who are high in CU traits constitute extreme ends of personality continua spanning the range from normal to abnormal functioning, rather than discrete classes or "natural kinds" (Meehl, 1992).

The most widely accepted dimensional model of normal-range human personality is the Big Five Model (or Five Factor Model), which describes individual differences along five broad dimensions: extraversion, agreeableness, conscientiousness, neuroticism and openness (Digman, 1990; John, Naumann & Soto, 2008; McCrae & John, 1992). A prodigious body of empirical evidence supports the construct validity of the Big Five, including convergent and discriminant validity across multiple raters and instrument types, high internal reliability, and predictive validity for a variety of important life outcomes (Deary, Weiss & Batty, 2010; DeYoung, 2006; John, Naumann & Soto, 2008; Judge, Higgins, Thoresen & Barrick 1999; Paunonen, 2003; Roberts, Kuncel, Shiner, Caspi & Goldberg, 2007).

Previous research on the phenotypic associations between CU traits and the Big Five is consistent with a dimensional model. In a large sample of adolescents, CU traits were negatively correlated with all Big Five domains (Essau, Sasagawa, & Frick, 2006). In another study, expert-generated psychopathy prototypes derived from Big Five personality items were used to create psychopathy scores, which correlated with self-report drug use,

delinquency, risky sex and aggression (Miller & Lynam, 2003). Results from two subsamples of the Pittsburgh Youth Study were consistent with interpreting juvenile psychopathy as a constellation of normal personality traits (Lynam et al., 2005). Moreover, meta-analytic reviews of associations between the Big Five and *DSM*-IV-TR personality disorders suggest Antisocial Personality Disorder is predominantly characterized by low agreeableness and low conscientiousness (Saulsman & Page, 2002; Samuel & Widiger, 2008).

Understanding the relation between CU traits and Big Five personality resonates with current research initiatives focused on identifying the biological bases for variables that cross-cut clinical constructs and diagnostic boundaries (Insel et al., 2010). Research on Big Five personality provides a theoretically rich and well-validated framework for understanding individual differences in biology, affect, cognition, and social relationships that have been linked to a wide variety of both internalizing and externalizing symptoms (Flory, Lynam, Milich, Leukefeld & Clayton, 2002; Kotov, Gamez, Schmidt & Watson, 2010; Malouff, Thorsteinsson & Schutte, 2005). Examining the relations among Big Five personality traits and CU traits, which have been studied more narrowly in relation to Conduct Disorder and Antisocial Personality Disorder, has the potential to both deepen our understanding of the origin of individual differences in CU traits, as well as broaden our understanding of how CU traits may be linked to dimensions of problematic psychological functioning beyond the externalizing disorders.

One method for investigating the biological mechanisms that putatively link CU traits and normal personality is to use a genetically informative design. Genetically informative data allow us to go beyond testing whether CU traits are correlated with Big Five personality traits to examine the extent to which these correlations are the result of shared genes or shared environments. In other words, we may shed light on the question: to the extent that CU traits are correlated with certain Big Five traits, is this due to common underlying genetic mechanisms? The current study measured broad dimensions of personality to test whether CU traits are influenced by genetic variants independent of those variants that influence a broad range of normal personality traits. Put differently, are genetic liabilities for CU traits common to– or unique of –genes that influence variation in normal personality? To evaluate this question, the current paper analyzes data from a sample of adolescent twins from the Texas Twin Project (Harden, Tucker-Drob, & Tackett, 2013).

Method

Participants

Participants were 535 adolescents from 264 families (257 twin pairs and 7 sets of triplets) ages 13–21 years (mean age = 15.82 years). The full sample was used for all phenotypic analyses. Zygosity information was missing for 1 twin pair; therefore, behavioral genetic analyses were performed on a subsample of 276 twin-pairs (255 pairs from twin families and 21 pairs from 7 triplet families). Adolescents were identified as twins or triplets from public school rosters and recruited via invitation by phone call or mailing. Verbal and written consent was obtained from parents and adolescents prior to participation. Parents completed an online survey, and adolescents visited a university campus for a laboratory

visit. All recruitment and testing procedures were approved by the university IRB. Moreover, the study was granted a federal certificate of confidentiality that exempts us from disclosing identifiable research information in response to legal demands.

Approximately 6% of participants' mothers had not received a high school diploma, 5% only graduated high school, 30% had some college or vocational training, 25% had completed college and 30% had education beyond college. The racial composition of the sample was approximately 60% non-Hispanic White, 20% Hispanic/Latino, 11% African-American, 1% Native American, 1% East Asian, 2% Southeast Asian and 5% mixed-race/other. Nearly all (99.9%) adolescents reported at least one symptom on the externalizing subscale of the Child Behavior Checklist (Lizotte, Chard-Wierschem, Loeber, & Stern, 1992), 83.9% of participants reported one or more delinquent behaviors on a self-report measure of delinquency (Survey, Huizinga, Esbensen & Weiher, 1991) and 75% of participants scored at or above the mean ICU composite score previously observed in a sample of detained juvenile offenders (Munoz, Frick, Kimonis & Aucoin, 2008). Adolescents' cognitive functioning, as measured on the Wechsler Abbreviated Scale of Intelligence (WASI-IV) fell within the expected range for a community sample (M full-scale IQ = 103, SD = 13.2).

Measures

Zygosity—All opposite-sex twin pairs are necessarily dizygotic (DZ). Zygosity for same-sex pairs was classified on the basis of questionnaire items regarding physical similarity and ease of being mistaken for the other twin. These items were completed by the twins' parents, two research assistants following the twins' lab visit, and both twins themselves. Responses were analyzed using latent class analysis (LCA), a statistical technique that assigns individuals to subgroups within a population (in this case, monozygotic [MZ] and DZ twins). Compared to zygosity classification by genotyping, LCA of questionnaire data has been found to have a misclassification rate of less than 1% (Heath et al., 2003). The LCA solution identified 35% of same-sex pairs as MZ and 65% as DZ. The LCA solution had an entropy statistic of 0.999, indicating very little uncertainty in classifying pairs.

