Early Warm-Rewarding Parenting Moderates the Genetic Contributions to Callous-Unemotional Traits in Childhood

Running head: WARM-REWARDING GENETIC CALLOUS-UNEMOTIONAL

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Abstract

Background: Previous gene-environment interaction studies of CU traits have relied on the candidate gene approach, which does not account for the entire genetic load of complex phenotypes. Moreover, these studies have not examined the role of positive environmental factors such as warm/rewarding parenting. The aim of the present study was to determine whether early warm/rewarding parenting moderates the genetic contributions (i.e., heritability) to callous-unemotional (CU) traits at school age. **Methods**: Data were collected in a population sample of 662 twin pairs (Quebec Newborn Twin Study – QNTS). Mothers reported on their warm/rewarding parenting. Teachers assessed children's CU traits. These reports were subjected to twin modelling. **Results**: CU traits were highly heritable, with the remaining variance accounted for by non-shared environmental factors. Warm/rewarding parenting significantly moderated the role of genes in CU traits; heritability was lower when children received high warm/rewarding parenting than when they were exposed to low warm/rewarding parenting. **Conclusions**: High warm/rewarding parenting may partly impede the genetic expression of CU traits. Developmental models of CU traits need to account for such gene-environment processes.

Keywords: Callous-unemotional traits, Warm/rewarding parenting, Gene-environment interaction, Twin studies.

Children with callous-Unemotional (CU) traits are characterized by a lack of guilt, a disregard for others' feelings (or lack of empathy) and a shallow display of emotions. These features are a distinguishing characteristic of psychopathy in adulthood (Cleckley, 1976; Frick, 2009), and index early risk of developing psychopathy and severe/stable antisocial behaviour across the lifespan (Frick, Ray, Thornton & Kahn, 2014). Accordingly, there is a need to understand the child and family factors involved in the development of CU traits.

Developmental theories of CU traits posit that they result from a failure to develop the moral emotions of guilt and empathy (i.e., conscience; Frick et al., 2014). These theories are grounded on the documented associations of CU traits with low empathy (Dadds, Cauchi, Wimalaweera, Hawes, & Brennan, 2012; Dadds et al., 2009; Frick, 2009), low guilt/remorse (Lotze, Ravindran, & Myers, 2010; Pardini & Byrd, 2012), and low prosocial behavior (Roose, Bijttebier, Decoene, Claes, & Frick, 2010; Sakai, Dalwani, Gelhorn, Mikulich-Gilbertson, & Crowley, 2012). Such failure in conscience development among children displaying CU traits could result from early atypical affective processing (Frick et al., 2014). Indeed, these children tend to show poor behavioral modulation following punishment (Frick & Viding, 2009), as well as reduced behavioral and neural responses to other people's distress (e.g., fearful faces; Blair, Leibenluft, & Pine, 2014; Jones, Laurens, Herba, Barker, & Viding, 2009; Marsh & Blair, 2008; Sebastian et al., 2014; Viding et al., 2012). Thus, learning about societal norms and what is morally wrong may be disrupted because children with high CU traits do not learn from punishments and do not find other people's distress aversive (Blair et al., 2014).

Past research indicates that an initial understanding of right and wrong emerges early in life (Eisenberg & Fables, 1998; Kochanska, Gross, Lin & Nichols, 2002), and that a substantial degree of variation in CU traits is accounted for by genetic factors (i.e., heritability; see Viding

& McCrory, 2012). This could also be the case for the affective processing variables underlying CU traits. At the same time, not all children who process affect atypically show later deficits in empathy and guilt (e.g., Cornell & Frick, 2007) and CU traits are not uniformly stable across children, partly due to environmental influences (Fontaine, Rijsdijk, McCrory & Viding, 2010; Pardini & Loeber, 2008). Thus, despite the importance of genetic factors in accounting for individual differences in CU traits, environments are likely to play a substantial role regarding how these traits emerge. While independent contributions of genetic vulnerability and environment have been extensively documented (Viding & McCrory, 2012), environments may combine with genetic vulnerability in shaping CU traits through gene-environment interactions (GxE; Frick et al., 2014; Viding & McCrory, 2015) and this has not been investigated systematically to date.

