Supplementary material

Participant recruitment

To ensure representativeness, over 600 public schools were randomly selected from all 18 districts and counties in Beijing municipality. All twins in these schools were invited to participate in this study. About 48% pairs and their parents agreed to participate. The remaining pairs refused to participate in the study, either because they were reluctant to provide saliva samples or they decided not to commit to a longitudinal study.

Representativeness in Beijing

To assess the representativeness of the sample, we compared the basic demographic characteristics of the Wave 1 twin sample to a general youth population in Beijing. We randomly selected one twin from each pair between the ages of 12 and 18 (N = 973). Using a frequency matching method, an age- and gender-matched sub-sample (N = 969) was randomly selected from a large population based representative youth sample in Beijing (Chen et al., 2009). Comparisons were conducted between the two samples in terms of basic demographic information. No significant differences were detected in terms of perceived family social economic status (*t* = –1.71, *p* = .09), fathers’ educational attainment (*t* = –1.65; *p* = .10), or parents’ marital status ( *χ2* = 0.71, *p* = .43) or marital quality (*t* = –0.99, *p* = .33), with one exception: mothers’ educational level was significantly higher in the twin sample than in the general youth sample, *t*(1,898) = –2.29, *p* < .05. Overall, these comparisons suggest that the representativeness of our twin sample was acceptable.

Zygosity determination

In the sample, zygosity of about 90% pairs were determined by DNA analyses, and the rest 10% of twin pairs whose saliva samples yielded insufficient DNA, were determined by the questionnaire method. For DNA analyses, nine short tandem repeat loci, which are highly heterogeneous in the Chinese population, were used. Same-sex twins with at least one different genetic marker were classified as DZ twins; otherwise, the twins were classified as monozygotic (MZ) twins. The posterior probability of being MZ for same-sex twins with the same genotype in all nine loci was estimated to be 99.99% (Chen et al., 2010). The validity of the questionnaire was tested by comparing to the DNA analyses results in previous pilot twin sample with predictive accuracy of 91% (Chen et al., 2010).

Table S1 *Covariance decomposition for variances/covariances of interest (Keller, 2010).*

|  |
| --- |
| *VP*=*σ2*=*a*2*q*+*f*2*x*+2*awf*+*e*2 +*d*2 +*s*2 |
| *VA*=*a2q, VD*=*d*2, *VS*=*s2*, *VF*=*f2x*, *VE*=*e2* |
| *CV*(*MZ,MZ*)=*a*2*q*+*d*2+*s*2+*f*2*x*+2*awf* |
| *CV*(*DZ,DZ*)=*a*2(*q*–1/2)+1⁄4*d*2+*s*2+*f*2*x*+2*awf* |
| *CV*(*Par,Child*)=1⁄2*a*(*qa*+*wf*)+1⁄2*a*(*qa*+*wf*)*μσ2*+*m*σ2+*mσ2μσ2* |

Table S2. *Parameter estimates in different age groups*

| Age group | Wave | Informant | A | D | S | E | *μ* |
| --- | --- | --- | --- | --- | --- | --- | --- |
| 10-13 | Wave 1 | Self-report | 0.240[0.154,0.323] | 0.292[0.126,0.396] | 0.000[0.000,0.139] | 0.469[0.403,0.544] | 0.494[0.421,0.559] |
| Parent-report | 0.488[0.407,0.563] | 0.139[0.000,0.312] | 0.109[0.000,0.263] | 0.264[0.223,0.313] | 0.511[0.432,0.583] |
| Wave 2 | Self-report | 0.008[0.000,0.118] | 0.266[0.035,0.504] | 0.225[0.018,0.405] | 0.500[0.414,0.604] | 0.403[0.313,0.482] |
| Parent-report | 0.180[0.061,0.295] | 0.467[0.253, 0.679] | 0.117[0.000,0.317] | 0.236[0.191,0.294] | 0.412[0.316,0.497] |
| 14-18 | Wave 1 | Self-report | 0.263[0.176,0.346] | 0.176[0.000,0.338] | 0.067[0.000,0.239] | 0.495[0.428,0.573] | 0.402[0.328,0.469] |
| Parent-report | 0.503[0.426,0.575] | 0.180[0.010,0.263] | 0.000[0.000,0.049] | 0.317[0.270,0.371] | 0.397[0.326,0.461] |
| Wave 2 | Self-report | 0.192[0.008,0.302] | 0.138[0.000,0.383] | 0.214[0.000,0.394] | 0.456[0.379,0.549] | 0.495[0.392,0.583] |
| Parent-report | 0.279[0.167,0.384] | 0.365[0.153,0.551] | 0.079[0.000,0.268] | 0.277[0.225,0.344] | 0.487[0.386,0.572] |

*Note.* Additive genetic, dominant genetic, sibling environmental, and non-shared environmental influences were represented by letters A, D, S, and E, respectively. *μ*: assortative mating. A, D, S, and E were all standardized variance components. Ninety-five percent confidence intervals were presented in square brackets.

References

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