Personality Traits—Broad personality domains were measured with the Big Five Inventory (BFI), which consists of 44 items comprising five scales (John, Naumann & Soto, 2008). Extraversion was indexed using 8 items, including "is talkative" and "takes charge, has an assertive personality." Agreeableness was indexed using 9 items, including "is helpful and unselfish with others" and "is considerate and kind to almost everyone." Conscientiousness was indexed using 9 items, including "does things carefully and completely," "is a reliable worker" and "keeps working until things are done." Neuroticism was indexed using 8 items, including "can be tense," "worries a lot" and "can be moody." Openness was indexed using 10 items, including "is original, comes up with new ideas," "is curious about many different things" and "likes to think and play with ideas." Adolescents rated items on a 5-point scale ranging from 1 (*Strongly Disagree*) to 5 (*Strongly Agree*). Scale scores for each of the five factors were computed using the method described by Soto, John, Gosling and Potter (2008), which includes ipsatization to control for individual

differences in response sets (i.e., extreme responding and acquiescence). Internal consistencies of BFI subscales showed high reliabilities (see Table 1).

Callous-Unemotional Traits—Individual differences in CU traits were measured using the Inventory of Callous-Unemotional Traits (ICU), which consists of 24 items comprising 4 scales: callous, uncaring, careless and unemotional (Kimonis et al., 2008). The callous scale includes items such as, "I do not feel remorseful when I do something wrong" and "What I think is right and wrong is different from what other people think." The uncaring scale includes items such as, "I am not concerned about the feelings of others" and "I seem very cold and uncaring to others." The unemotional scale includes items such as, "I do not let my feelings control me" and "I do not show my emotions to others." The careless scale includes items such as, "I do not care about doing things well" and "I do not like to put the time into doing things well." Adolescents rated items on a 4-point scale ranging from 1 (*Disagree*) to 4 (*Agree*). Controlling for age and gender, ICU composite scores were positively correlated with aggression ($r = .37$, $p < .001$) and rule-breaking behavior ($r = .38$, $p < .001$), and negatively correlated with prosocial behavior ($r = −.42$, p < .001) and peer relationship quality ($r = −.32$, $p < .001$), providing additional evidence of construct validity for the ICU in the current sample.

Results

Descriptive statistics (means and standard deviations), internal consistencies (Cronbach's alphas) and histograms were first examined to ensure normality and reliability of study variables (see Table 1). Careless and uncaring scales were log-transformed to correct for positive skew[1], and the distributions of all remaining scales approximated normality. Analyses were conducted in four steps using M*plus* software version 7.1. Using the categorical option (Muthén & Muthén, 1998–2010), items were treated as ordered categorical indicators in confirmatory factor analysis models, which were estimated using robust weighted least squares (Flora & Curran, 2004). For all analyses, standard errors and model statistics were adjusted for nonindependence of data from children living in the same household (i.e. sibling clusters; Asparouhov & Muthén, 2006) using the Complex Survey option (Muthén & Muthén, 1998–2010). For phenotypic analyses, this approach was necessary because siblings from the same family contributed multiple observations. For behavior genetic analyses, this approach was necessary because triplet pairs from the same family contributed multiple observations. Twin-pair correlations and behavioral genetic model parameters control for the main effects of age, sex and age × sex interaction (McGue & Bouchard, 1984).

Step #1: Confirmatory Factor Analysis Models (CFAs) of the ICU

To inform the construction of valid scale scores to be used in behavior genetic analyses, we first examined the factor structure of CU traits. Although the ICU was originally designed to have 4 subscales, CFA models were necessary, because exploratory factor analytic research

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[1]For careless and uncaring traits, multivariate twin models were fit using both log-transformed and non-transformed scales. Results remained largely unchanged in terms of parameter estimates and confidence intervals. M*plus* output scripts are available from first author upon request.

has found evidence for a 3-factor structure of CU traits in adolescence, and the best-fitting factor structures have varied across studies (Kimonis et al., 2008; Essau, Sasagawa & Frick, 2006). Because the factor structure of the Big Five (including using unit-weighted sum scores) has been well validated (Chiorri, Marsh, Ubbiali & Donati, 2015; John, Naumann, & Soto, 2008; Marsh et al., 2010; Marsh, Nagengast, & Morin, 2013), we did not investigate its factor structure here.

A unidimensional model was fit to provide a baseline model for evaluating various three-factor and four-factor structures. In this model, all 24 items from the ICU were specified as categorical indicators of a single latent construct. Next, a correlated three-factor model was fit to the data, which had items load onto three correlated, latent factors: callousness, uncaring and unemotional (Kimonis et al., 2008). The third measurement model was a hierarchical three-factor solution, which assumed a general dimension common to three specific factors. In this model, all items loaded onto three distinct (uncorrelated), lower-order factors, which in turn loaded onto a general, higher-order factor. The fourth measurement model was a three-factor bifactor solution, which had all items individually load onto a single general factor, as well as one of three specific, uncorrelated factors. Finally, following the original construction of the ICU scale, we fit a series of four-factor solutions. Model structure and specifications for four-factor solutions were identical to the three-factor solutions outlined above, except items loaded onto four distinct factors: callous, uncaring, careless and unemotional.

Seven models were tested, and fit indices (Model χ^2, RMSEA, and CFI) for the four-factor models were superior to those of the unidimensional and three-factor models (see Table S1 in the Online Supplement), both when controlling for the effects of age, sex and their interaction and in a model without covariates. Consistent with the original development of the ICU, a four-factor bifactor solution with correlated residuals for items of negative valence (e.g. "I do not…") was the best fitting model. In this solution, after loading onto the bifactor, items from the callous subscale had negative loadings or did not significantly load onto the unique callous factor. This suggests the callous subscale was largely isomorphic with a general CU factor, which may account for why it had relatively low internal consistency ($\alpha = .50$). Based on this solution, we constructed callous, careless, uncaring and unemotional subscale scores for use in behavioral genetic analyses by averaging scores on representative subscale items, which correspond to the original development of the ICU[2]. Observed scores, as opposed to latent measurement models, were carried forward to behavior genetic analyses for pragmatic reasons – to decrease the required number of freely estimated parameters and to facilitate model convergence.

