

Supplementary Online Content

van der Aa N, Bartels M, te Velde SJ, Boomsma DI, de Geus EJC, Brug J. Genetic and environmental influences on individual differences in sedentary behavior during adolescence: a twin-family study. *Arch Pediatr Adolesc Med*. Published online February 6, 2012. doi:10.1001/archpediatrics.2011.1658.

eAppendix. Methods and eFigure.

This supplementary material has been provided by the authors to give readers additional information about their work.

eAppendix

Methods

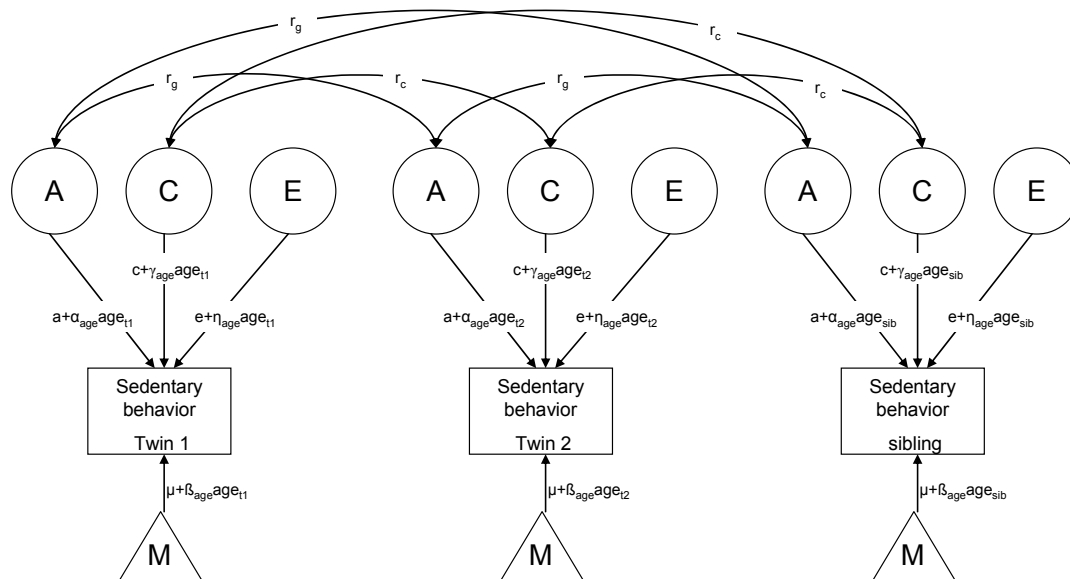
Resemblance in sedentary behavior for twin and twin-sibling pairs was expressed in twin and twin-sibling correlations. In a so called saturated model, means, variances, and the twin and twin-sibling correlations were estimated for each of the 5 sex by zygosity groups (i.e. monozygotic male: MZM, dizygotic male: DZM, monozygotic female: MZF, dizygotic female: DZF, and dizygotic opposite-sex: DOS), making use of the software package Mx.¹ The saturated model specifies for each sex by zygosity group that the data from the first- and second-born twin and the non-twin sibling are correlated without attempting to model these correlations as a function of genes or shared environment.

Means, variances, and correlations were estimated conditional on sex by allowing, means and variances to be different for boys and girls and correlations to depend on both sex (male-male, female-female, and male-female pairs) and zygosity. Sex differences in means and variances were assessed by constraining them to be equal between boys and girls and it was tested if this resulted in a significant deterioration of model fit.

Age, which was transformed into a z-score, was included as a fixed effect (covariate) in the means model. We tested whether constraining the regression weight of age at zero led to a significant deterioration of model fit.

With respect to correlations, we assessed whether twin-sibling correlations were significantly different from DZ twin correlations (thereby testing for specific twin effects), whether MZ twin correlations were significantly different from DZ twin and twin-sibling correlations (thereby testing if genes play a role in familial resemblance), and whether the correlations differed as a function of sex. All tests were done by constraining the appropriate sets of correlations to be equal and test whether the constraint resulted in a significant deterioration of model fit.

eFigure. Genetic model for sedentary behavior with moderating effects of age on genetic and environmental path coefficients



Squares represent the measured sedentary behavior. Triangles represent the theoretical level of sedentary behavior, whose influence can be modified by age. Sedentary behavior is modeled as a function of a person's genes and environment. Genetic and environmental factors are shown as latent (unmeasured) factors and include A (additive genetic influences), C (common or shared environment), and E (nonshared environment). The influence of A, C and E is given by a , c and e which represent unmoderated path coefficients. The influence of latent factors can be moderated by age and α -, γ -, and η -coefficients represent the moderating effects of age. If for example, α is significantly different from zero, the magnitude of A changes as a linear function of age. Path coefficients a , c and e , as well as α -, γ -, and η -coefficients were allowed to differ for boys and girls. Genetic correlation (r_g): MZ twin pairs = 1, DZ twin pairs and twin-sibling pairs = 0.5; shared environmental correlation (r_c) = 1. The latent factors have been standardized to have unit variance.

Next, using genetic structural equation modeling in Mx, genetic models were fitted to the data to estimate the influence of genetic, shared environmental, and nonshared environmental factors to variation in sedentary behavior (eFigure). To assess whether there was evidence for changes in the genetic architecture of

sedentary behavior throughout adolescence, a moderator model was used.² Under this model, genetic, shared environmental, and nonshared environmental effects can be moderated by a measured variable such as age. The effect of age (z-score) was included as a moderator on the genetic and environmental path coefficients a , c , and e . The influence of A, C, and E is represented by the paths:

- (1) $a + \alpha_{age}age$
- (2) $c + \gamma_{age}age$
- (3) $e + \eta_{age}age$

The variance due to A, C, and E was computed by squaring these paths. In order to assess sex differences in the genetic, shared environmental, and nonshared environmental contribution to variation in sedentary behavior, the α -, γ -, and η -coefficients as well as the unmoderated path coefficients a , c , and e were allowed to be different for boys and girls and it was tested whether constraining these parameter estimates to be equal for boys and girls resulted in a significant deterioration of model fit. The unmoderated estimates of a , c , and e represent the parameter estimates used to calculate the variance components A, C, and E at the mean age in the sample. The significance of the age effects was assessed by testing whether constraining the α -, γ -, and η -coefficients at zero resulted in a significant deterioration of model fit. To assess whether genetic and shared environmental factors contributed significantly to individual differences in sedentary behavior, it was tested whether constraining the unmoderated parameter estimates for A and C (i.e. a and c) at zero resulted in a significant deterioration of model fit.

Submodels were nested in the sense that one model could be derived from the other by the imposition of one or more constraints on the parameters. The fit of the different models was compared by means of the likelihood ratio test (LRT). The difference in minus two times the log-likelihood (-2LL) between a more general and a nested model has a χ^2 distribution with the degrees of freedom (df) equaling the difference in df between the two models. If a p-value higher than 0.05 was obtained from the χ^2 -test the fit of the constrained model was not significantly worse than the fit of the more general model. In this case, the constrained model was kept as the most parsimonious and best fitting model. The fit of the genetic models was also compared to the full ACE model by means of Akaike's Information Criterion (AIC), keeping the model with the lowest AIC as the best fitting model.¹

References

- (1) Neale MC, Boker SM, Xie G, Maes HM. *Mx: Statistical modeling (7th ed.)*. Richmond, VA: Department of Psychiatry; 2006.
- (2) Purcell S. Variance components models for gene-environment interaction in twin analysis. *Twin Research* 2002;5(6):554-71.