Previous twin studies of CU traits decomposed the variance attributable to latent genetic and environmental factors but did not consider measured environmental risk factors and, therefore, did not test whether GxE account for the manifestation of these traits. There is preliminary, molecular genetic evidence suggesting that the expression of genetic risk for CU traits is affected by environmental conditions. A first, cross-sectional study found that having the long allele of 5-HTTLPR, a gene involved in the metabolism of serotonin, increased risk for CU traits in low (as compared to higher) socioeconomic backgrounds (Sadeh et al., 2010). Second, Willoughby, Mills-Koonce, Propper and Waschbusch (2013) reported that the association between a specific methionine allele of the brain-derived neurotrophic factor – a gene involved in neuronal survival and growth – and CU traits was moderated by the degree of harsh-intrusive parenting in infancy.

Previous studies have documented GxE through a limited number of candidate genes, which does not capture the full genetic load for complex phenotypes. Furthermore, they only examined the role of adverse environment. Yet, positive aspects of the early environment – particularly warm/rewarding parenting – have been more consistently associated with CU traits than adverse environments (Kroneman, Hipwell, Loeber, Koot, & Pardini, 2011; Pasalich, Dadds, Hawes, & Brennan, 2012; Pasalich, Witkiewitz, McMahor & Pinderhughes, 2016). Recently, warm and rewarding forms of parenting have been shown to mitigate the contributions of genetic factors – as indexed by proxies such parent history of antisocial behavior and fearless temperament – to CU traits (Hyde et al., 2016; Waller et al., 2016). In other words, parental warmth and rewards may help shape aspects of norm compliance and conscience development that protect from a genetic vulnerability for developing CU traits. One above-mentioned study has probed the role of sensitive parenting to the development of CU traits, but the measure was general, including aspects pertaining to attachment, animation and stimulation of development (Willoughby et al., 2013; see above). Finally, available studies were either cross-sectional (Sadeh et al., 2010) or contiguously assessed environment and CU traits (Willoughby et al., 2013), thus limiting inferences regarding the direction of associations.

In summary, past research indicates that warm/rewarding parenting can buffer the development of CU traits. However, no study has examined the degree to which the relative importance of genetic and environmental factors in accounting for CU traits vary as a function of warm/rewarding parenting. The goal of this study was to determine whether early warm/rewarding parenting (63 months) moderates the relative importance of genetic contributions to childhood CU traits (7, 9, 10 and 12 years). Given the caveats of the candidate gene approach, we turned to twin modelling, which provides a general assessment of genetic

contributions to a given phenotype (i.e., heritability). To provide a more robust assessment of children's CU traits, the present study relied on repeated assessment across childhood. Warm/rewarding parenting was assessed before school entry to evaluate its predictive and interactive role with respect to later CU traits. Furthermore, because children's initial disruptive tendencies tend to consolidate with age, and progressively evoke parental reactions (i.e., evocative rGE; Scarr & McCartney, 1983), the late preschool period was more likely to index the full challenging context of parenting children with CU traits. Accordingly, we controlled for possible rGE between CU traits and warm/rewarding parenting in testing for GxE.

Methods

Participants. Participants were from the Quebec Newborn Twin Study (QNTS; Boivin et al., 2013). Over 660 families from the Greater Montreal area were initially enrolled (1995-1998) and followed annually from birth on a host of individual, social, family, and school characteristics. Parents' consent was obtained before each data collection. Teachers' consent was also obtained for those who acted as respondents on the CU assessments. Zygosity was initially assessed via questionnaire (Goldsmith, 1991), and ascertained with a 96% correspondence through genotyping (Forget-Dubois et al., 2003). The ethics boards of St.-Justine Hospital and Laval University, as well as the boards of the participating schools approved all procedures. As the number of twins varied across measures, we employed a Full Information Maximum Likelihood (FIML) approach in order to include a maximum of participants with missing data (see Table 1).

Measures. Warm/rewarding parenting was self-reported when the twins were on average 63 months old. The items assessed mothers' perceptions of their own tendencies to encourage, reward and spend time with their child: "I have talked and/or played games with my child", "I

told my child I was proud of him/her", "I have spent time with my child playing sports and/or doing activities", "I have praised my child for a good deed" (0–5 Likert scale). In the present study, all internal consistencies were verified by selecting one twin per pair. The internal consistency of the warm/rewarding parenting scale was acceptable ($\alpha = .70$). Mean scores were computed, with high mean scores indicating high levels of warm/rewarding parenting. As twin concordance was very high for this measure (.83), we computed a mean family score by averaging the warm/rewarding parenting means for both twins. Thus, warm/rewarding parenting varied across, but not within families, and was used as a family-wide environmental moderator in GxE testing.