Step #2: Univariate Twin Models

The classic twin model decomposes observed variance in a phenotype into *additive* genetic variance (*A*), nonshared environmental variance, plus measurement error (*E*), and either *dominance* genetic variance (*D*) or shared environmental variance (*C*).[3] For MZ twins,

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[2]A composite score (mean) of all 24 ICU items, representing the general factor, was constructed and subjected to the same univariate and multivariate data analytic procedures as the other CU subscales; for the sake of brevity, these results are only presented in the Online Supplement.

cross-twin correlations between A factors and between D factors are both fixed to 1.0, reflecting the fact that MZ twins share 100% of segregating genes. For DZ twins these constraints are .50 and .25 for A and D factors, respectively. By definition, MZ and DZ cross-twin correlations between C factors and between E factors are fixed to 1.0 and 0, respectively.

Twin-pair correlations were estimated for each of 9 phenotypes (4 ICU subscales and 5 BFI subscales) and are reported in Table S2 found in the Online Supplement. To guide multivariate analysis, the total phenotypic variance in each of the CU traits and Big Five personality domains was decomposed into latent genetic and environmental factors using univariate twin models. First, models that estimate additive genetic, shared environmental and nonshared environmental variance (ACE) were fit to determine whether it was necessary to model shared-environmental influences, and results revealed no evidence of shared environmental variance in any phenotype (see Table S3 in the Online Supplement). Consistent with nonadditive genetic influence, MZ twin-pair correlations were routinely more than double the DZ correlations. Therefore, models that estimate additive genetic, dominance genetic and nonshared environmental variance were fit to each phenotype. For 8 of 9 phenotypes, estimates were greater than zero, although confidence intervals were wide for agreeableness ($d^2 = .134$, CI.95% = $-.579, .846$, $p > .10$), neuroticism ($d^2 = .224$, CI.95% = $-.007, .455$, $p > .10$), careless ($d^2 = .279$, CI.95% = $-.396, .954$, $p > .10$), and uncaring traits ($d^2 = .150$, CI.95% = $-.555, .855$, $p > .10$). There was stronger evidence of dominant genetic influences for extraversion ($d^2 = .445$, CI.95% = $.225, .665$, $p < .001$), conscientiousness ($d^2 = .422$, CI.95% = $.263, .580$, $p < .001$), neuroticism ($d^2 = .224$, CI.95% = $-.007, .455$, $p = .057$), openness ($d^2 = .445$, CI.95% = $.298, .593$, $p < .001$) and callous traits ($d^2 = .418$, CI.95% = $.285, .510$, $p < .001$). For certain traits (e.g. agreeableness) nested model comparisons and predictive fit indices led to marginal or equivocal decisions regarding best fitting models (see Table S4A and Table S4B in Online Supplement). However, given that estimates of non-additive genetic influence were often greater than zero, and that power increases in a structural equation modeling framework as the number of observed variables increases, ADE models were selected for use in multivariate analyses. The substantial non-additive genetic variances in Big Five personality

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[3] A person inherits two copies of each gene -- one from his or her mother and one from his or her father. Importantly, these two copies may be identical to one another (*homozygous*), or the person may inherit a different version from each parent (*heterozygous*). A person may therefore have 0, 1, or 2 copies of a particular version of a gene (alternate versions of a gene are called *alleles*). *Additive genes* differ from *dominant genes* in terms of what phenotype is expected for a person who has only 1 copy of an allele, i.e., for heterozygotes. For additive genes, someone with 1 copy of an allele is expected to have a phenotype intermediate between having 0 copies and having 2 copies. For example, if the G allele of a gene causes a person to be taller, then a person who inherits 2 copies of G is expected to be taller than a person than who inherits 1 copy. For dominance genetic effects, one allele (the dominant allele) suppresses the effect of the other allele (the recessive allele), such that a person with 1 copy of a dominant allele is expected to have the same phenotype as a person with 2 copies, and the recessive phenotype is not expressed unless the person has 0 copies of the dominant allele. For example, a person typically needs to inherit two copies of the (recessive) genetic variant that causes blue eyes in order to have blue eyes. Thus, dominance genetic effects will *reduce* the phenotypic similarity of dizygotic twins (who *are not* necessarily matched on the other copy of the gene) relative to what would be expected under an exclusively additive model, but will have equivalent effects on phenotypic similarity on monozygotic twins (who *are* necessarily matched on the other copy of the gene) relative to what would expected under an exclusively additive model. In addition to shared genes, shared environmental factors that occur at the family-level (such as socio-economic status, family structure, culture and religion) may also contribute to sibling similarity. Non-shared environmental factors that are uniquely experienced by each twins (such as differential parenting or peer groups), on the other hand, make siblings different from one another. The non-shared environment may also include the effects of measurement error and any genetic differences (e.g., mutations) between identical twins (Charney, 2012).

traits are largely consistent in magnitude with previous results obtained in a larger sample (n > 2000 pairs) of adolescent twins (Lewis, Haworth, & Plomin, 2014).

Step #3: Multivariate Twin Models

Guided by the results of Step #2, multivariate Cholesky decompositions were used to identify genetic and environmental influence on CU traits common to Big Five personality. Cholesky decompositions partition the total variance in two or more phenotypes *and their covariance* into latent genetic and environmental components. Results are displayed in the form of path diagrams (see Figure 1 and Table S6 in the online supplement for a comprehensive report of parameter estimates). Past research on the Big Five has found evidence that antisocial personality is most closely related to agreeable, conscientious and neurotic personality traits (Lynam et al., 2005; Samuel & Widiger, 2008). Therefore, these scales were selected as primary to CU traits in multivariate analyses.

