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Genes and Behavior in Preschool Children: The Relation between Dopamine Genotype and Latent Executive Control
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**Dopamine and Executive Control**
- Dopaminergic neurotransmission is implicated in the executive control of cognition and behavior (Braver & Cohen, 2000).
- The prefrontal cortex is thought to modulate activity in other brain regions through “biases signals” boosting activation of task-relevant neural pathways, likely through the action of dopamine (Montague, 2004).
- A number of studies have found associations between executive control and dopamine-related candidate genes, likely because of variation in the availability of dopamine in the synapse and/or efficiency of dopaminergic neurotransmission (Casey, 2002; Roesch-Ely, 2005).

**Method**
- 133 preschool children (mean age 4 years 1 month, range 2.5 to 6 years) were administered an executive control battery that included the following tasks: Delayed Alternation, Continuous Performance Task, DAS Digit Span, Delayed Response, Six Boxes, Shape School, NEPSY Statue, NEPSY Visual Attention, and Tower of Hanoi.
- Children were genotyped on the COMT, DAT, DRD2, and DRD4 polymorphisms of interest from cheek swabs obtained using a preschooler-friendly “lipswab” game procedure (Espy, 2002).
- Children were assigned dummy codes of 0 or 1 for each gene, where 1 indicated the presence of the “risk allele.”

**Genes and Executive Control: Model 1**
- First, a summary variable was calculated by simply adding up “risk scores” for all dopamine genes of interest.
- This risk score was used to predict latent executive control.
- Age was also included as a covariate, to account for age differences in executive control.

**Genes and Executive Control: Model 2**
- To look at the contributions of individual genes, individual dummy variables were used to create a latent Genetic Risk variable, in a Multiple Indicator Multiple Cause (MIMIC) model.

**Dopamine Gene Alleles associated with Risk**

**References**
Bakermans-Kranenburg, M. & van Ijzensoorn, M. (2006). Gene-environment interaction of to look at the contributions of individual genes, individual dummy variables were used to create a latent Genetic Risk variable, in a Multiple Indicator Multiple Cause (MIMIC) model.

**Discussion**
- This model also demonstrated good fit to the data, as evidenced by a non-significant chi-square test.
- However, the effect of genetic risk was statistically significant (p < .05).
- As shown by the loadings of the individual genetic risk dummy variables on the Genetic Risk latent variable.
- The effect can be largely attributed to DRD2 and COMT, as model results do not change substantially when DRD4 and DAT are dropped.

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