**Supplementary Information**

**Heritability of Reflexive Social Attention Triggered by Eye Gaze and Walking Direction: Common and Unique Genetic Underpinnings**

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**Genetic Data Analysis**

*Univariate Analysis*

To assess the relative importance of genetic and environmental factors to the total phenotypic variations of reflexive attentional orienting effects (i.e., gaze induced attentional effect, walking direction induced attentional effect, and arrow induced attentional effect) and the core social attention ability (i.e., the differentiation between social and non-social attentional effect), univariate genetic analyses, as described in Neale and Cardon (1992), were conducted with the statistical package Mx (Neale Michael *et al.*, 2003). Linear structural equation models were separately fitted to variance-covariance matrices for MZ and DZ twins. These models assume that phenotypic variation arises from the factors of additive genetic (A), common environmental (C) and non-shared environmental (E) influences. The effect of additive genetic factors (A) is assumed to be the sum of multiple genes (polygene) whose effects are small and additive to form a quantitative phenotype. Common environment (C) is the effect that makes twins alike not from heredity but from the environment shared by family members. Non-shared environment (E) is the effect from individually unique environment that makes twins different, such as differential parental treatment, prenatal or postnatal traumas and peer group. Non-shared environment (E) also includes measurement errors. In order to reveal which factors significantly contribute to phenotypic variance, different models were systematically compared in terms of goodness-of-fit statistics and parsimony. These are the ACE model in which phenotypic covariances are explained by A, C and E; the AE model explained by just A and E; the CE model explained by just C and E; and the E-only model. After fitting the full ACE model to the data, we also separately tested the AE, CE, and E submodels and compared to the full models. Chi-square statistic was used to assess the goodness-of-fit of each model, where low values indicate a good fit. If dropping a factor significantly reduced the goodness of fit, the factor was retained in the model, otherwise the factor was dropped and the model with a fewer number of factors was chosen (i.e., the more parsimonious model). In addition, different models were also compared using Akaike’s Information Criteria (AIC) that reflects a model’s goodness of fit as well as its parsimony, and the model that results in the smallest AIC is regarded as the best.

Table 1 shows the fit statistics for the full and the best genetic models for reflexive attentional orienting effects and the core social attention ability. In Experiment 1, for gaze induced attentional effect, dropping the A factor from the full model (i.e., CE model) led to significant worsening of the model fit (Δχ2 (1) = 6.64, *p* = .02). In contrast, dropping the C factor (i.e., AE model) did not reduce the fit of the model (Δχ2 (1) = 0). The C factor was thus dropped and AE model was chosen as the best model. For walking direction induced attentional effect, the most parsimonious and best-fitting model was the AE model (CE: Δχ2 (1) = 14.52, *p* = 0.001; AE: Δχ2 (1) = 0). In Experiment 2, for gaze induced attentional effect, the AE model also provided the best fit (CE: Δχ2 (1) = 4.62, *p* = .09; AE: Δχ2 (1) = 0), which is consistent with that observed in Experiment 1. For arrow induced attentional effect, a different pattern of results emerged. Dropping the A factor (i.e., CE model) or the C factor (i.e., AE model) did not show significant change in χ2 from the full model (CE: Δχ2 (1) = 0; AE: Δχ2 (1) = 0), and E-only model resulted in no significant decrement of the model fit (Δχ2 (2) = 0). Therefore, E-only model was chosen as the best model. For the core social attention index, the best-fitting model was AE model (CE: Δχ2 (1) = 7.62, *p* = 0.02; AE: Δχ2 (1) = 0).

*Bivariate Analysis*

In order to further examine genetic and environmental contributions to the covariance between the two types of social attentional effects (i.e., gaze induced and walking direction induced attentional effects) and that between the social and non-social attentional effects (i.e., gaze induced and arrow induced attentional effects), bivariate genetic analysis was applied to the twin data using the Mx program. The bivariate correlated factors model was fit to the covariance matrices. This model allows the covariance of two phenotypes to be partitioned into covariance that is due to additive genetic, common environmental and non-shared environmental factors. Three parameters were calculated to respectively estimate the additive genetic (*r*g), common environmental (*r*c) and non-shared environmental (*r*e) correlations. The additive genetic correlation (*r*g) indicates the degree to which genetic influences on one phenotype overlap with those on the second phenotype (independent of their individual heritability). Based on the genetic correlation (*r*g) and the individual heritability of each phenotype (i.e., a112, a222), the extent to which overlapping genetic influences account for the phenotypic correlation between two phenotypes can be obtained. The square root of the heritability of each variable were multiplied with the genetic correlation (a11 × a22 × *r*g) and then converted to the proportion by dividing the observed overall phenotypic correlation. The common environmental and non-shared environmental contributions to the phenotypic correlation can be calculated in similar ways. The sub-models, in which *r*g, *r*c, or *r*e was dropped, were tested and compared with the full model to determine if the three parameters (*r*g, *r*c, and *r*e) were significant. A significant difference in chi-square indicates a worse fit and the parameter (*r*g, *r*c, or *r*e) dropped from the model is significant and should be retained in the model. Based on the univariate analyses of gaze induced attentional effect and walking direction induced attentional effect, the bivariate AE model was fitted. The bivariate AE model fitted well, χ2 = 14.06, df = 14, *p* = 0.45, AIC = -13.94. Dropping the genetic correlation (*r*g) significantly reduce the fit of the model (Δχ2 (1) = 5.90, *p* = 0.02), whereas the non-shared environmental correlation (*r*e) could be dropped with no significant change in χ2(Δχ2(1) = 0.07, *p* = 0.79).

All data submitted to the intraclass correlation and the genetic modeling analyses had been controlled for age, gender, and zygosity based on multivariable regression.

**References**

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**Neale Michael, C., Boker Steven, M. & Xie Gary, M. H. H.** (2003). *Mx: Statistical Modeling*. Richmond: Virginia Commonwealth University, Department of Psychiatry.