Callous—The callous scale was regressed on the latent genetic and environmental factors that influence agreeable, conscientious and neurotic personality traits, and additionally allowed to have unique genetic and environmental components. This model showed good fit to the data ($\chi 2 = 61.961$, $p = .213$, *RMSEA* = .033, *CFI* = .965). First, the additive genetic cross-path from agreeableness ($b = -.380$, $p < .001$) to callous traits was significant. Second, the additive genetic ($b = .000$, $p = .085$) and dominance genetic ($b = .005$, $p = .853$) paths unique to callous traits approached zero. Finally, the non-shared environmental path from agreeableness to callous traits was significant ($b = -.199$, $p < .01$), as well as the non-shared environmental path unique to callous traits ($b = .743$, $p < .001$). These results indicate that additive genetic and non-shared environmental influences both contribute to the observed association between callous traits and agreeableness. Additionally, these results suggest that there is a substantial portion of non-shared environmental variance in callous traits unique of normal personality, but nearly no genetic variance that is unique of normal personality.

Careless—The model of carelessness predicted by agreeable, conscientious and neurotic personality showed good fit to the data ($\chi^2 = 67.037$, $p = .109$, *RMSEA* = .042, *CFI* = . 965,). First, the additive genetic cross-path from agreeableness to carelessness ($b = -.423$, $p = .001$) and the dominance genetic cross-path from conscientiousness ($b = -.405$, $p < .01$) to carelessness were significant. Second, the non-shared environmental cross-path from conscientiousness ($b = -.318$, $p < .001$) to careless traits was also significant. Finally, the additive genetic ($b = .002$, $p = .589$) and dominance genetic ($b = .001$, $p = .273$) paths unique to careless traits were estimated at approximately zero. These results indicate that non-additive genetic and non-shared environmental variance shared with conscientiousness, and to a lesser extent additive genetic variance shared with agreeableness, drives the observed association between careless traits and normal personality. Moreover, these results suggest that the entirety of genetic influences on careless traits is shared with conscientiousness and agreeableness. Thus, the current study provides little to no evidence of genetic influence on careless traits that is unique of normal personality.

Uncaring—Uncaring traits were modeled identically to callous and careless traits. This model showed good fit to the data ($\chi^2 = 47.661$, $p = .716$, *RMSEA* = .000, *CFI* = 1.000,).

Noteworthy results include additive genetic ($b = -.512$, $p < .001$) and non-shared environmental ($b = -.301$, $p < .001$) cross-paths from agreeableness to uncaring traits. Moreover, the additive genetic ($b = .000$, $p = .735$) and dominance genetic ($b = .015$, $p = .881$) paths unique to uncaring traits were not significant and approached zero. Thus, similar to callous and careless traits, these results indicate that genetic and non-shared environmental influences on agreeableness drive the association between uncaring traits and normal personality. Moreover, these results suggest that the genetics of uncaring traits are neither independent nor distinct from the genetics of normal personality.

Unemotional—Unemotional traits were modeled identically to the other CU traits. This model showed good fit to the data ($\chi^2 = 66.893$, $p = .112$, *RMSEA* = .042, *CFI* = .915). The additive ($b = .000$, $p = .318$) and dominance ($b = .001$, $p = .476$) genetic paths unique to unemotional traits were not significant and equal to zero. Additionally, all genetic cross-paths were estimated near zero ($b_{range} = .000$–.095) and failed to reach significance (i.e. $p > .10$), which was expected given univariate twin models revealed no evidence of additive or non-additive genetic influences on unemotional traits.

Compared to other CU traits, unemotional traits showed unique phenotypic associations with Big Five personality traits. Mainly, unemotional traits showed relatively strong associations with extraversion ($r = -.406$, $p < .001$) and openness ($r = .141$, $p < .001$), and no association with conscientiousness ($r = -.009$, $p = .840$). Therefore, a second model was fit, in which the unemotional scale was regressed on the latent genetic and environmental factors that influence extraversion, openness, and neuroticism. This model showed improved fit to the data (model $\chi^2 = 54.976$, $p = .437$, *RMSEA* = .011, *CFI* = .995). Again, additive ($b = .000$, $p = .439$) and dominant ($b = .000$, $p = .377$) genetic paths unique to unemotional traits were not significant and approximated zero. However, non-shared environmental cross-paths from extraversion ($b = -.472$, $p < .001$) and neuroticism ($b = -.220$, $p = .013$) to unemotional traits were significant. Similar to the first model, all genetic cross-paths failed to reach significance (i.e. $p > .10$). These results indicate that non-shared environmental influences common to extraversion and neuroticism predominantly drives the association between unemotional traits and normal personality. These results also suggest that unemotional traits have patterns of heritability and relationships with normative trait continua that are distinct from other CU traits.

Results of multivariate twin models are summarized in Figure 2. These results suggest that genetic variance underlying CU traits overlaps entirely with genetic variance underlying Big Five personality, specifically agreeableness and conscientiousness. To the extent that there is phenotypic variance in CU traits distinct from normal personality, it reflects environmental influences unique to the individual (plus measurement error).

Step #4: IRT Analyses

The results of step #3 indicated that CU traits, measured by the ICU, are largely affected by the same genetic liabilities as those affecting Big Five personality traits. Although this might, *at face*, undermine the utility of the ICU as a clinical instrument, the ICU may be more sensitive at detecting scores at extreme, clinically relevant, ends of trait continua.

Therefore, we conducted an Item Response Theory (IRT) analysis to compare the performance of BFI and ICU items in measuring personality variation at the extreme ends of normal dimensions of personality. Specifically, we fit a multivariate two parameter logistic IRT model with five latent factors defined by ordered categorical responses from items of the five subscales of the BFI. Guided by the results of step #3, subsets of the ICU items, also specified as ordered categorical indicators, were allowed to load onto one or more latent Big Five factors (e.g., callous items were allowed to load onto factors defined by agreeableness, conscientiousness, and neuroticism items). Response thresholds and item discrimination parameters are reported in Table S5 in the online supplement.