Teachers rated CU levels at 7, 9, 10 and 12 years via a five-item questionnaire assessing their perceptions of target children (0–2 Likert scale). Three items came from the Inventory of Callous-Unemotional Traits (Frick, 2003), currently the most detailed measure of CU traits in youths: "he/she did not seem to feel guilty after misbehaving", "his/her emotions appear superficial", "he/she has been insensitive of other people's feelings". The remaining two items were selected from the Antisocial Process Screening Device (APSD; Frick & Hare, 2001): "he/she does not keep promises", "he/she used or conned others". Means were computed, with a high mean score indicating high levels of CU traits ($\alpha = .73–.76$). An aggregate CU score was created by averaging the mean scores as they were all correlated ($r_{7\text{-}9} = .40$, $p < .001$; $r_{7\text{-}10} = .36$, $p < .001$; $r_{7\text{-}12} = .26$, $p < .001$; $r_{9\text{-}10} = .49$, $p < .001$; $r_{9\text{-}12} = .35$, $p < .001$; $r_{10\text{-}12} = .41$, $p < .001$).

Statistical analysis. The CU scale was positively skewed. Thus, we applied a logarithmic transformation. We report the findings using the transformed scale, except in Table 1. Scores were Z-standardized for genetic analysis.

GxE testing requires determining whether the outcome has statistically significant genetic contributions. Thus, we first conducted a full univariate ACE twin model on the CU traits scores. The twin design's basic principle is to determine whether, on a given phenotype, similarity between monozygotic (MZ) twins, sharing 100% of their genes, exceeds similarity between dizygotic (DZ) twins, who share on average 50% of their genes. This allows individual differences on a given phenotype to be disentangled into additive genetic (A), shared environmental (C; environments that increase sibling similarity), and nonshared environmental (E; environments that increase sibling differences) sources of variance. Additive genetic influences reflect the extent to which MZ twin pairs are more similar than DZ twin pairs.

Second, we tested the presence of gene-environment interaction through a GxE model for continuously distributed variables (Price & Jaffee, 2008). In this model, the latent sources of variance A, C and E load on CU traits with unstandardized beta coefficients *a*, *c* and *e*, respectively. A variable assessing a family-level measured environment (i.e., warm/rewarding parenting) is posited to contribute to CU traits (*b*), and may also be correlated with *a* due to a potential rGE (*r*). An interaction term is also incorporated into *a*, therefore testing moderation of the family environment on the genetic contributions to CU traits (*ma*). In other words, *a* is a beta coefficient reflecting the main genetic contribution, and *ma* indicates to what extent the genetic contribution varies linearly as a function of the family environment.

To test whether the parameters were statistically significant, we compared models where parameters were freely estimated versus fixed to zero. We first considered a full model where *a*, *c*, *e*, *b*, *ma* and *r* were all freely estimated. Second, we tested a nested model where *r* was fixed to zero. Then, we tested a nested model where *ma* (in addition to *r*) was fixed to zero. The *ma* interaction term was considered statistically significant only if the *r* parameter was not. Finally, a

statistically significant *ma* interaction was decomposed to assess heritability of CU traits across different absolute values of warm/rewarding parenting.

Descriptive statistics and Pearson's correlations were obtained using the Statistical Package for the Social Sciences (SPSS 20.0, IBM Corp, 2011). Mplus 6.11 (Muthén & Muthén, 1998-2011) was used to perform the genetic models. As the default estimator when using Mplus, FIML permitted the use of all available data. In univariate analysis, model fit was assessed through chi square goodness of fit statistic (χ2), Akaike's Information Criterion (AIC), Scaled Comparative Fit Index (CFI), Scaled Root Mean Square Error of Approximation (RMSEA), and Standardized Root Mean Square Residual (SRMR). The likelihood-ratio chi-square tests, the AIC and the BIC were used in multivariate genetic analysis.

Results

Descriptive statistics are displayed in Table 1. Boys (M = .32, SD = .34) displayed significantly higher CU traits than girls (M = .20, SD = .27); $t_{1031.29}$ = 6.16, p < .001, but did not differ from girls in warm/rewarding parenting; t_{880} = -.45, p = .651. CU traits were modestly negatively correlated with warm/rewarding parenting (r = -.14, p < .001).

(Insert Table 1 here)

The intra-class correlations in CU traits for MZ (*ICC* = .65; p < .000) versus DZ twins (*ICC* = .33; p < .001) suggested a significant heritability of CU traits (see Table 2). Accordingly, a full ACE model was tested, and revealed that genetic factors (A) accounted for 65% of the variance in CU traits, the remaining variance being associated with nonshared environmental factors (E).

