

ONLINE SUPPLEMENT  
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**The Integration of Genetic Propensities into Social-Control Models of Delinquency and Violence among Male Youths**

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**THE SERIOUS DELINQUENCY SCALE AND THE VIOLENT DELINQUENCY SCALE**

1. In the past twelve months, how often did you hurt someone badly enough to need bandages or care from a doctor or nurse?
2. In the past twelve months, how often did someone hurt you badly enough to need bandages or care from a doctor or nurse?
3. In the past twelve months, how often did you use or threaten to use a weapon to get something from someone?
4. In the past twelve months, how often did you take part in a fight where a group of your friends was against another group?
5. In the last twelve months, how often did you deliberately damage property that didn't belong to you?
6. In the past twelve months, how often did you carry a handgun to school or work?
7. In the past twelve months, how often did you steal something worth more than \$50?
8. In the past twelve months, how often did you steal something worth less than \$50?
9. In the past twelve months, how often did you go into a house or building to steal something?
10. In the past twelve months, how often did you sell marijuana or other drugs?
11. In the past twelve months, have you shot or stabbed someone?
12. In the past twelve months, have you pulled a knife or gun on someone?

Questions 1 to 10. For these questions, we determined the score value on the scale in the following manner: the score is coded 0 if the event did not occur in the past 12 months, 1 if the

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event occurred once or twice in the past 12 months, 2 if the event occurred three or four times in the past 12 months, and 3 if the event occurred five or more times in the past 12 months.

Questions 11 and 12. For these questions, we determined the score value on the scale in the following manner: the score is coded 0 if the event did not occur in the past 12 months and 3 if the event did occur once or more during the past 12 months.

In the construction of the serious delinquency scale, individuals with more than two missing responses were excluded from the analysis. In the construction of the violent delinquency scale, individuals with more than one missing response were excluded from the analysis.

### **MEASURES OF GENETIC POLYMORPHISMS**

Genomic DNA was isolated from buccal cells using a modification of published methods (Freeman et al. 1997; Lench, Stanier, and Williamson 1988; Meulenbelt et al. 1995; Spitz et al. 1996). All the methods employed Applied Biosystems instruments and reagents. Microsatellite and VNTR polymorphisms were done using fluorescent primers analyzed on an ABI (Applied Biosystems) capillary electrophoresis instrument. Single nucleotide polymorphisms were analyzed using an ABI Sequence Detection System and 5'-nuclease (Taqman) methodology. To reduce errors, two individuals independently scored all genotyping. The additional details on DNA collection and genotyping can be found at the Add Health Web site (Smolen and Hewitt <http://www.cpc.unc.edu/projects/addhealth/>).

A 40 bp VNTR polymorphism in the 3' untranslated region of the *DAT1* gene has been genotyped with a modified method of Vandenberg and colleagues (1992). The primer sequences are as follows: forward, 5'-TGTGGTGTAGGGAACGGCCTGAG-3' (fluorescently labeled), and reverse, 5'-CTTCCTGGAGGTCACGGCTCAAGG-3'. This VNTR ranges from 3 to 11 copies with the 9-repeat (9R or 440 bp) and 10-repeat (10R or 480 bp) polymorphisms being the two most common alleles in Caucasian, Hispanic, and African American populations (Doucetestamm et al. 1995). In our male analysis sample, the 9R and 10R account for about 21 and 76 percent of all alleles, respectively; 34.8, 59.9, and .053 percent of the respondents possess one 10R, two 10Rs, and two 9Rs, respectively. The variation across ethnic groups appears to be moderate, with the 10R allele accounting for 80, 86, 80, and 90 percent of all alleles in whites, blacks, Hispanics, and Asians, respectively.

The *DRD2* gene has a polymorphic Taq1A restriction endonuclease site about 2,500 bp downstream (3' untranslated region) from the coding region of the gene. The A1 allele of this polymorphism has a point mutation C→T (TCGA to TTGA). The *DRD2* Taq1A genotyping was performed using the fluorogenic 5'-nuclease (Taqman, Applied Biosystems, Foster City, CA) method with reagents (VIC and 48 FAM labeled probes and TaqMan Universal PCR Master Mix without AMPerase UNG) obtained from Applied Biosystems (ABI) (Haberstick and Smolen 2004). In our male sample, the proportions of *DRD2*\*A1/A2, A2/A2, and A1/A1 are 37, 55, and 8 percent, respectively.

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The *MAOA-uVNTR* polymorphism was assayed by a modified method (Haberstick et al. 2005; Sabol et al. 1998). The primer sequences for the 30bp VNTR in the promoter region of the *MAOA* open reading frame were as follows: forward, 5'ACAGCCTGACCG-TGGAGAAG-3' (fluorescently labeled), and reverse, 5'-GAACGTGACGCTCCATTCGGA-3' (Sabol, Hu, and Hamer 1998). The reaction yielded five fragment sizes that included 291, 321, 336, 351, and 381 bps (2, 3, 3.5, 4, and 5 repeats, respectively). The focus allele in *MAOA* in this study is the rare 2R. A series of tests for each polymorphism and for each self-reported ethnic group (European, African American, Hispanic, and Asian) shows no deviation from the Hardy–Weinberg equilibrium.<sup>1</sup>

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<sup>1</sup> A population is said to be in Hardy–Weinberg equilibrium (HWE) if the genotype frequencies are equal to the product of the allele frequencies, indicating the absence of disturbing forces such as selection, mutation, or migration and the presence of random mating in a population.