This model was used to estimate *total item information* for BFI and ICU items that contributed to each latent factor. Information is inversely related to the standard error of measurement; that is, constructs are measured most reliably at the point in the latent trait continuum where information is maximized (Baker, 2001, p. 104). Item information is maximized when items are matched in "difficulty" to the sample being measured; for example, an item from the quantitative GRE is very informative regarding math ability among college graduates but not at all among 1st graders (Embretson & Reise, 2000). Item information curves are additive, such that information from a set (or subset) of items comprising a test can be aggregated. A test composed of items that span a broad range of difficulties will yield a total information curve that is flat across the range of the latent trait; individuals who are high, low, and intermediate on the latent trait will all be measured with more or less equal precision (Embretson & Reise, 2000, p. 270). In contrast, a test composed of items that are concentrated in a circumscribed range of difficulties will yield a peaked information curve; a focused subset of individuals will be measured very well but others will be measured with less precision. In some applications, such as characterizing individual differences in the general population, the former type of test might be preferred. In other cases, such as determining whether an individual meets a clinical cut-off or when screening for a rare disorder, the latter type of test might be preferred.

Of key interest in this analysis were the total item information curves for the latent traits defined by each of the five subscales of the BFI. Figure 3 plots the total information provided by items from the BFI (red/solid lines) and the ICU (blue/dashed lines) as a function of the (*z*-scored) latent trait. The bands above the test axis show the range of latent trait scores for which the total information provided by ICU items exceeds the total information provided by BFI items. The red squares and blue triangles above the top axis denote the points in the latent trait continuum at which the BFI and ICU items, respectively, were most informative.

BFI items behaved in our sample as one would expect. Across all five dimensions, the information curves are gently sloping, approximately symmetrical bells centered on the mean of the latent trait. Reflecting the assumption that common personality traits are normally distributed, with the majority of the population near the mean, BFI items are matched in difficulty to this trait distribution. Although not completely uninformative, BFI items are not well-suited for measuring individuals at the extreme ends of personality continua.

For agreeableness and conscientiousness, the information curves for ICU items are more peaked than the information curves for BFI items; the location of that peak is lower than the location of the BFI peak; and the total item information from ICU items exceeds information from the BFI items for the left half of the distribution. This suggests that ICU items are more informative than BFI items in differentiating disagreeable and non-conscientious adolescents from *very* disagreeable and *very* non-conscientious adolescents, but are less informative regarding the positive end of these dimensions.

For neuroticism, the information curve was relatively flat across the trait distribution, and total information from ICU items matched BFI information at the extreme low end of neuroticism. For extraversion, the information curve for ICU items was approximately parallel to the information curve for BFI items, but total information for ICU items was lower across the entire range of the latent trait, which suggests that the unemotional scale is not "targeting" individuals at the extreme ends of the extraversion continuum. Finally, the information curve for ICU items was flat and negligible across the range of openness. Consistent with results from multivariate genetic models that found no significant associations between openness and ICU subscales, these results indicate that CU traits are largely uninformative regarding individual differences in openness.

Overall, results from IRT analyses suggest that the BFI performed in our sample as intended: It is an all-purpose measure that characterizes all five dimensions of normal personality, and scales are informative across the full range of the latent traits but best suited for measuring the "average" individual. In contrast, the ICU is a more targeted measure that is particularly well-suited for discriminating among individuals who have average to very low levels of agreeableness and conscientiousness. Clinicians and researchers can capitalize on these measures' complementary strengths by incorporating both in studies designed to characterize the full spectrum of personality risk for antisocial behavior outcomes, spanning from normal range agreeableness and conscientiousness to more extreme ranges of these dimensions, which characterize the highly callous and unemotional.

Discussion

The primary goal of the current study was to examine the genetic and environmental etiology of CU traits that is common to and unique of a general model of personality. This study provides novel behavior genetic evidence in favor of a dimensional perspective that emphasizes the continuity between normal variations in common personality and CU traits. Results suggest that the genetics of CU traits are neither independent nor distinct from the genetics of normal personality. Rather, non-shared environmental influence on CU traits (including measurement error) differentiates these behavioral dispositions from normal dimensions of personality. More specifically, the genetic basis of callous, careless and uncaring traits can be effectively described by the genes that underlie agreeableness and conscientiousness. The etiology of unemotional traits, on the other hand, was predominantly shared with environmental liabilities for extraversion and neuroticism. Thus, results of the current study are consistent with conceptualizing CU and normal personality traits as manifestations of the same underlying dimensions of genetic risk.

However, our findings of nearly complete genetic overlap between CU traits and normal personality should not be interpreted to suggest the ICU lacks utility as a theoretical construct or clinical measure. First, CU traits were associated with multiple dimensions of personality, primarily agreeableness and conscientiousness and, to a lesser extent, neuroticism and extraversion. This suggests that individuals who score highly on subscales of the ICU occupy a specific zone of multivariate personality space – non-conscientious, highly disagreeable, lacking anxiety and expressive affect. More specifically, results of the current study suggest callous and uncaring traits lie at the multivariate intersection of extremely low levels of agreeableness, conscientiousness and neuroticism. Careless traits show weaker associations with neurotic tendencies and, rather, are predominantly characterized by low levels of agreeableness and conscientiousness. Finally, unemotional traits denote behavioral and affect dispositions that emerge from the concurrence of extremely lows levels of extraversion, neuroticism and openness to experience. Second, IRT analyses indicate that the ICU is a targeted measure that is more informative than the BFI in characterizing individuals at the low end of the agreeableness and conscientiousness spectra.

The current study measured general personality functioning in terms of five broad dimensions, each of which taps a set of genes that influence an array of affective, behavioral and cognitive dispositions. Past research, however, suggests that fine-grained personality facets may provide greater insight into *specific* psychopathologies (Paunonen & Ashton, 2001; Paunonen, 1998; Samuel & Widiger, 2008). For example, a meta-analysis of facet-level associations between the Big Five and DSM-IV-TR personality disorders indicate that the negative association between antisocial personality and conscientiousness is driven more by low levels of deliberation, self-discipline and dutifulness, as opposed to order and achievement striving (Samuel & Widiger, 2008). Moreover, recent behavioral genetic research has found that unique genetic influences act on personality facets above and beyond common influences mediated by higher-order personality traits (Briley & Tucker-Drob, 2012). Thus, additional future research could investigate the genetic associations between CU traits and personality measured at the facet level, in order to identify specific facets of, for example, agreeableness that drives its relation with CU traits.