(Insert Table 2 here)

Table 3 reports the full and nested multivariate genetic models. Examination of loglikelihood ratios and other fit indices indicated that fixing *r* to zero in the second model did not deteriorate the fit compared to the full model. The third model, where both *r* and *ma* were fixed to zero, had a significantly worse fit than the second model. Thus, the second model, where *ma* (but not *r*) was freely estimated, provided the best fit to the data, thus indicating significant GxE (*ma* = -14; $p < .01$). In this model, *a* (.68, $p < .001$), *e* (.60, $p < .001$) and *b* (-.11, $p < .01$) were also significant. There were no shared environment by warm/rewarding parenting (*mc*) or non-shared environment by warm/rewarding parenting (*me*) interaction (data not shown).

(Insert Table 3 here)

Figure 1 provides a graphical illustration of the significant interaction by depicting the values of additive genetic variance across different levels of warm/rewarding parenting. The role of genetic factors in CU traits decreased as child exposure to warm/rewarding parenting increased (values of warm/rewarding parenting = standardized additive genetic variance: -2 = .67; -1 = .62; 0 = .56; 1 = .48; 2 = .40). In other words, when children were exposed to higher levels of warm/rewarding parenting, their genetic contributions to CU traits were lower than when children were exposed to lower levels of warm/rewarding parenting.

(Insert Figure 1 here)

Discussion

The goal of the present study was to determine whether the relative importance of genetic and environmental factors on CU traits across childhood vary as a function of the degree of warm/rewarding parenting that the child receives at 63 months. Our univariate twin modelling showed that genetic factors accounted for a substantial degree of individual differences in CU traits, but the multivariate genetic modelling indicated that the degree of genetic influence on

variation in CU traits was less strong in environments characterised by early warm/rewarding parenting.

The high heritability of CU traits is consistent with past twin studies (43–70%; Viding & McCrory, 2012). The present study also found only a modest predictive (negative) association between warm/rewarding parenting and CU traits. This finding is in line with previous studies where modest/moderate, yet persistent correlations between early parenting and CU traits were found regardless of assessment method for parenting (i.e., observed [Hyde et al., 2016; Waller et al., 2012, 2014] vs. self-reported [Barker, Oliver, Viding, Salekin & Maughan, 2011; Hawes, Dadds, Frost & Hasking, 2011]), CU rater (i.e., mother [Barker et al., 2011; Hawes et al., 2011; Waller et al., 2012, 2014] vs. teacher [the present study]) and age at outcome (i.e., preschool [Hyde et al., 2016; Waller et al., 2012, 2014], middle childhood [the present study], adolescence [Hawes et al., 2011]).

Most importantly, the present study allowed the investigation of gene-environment interplay with respect to the relative importance of genetic and environmental factors in accounting for individual differences in CU traits in parenting environments varying in warmth/rewards. The genetic contributions to individual differences in CU traits were found to be lower in environments characterised by higher warm/rewarding parenting, compared with environments characterised by lower warm/rewarding parenting. In addition, the initial modest phenotypic association between warm/rewarding parenting and CU traits was not accounted for by genes (no rGE), and thus could not account for this GxE. All of this points to warm/rewarding parenting as a protective environmental factor that can counter genetic vulnerability to CU traits. This finding is in line with that of a recent adoption study that demonstrated that higher levels of adoptive mother positive reinforcement at 18 months predicted lower levels of CU traits at 27

months in children of biological mothers with history of antisocial behavior, thus indicating that the adoptive mother's positive reinforcement partly buffered the contribution of genetic risk for CU traits (Hyde et al., 2016; see also Waller et al., 2016).