Finally, and most importantly, there was substantial variation in the ICU that was unique of general personality, and this unique variance was due to environmental influences particular to each twin. In fact, there was no evidence of additive or non-additive genetic influences on unemotional traits, an essential component of the CU construct. Identifying which specific environmental experiences and contexts differentiate twins who share the same underlying genetic dispositions, such that one becomes more callous than the other, remains a perplexing and important question for future research. Differential parenting is an obvious potential culprit, as longitudinal research in children and adolescents has found that harsh and inconsistent parenting prospectively predicts increases in CU traits (see review by Waller, Gardner, & Hyde, 2013). However, the only genetically informed study of parenting and CU traits failed to find an association between negative parental discipline and CU traits when comparing within MZ twin pairs (Viding, Fontaine, Oliver, & Plomin, 2009), suggesting that associations between parenting and child CU traits may reflect passive or evocative gene-environment correlations (Plomin, DeFries, & Loehlin, 1977). More generally, research using 7-year old twins suggests that the unique environmental influences

on CU traits overlap only modestly with unique environmental influences on conduct disorder symptoms (r = .40 in boys and .19 in girls; Viding, Frick, & Plomin, 2007). Additional longitudinal and genetically-informed research is necessary to parse the particular environmental experiences that push genetically vulnerable youth toward the CU phenotype.

These results were obtained in an ethnically diverse sample of adolescents who were recruited from public schools and who are broadly representative of the community with regards to cognitive functioning and involvement in antisocial behavior. Nearly all participants reported at least one delinquent act. It remains an open question whether the genetic and environmental relations between normal personality and CU traits are consistent in other populations, such as clinical or forensic samples. However, the current sample of adolescents reported levels of CU traits similar to those observed in a sample of detained juvenile offenders (Munoz, Frick, Kimonis & Aucoin, 2008). Thus, despite being originally developed and implemented to identify extreme forms of antisocial behavior, our results suggest that a certain degree of callousness and unemotionality is normative among teenagers. This finding is consistent with results from a very large (N > 1,000,000), cross-national study of age differences in Big Five personality, which found pronounced declines in average levels of conscientiousness and agreeableness during adolescence, followed by rebounds in these traits in young adulthood (Soto, John, Gosling, & Potter, 2011).

In the current study, CU traits and Big Five personality were measured exclusively by adolescent self-report. Previous research has found that the stability of CU traits depends on reporter, with highest rank-order stability seen for parent-reported CU and lowest for self-reported (reviewed in Frick, Ray, Thornton, & Kahn, 2014). It is unclear whether the pattern of personality correlates depends on reporter. Therefore, the current results would be further substantiated by measuring these constructs using parent, peer, and teacher report. Finally, analyses were conducted with a moderately sized sample of adolescents, which is small enough to warrant some caution when interpreting results. While we were able to detect significant genetic overlap between the Big Five and the ICU, future work with larger sample sizes will be necessary to determine more precisely the magnitude of residual genetic effects on callous-unemotional traits. Notably, however, the current results are highly consistent with a behavioral genetic analysis of Big Five traits in a considerably larger sample of adolescent twins (Lewis et al., 2014).

Our results may also be informative about ongoing efforts to identify molecular genetics correlates of CU traits. Specifically, both genome wide association studies (GWAS) and genome wide complex trait analysis (GCTA) have been used to search for the genetic underpinnings of CU traits and associated behavior problems (Viding et al., 2013; Trzaskowski, Dale & Plomin, 2013). GWAS tests the associations between individual polymorphisms and a trait (Hirschhorn & Daly, 2005), whereas GCTA estimates the aggregate variance in a trait collectively explained by all measured polymorphisms across the entire genome (Yang, Lee, Goddard & Visscher, 2011). Notably, GWAS has largely failed to identify genetic loci associated with CU traits (Viding et al., 2013), and GCTA has failed to recover twin-based estimates of heritability of childhood behavior problems (Trzaskowski et al., 2013). Despite their sophistication, a shared weakness of both methods

is extremely low power for detecting non-additive genetic effects (McCarthy et al., 2008). The results of the current study suggest a non-negligible portion of the genetic variance that underlies CU traits is non-additive and, moreover, is shared with normal personality, for which GWAS and GCTA have also produced underwhelming results (De Moor et al. 2012; Verweij et al., 2010).

In this study, all analyses controlled for the gender differences in mean levels of CU traits, but because of our moderate sample size, we did not model qualitative or quantitative sex differences in the etiology of CU traits. Thus, our models assume that the same genes and same environmental factors affect both males and females, and that the magnitudes of these genetic and environmental influences are equal in both males and females. Although males tend to be higher on CU traits than females, the ICU scale has been found to be invariant across gender (Essau, Sasagawa & Frick, 2006). Moreover, a recent longitudinal study found that the number and shape of CU trajectories were highly similar across gender (Fontaine, Rijsdijk, McCrory & Viding, 2010), and results of a large-scale behavioral genetic study revealed no evidence for sex differences in the genetic and environmental etiology of CU traits (Forsman, Lichtenstein, Andershed & Larsson, 2008). Future research could aim to identify mechanisms that explain observed gender differences in CU traits, which currently remain largely unknown.

Future efforts to understand the development of CU traits in infancy, childhood, and adolescence may be informed by research on the developmental dynamics of normal personality. That is, understanding genetic risk for CU traits depends on understanding the basic mechanisms underlying the emergence of individual differences in agreeableness, conscientiousness, neuroticism, and extraversion over the course of development. This proposition is consistent with Frick and colleagues' (2009, 2014) theoretical model of the development of CU traits, which posits that children with certain temperamental factors – which are not, in and of themselves, necessarily pathological – are more likely to experience deficits in the development of empathy and guilt in early childhood. In fact, there is already evidence that the developmental dynamics of normal personality and CU traits are similar. For example, a recent meta-analysis of longitudinal behavioral genetic studies of Big Five personality traits found that Big Five personality traits show moderate stability even in very early childhood and this early stability is primarily due to genetic factors (Briley & Tucker-Drob, 2014). This pattern of results is consistent with emerging research on the longitudinal stability of CU traits, which also show substantial phenotypic and genetic stability in early childhood (Frick et al., 2014). Overall, the finding that genetic influences on CU traits are indistinguishable from genetic influences on general personality underscores the importance of a developmental psychopathology perspective, which views the study of normal and atypical development as mutually informative. The multi-level cascade of proximate mechanisms that link genes to behavior, including behaviors characterized by callousness and unemotionality, remains largely unknown. However, results of the current study suggest that understanding the developmental dynamics of normal personality will informing a deeper understanding of the development of callous and unemotional behavior.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

Acknowledgments

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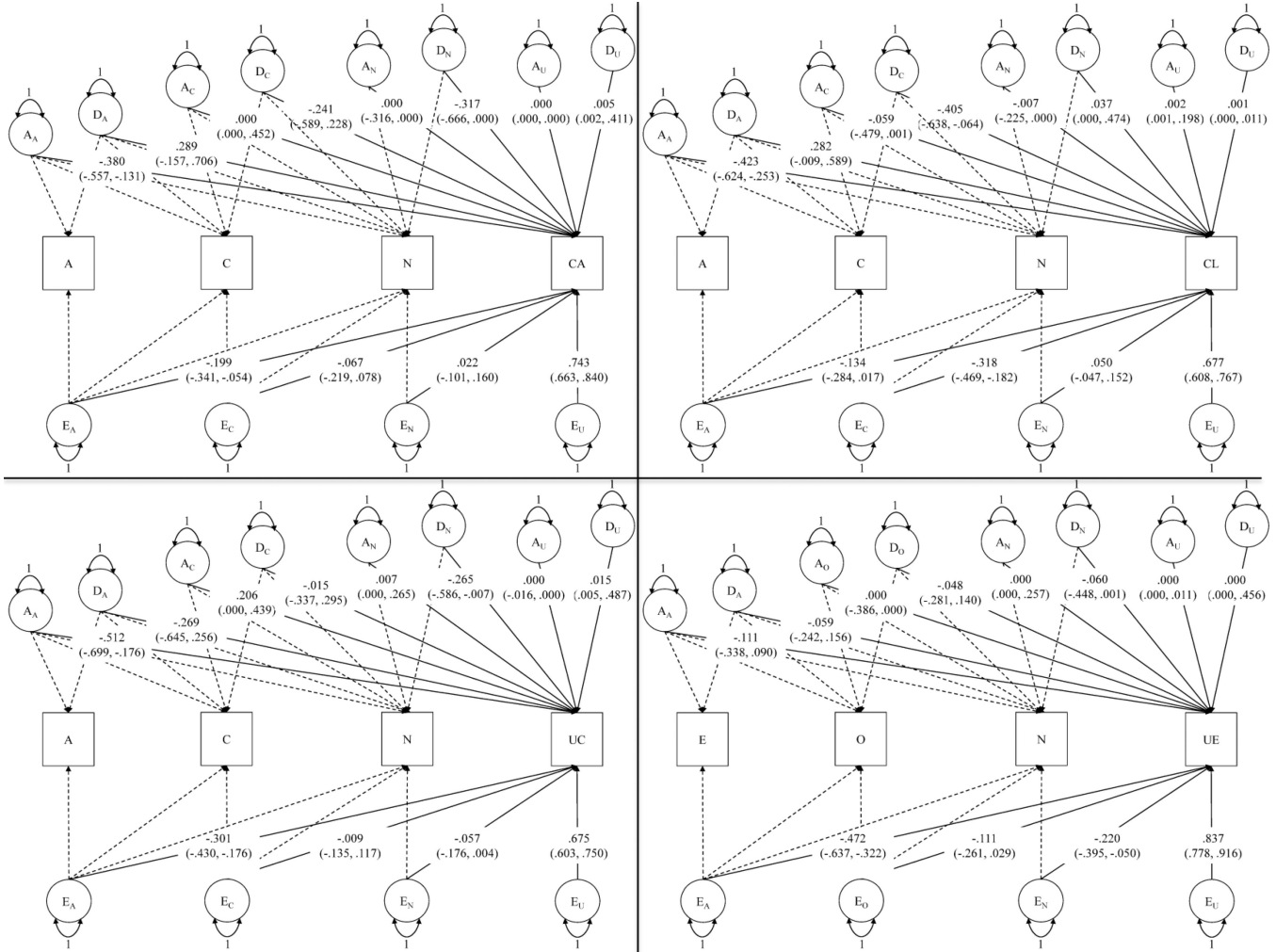
Figure 1.
Path Diagrams for Multivariate Twin Models of CU Traits & Big Five Personality
Note. Additive genetic, dominance genetic and non-shared environmental variance in callous
(CA), careless (CL), uncaring (UC), and unemotional (UE) traits common to –and unique
of– agreeableness (A), conscientiousness (C), neuroticism (N), extraversion (E) & openness
(O). Unstandardized parameter estimates are reported. All pathways were estimated, but
estimates for dashed pathways were omitted to ease presentation. See Table S5 in the online
supplement for a comprehensive report of parameter estimates for each model. Parameter
estimates for a multivariate twin model of the ICU composite scale also reported in Table
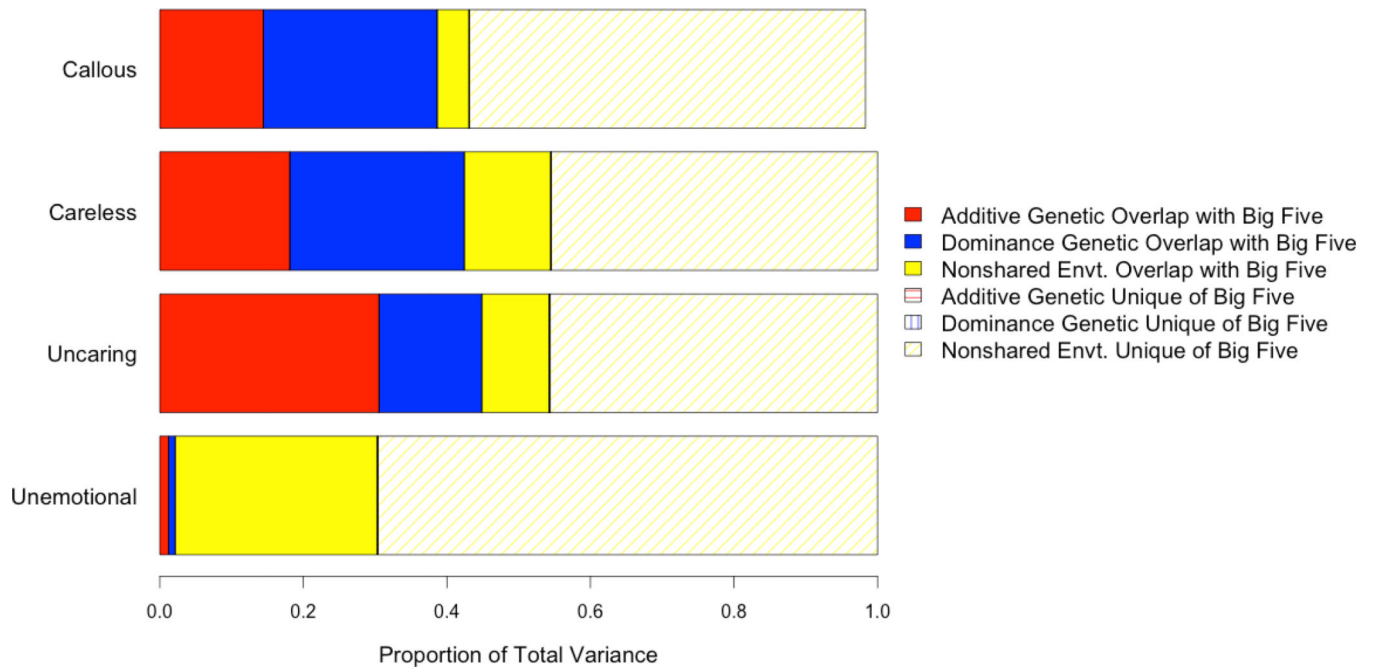S5.