The present GxE findings indicate that positive aspects of parent-child relationship can moderate the expression of genetic risk to CU traits and add to the evidence base regarding the importance of environmental factors in contributing to the developmental trajectories of CU traits (Fontaine et al., 2010; Pardini & Loeber, 2008). It has been proposed that warm/rewarding parenting *in response to prosocial behavior,* particularly early in life when such parenting behaviors can be implemented consistently, has a specific role in shaping the aspects of norm compliance and moral behavior in children at risk of developing antisocial/CU behavior (Frick et al., 2014). Warm/rewarding forms of parenting are more predictive of reduction in conduct problems in children with high CU traits (Kroneman et al., 2011; Pasalich et al., 2012, 2016), while harsh/hostile practices are more closely related to increased conduct problems in children without elevated levels of CU traits (Hipwell et al., 2007; Oxford, Cavell, & Hughes, 2003; Wootton, Frick, Shelton, & Silverthorn, 1997). Buffering the genetic risk for CU traits could be one reason why high warm/rewarding parenting is associated with lower CU traits over time (i.e., suppression process; Shanahan & Hofer, 2005). Caregiving environments encouraging prosocial behavior through consistent rewards could be protective for all children, but especially for those at risk for CU traits. Another possibility is that warm/rewarding parenting rather promotes genetic expression for empathy and prosocial behavior, thus protecting against the development of CU traits (i.e., facilitation process; Shanahan & Hofer, 2005). We need carefully conducted, longitudinal neurocognitive data to examine these two possibilities more closely. In

any case, the low magnitude of this moderation (i.e., heritability is still substantial for children exposed to high warm/rewarding parenting) suggests that the protective effect may be limited.

Our study employed a broad and powerful indicator of genetic vulnerability (i.e., heritability). This GxE test was also original in its use of warm/rewarding parenting as a moderator; this was warranted by the current stage of knowledge in the field. This study also relied on repeated measures of CU traits provided by different raters at each wave, thereby optimizing reliability and validity. Yet, several limitations are of note. First, all results were obtained from a non-normal and transformed CU variable. Log transformation considerably improved its distribution, but normality criteria were not reached. It is however common in population-based samples to have non-normal CU variables. Second, a limited number of items were included in the warm/rewarding and CU scales; this may have increased measurement error. In the case of CU traits, this problem was partly taken care of by averaging repeated measures, and despite the limited number of items on the warm/rewarding parenting scale, several statistics indicated limited measurement error on this variable (e.g., acceptable internal consistency, modest 'E' parameter in twin modelling).

The present GxE pattern points to the malleability not only of the CU construct, but also of its underlying genetic predisposition. Theoretical conceptualizations need to explicitly consider complex GxE processes as part of the development of CU traits. Developmental mechanisms underlying these GxE processes should also be clarified. In this regard, warm and rewarding forms of parenting may contribute to CU traits in part because children at risk for these traits have a reward-oriented response style and may particularly benefit from consistent rewarding of norm compliant behavior. If that is the case, children with a reward-oriented response style should benefit more than other children from high levels of warm/rewarding

parenting, and the absence of warm/rewarding parenting should impact them more. This possibility should be tested formally as this may not only inform developmental models, but could also help determine which groups of children benefit more from parenting training interventions in terms of increase in norm compliance and/or conscience development.

The nature of warm/rewarding parenting's contribution to CU traits could also be clarified at the molecular level. For instance, variations in heritability depending on an environment could reflect variations in gene coding and expression. The field of epigenetics in behavioral science is growing rapidly, providing us with unrivaled opportunities to understand how social stressors have lasting effects on development. A first step would however be to identify genes and genomic networks likely involved in neurobiological (e.g., amygdala hyporeactivity) and cognitive (e.g., poor emotion recognition) deficits at the core of CU traits. While the polygenic nature of inheritance is a challenge to the identification of risk genes, the need to understand what makes high CU children different from their peers is vital.

Conclusion. In brief, this was the first published study to document variations in the heritability of CU traits according to an environmental condition. Developmental models of CU traits will need to account for such G-E transactions in the future but first, our understanding of these processes should be informed by a detailed examination of the genetic roots of CU traits, as well as more systematic replication.

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Key points

- Previous studies that tested gene-environment interactions involved in CU traits relied on a candidate gene approach, which does not account for the entire genetic load of complex phenotypes. To our knowledge, our study is the first to address this question using a global indicator of genetic risk for CU traits (i.e., its heritability).
- Our study shows that the heritability of CU traits is lower when children receive more warm/rewarding parenting. In others words, high warm/rewarding parenting may be a protective factor against the genetic expression of CU traits.
- More data is needed to understand the nature of warm/rewarding parenting's contribution to CU traits. This could inform developmental models and intervention efforts.

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Table 1

Descriptive Statistics for Warm/Rewarding Parenting (WRP) and Callous-Unemotional (CU) Traits

Variables	*M* (*SD*)	Skewness (±2**SE*)	Kurtosis (±2**SE*)	*n*
WRP	3.75 (.61)	-.10 (-.27-.06)	-.21 (-.54-.12)	890
CU	.26 (.31)	1.79 (1.64-1.94)	3.56 (3.26-3.85)	1073

Note. The alpha for the warm/rewarding scale was derived at the item level, before averaging means over twins 1 and 2. The alpha for the CU scale was derived at the scale level.