Figure 2.
Proportions of Variance in Callous-Unemotional Traits Due to Additive Genetics, Dominance Genetics and Non-Shared Environmental Overlap with Normal Personality.
Note. Proportions of variance calculated from parameter estimates presented in Figure 1.
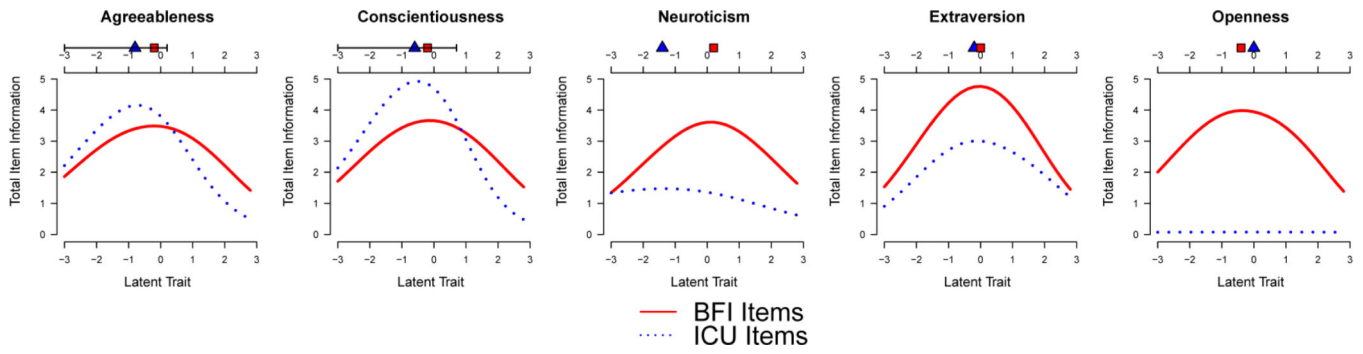
Figure 3.
Total Item Information Curves for BFI and ICU Item

Note. Information curves based on Item Response Theory model summarized in Table S1 of Online Supplement. BFI = Big Five Inventory. ICU = Inventory of Callous Unemotional Traits.

Table 1

Correlations, Descriptive Statistics & Internal Consistencies for Study Variables

N = 535		M (SD)	A	C	N	O	ICU	CA	CL	UC	UE
E	(α = .831)	3.275 (.721)	.124*	.044	−.133*	.046	−.257**	.021	−.080	−.131*	−.406**
A	(α = .779)	3.741 (.552)		.281**	−.235**	−.021	−.454**	−.326**	−.209**	−.568**	−.119*
C	(α = .791)	3.358 (.619)			−.210**	.031	−.399**	−.271**	−.578**	−.237**	−.009
N	(α = .788)	2.828 (.666)				.020	−.012	−.001	.113	.036	−.136*
O	(α = .740)	3.813 (.508)					−.090	−.011	−.055	−.008	−.141*
ICU	(α = .804)	1.880 (.311)						.692**	.619**	.713**	.563**
CA	(α = .500)	1.912 (.415)							.372**	.437**	.106
CL	(α = .782)	1.548 (.456)								.354**	−.019
UC	(α = .734)	1.505 (.430)									.164**
UE	(α = .757)	2.558 (.567)									

Note. Descriptive statistics are reported for non-transformed variables. α = Cronbach's alpha. M = mean. (SD) = standard deviation. Partial correlations controlling for age, gender and their interaction are reported for transformed variables; Careless and uncaring subscales were log-transformed and Big Five scales were computed from ipsatized items. E = Extraversion. A = Agreeableness. C = Conscientiousness. N = Neuroticism. O = Openness. ICU = Callous-unemotional composite score. CA = Callous subscale. CL = Careless subscale. UC = Uncaring subscale. UE = Unemotional subscale. CL = Careless subscale. UE = Uncaring subscale.

*
P(2-tailed) < .01.

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P(2-tailed) < .001