Table 2

Monozygotic (MZ) and Dizygotic (DZ) Intraclass Correlations and Estimates of Heritability (A), Shared Environment (C), and Nonshared Environment (E) for Callous-Unemotional (CU) Traits with 95% Confidence Intervals, from the Full Univariate Model

	MZ		DZ				
	ICC	*n*	ICC	*n*	A	C	E
CU	.65	218	.33	318	**.65 (.58-.72)**	.00 (-.00-.00)	**.35 (.28-.42)**

Note. ICC = Intraclass correlation; *n* = Number of participants for each variable. **Statistically significant ACE parameters are highlighted in bold.**

Table 3

*Full and Nested Multivariate Genetic Models Parametrizing Gene-Environment Correlation and Interaction Processes Linking Callous-Unemotional Traits (Outcome) and Warm/Rewarding Parenting (Moderator) (*N = *890)*

Model	*a*	*c*	*e*	*b*	*ma*	*r*	Δ-2LL	AIC	BIC
Full	-.681**	.000	.602**	-.187	-.135*	-.11	–	4932.10	4981.22
***r*=0**	**.676****	**.000**	**.603****	**-.114****	**-.137****	**–**	**.056**	**4930.16**	**4975.18**
r= 0,*ma*=0	.683**	.000	.602**	-.112**	–	–	7.75**	4935.90	4976.84

Note. *a* = Additive genetic path parameter; *c* = Shared environment path parameter; *e* = Nonshared environment path parameter; *b* = Main effect of warm/rewarding parenting; *ma* = Linear moderation of genetic path by warm/rewarding parenting (GxE); *r* = Warm/rewarding parenting/CU traits correlation due to rGE; Δ-2LL = Difference in -2LL (twice the negative loglikelihood) between the previous model and the model that is tested; AIC = Akaike's Information Criterion; BIC = Bayesian Information Criterion. **The best-fitting model is highlighted in bold.**

* $p < .05$

** $p < .01$

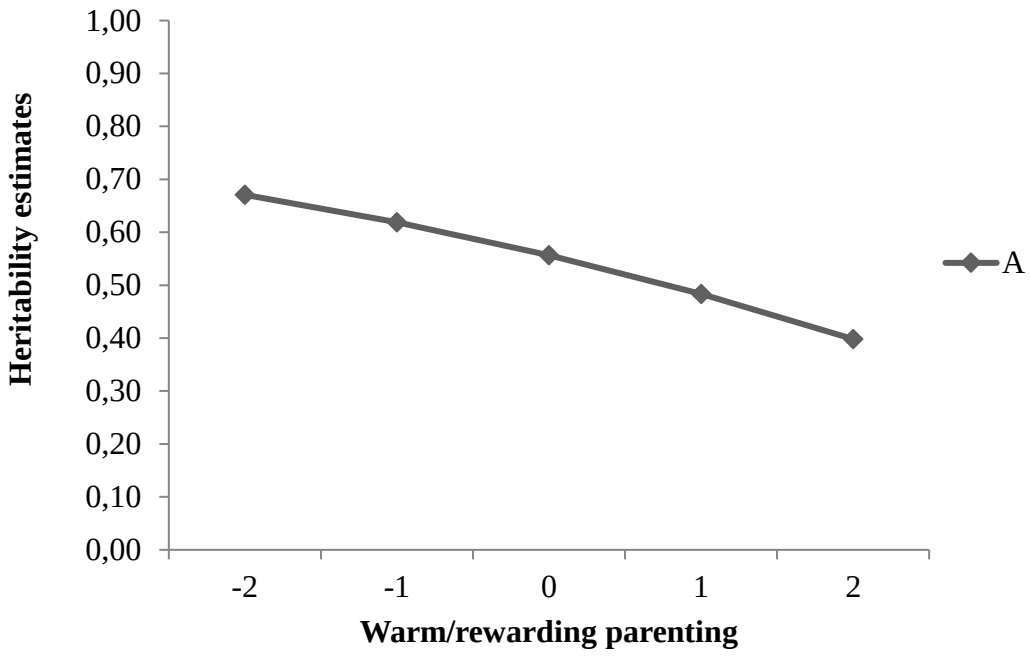

Figure 1. Moderation Effect of Warm/Rewarding Parenting on the Heritability of Callous-Unemotional Traits.