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Human Genetics

Childhood Dysregulation is Associated with Brain-Derived Neurotrophic Factor and the Serotonin 2A Receptor

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Introduction

While the CBCL-Dysregulation Profile (CBCL-DP) is known to have high heritability, genomewide association studies of the phenotype to date have not revealed significant findings.¹ We undertook an *a priori* selection of 7 candidate genes from a 36 gene SNP chip along with analysis of 2 common VNTRs. (Table 1).

We used latent class analysis (LCA) to determine a profile of responses consistent with the CBCL-DP to allow for an empirical, data-driven manner of grouping individuals with high attention problems (AP), aggressive behavior (AGG), and anxious-depression (AD).²

Table 1. Candidate genes selected for analysis.

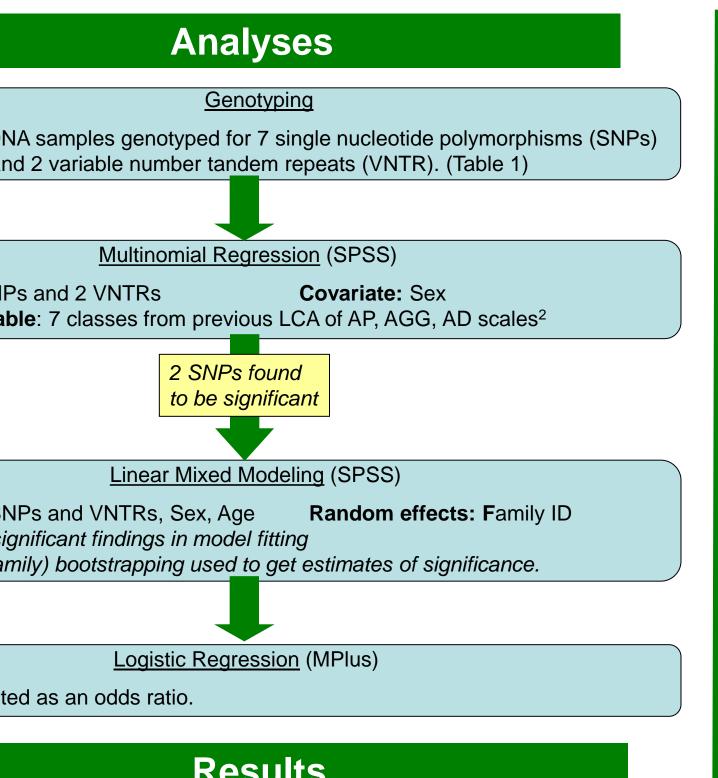
System	Gene	Polymorphism
Adrenergic	Steroid receptor co-activator-1 (SRC1)	SNP C>G rs11125744
	Adrenergic receptor alpha-2A (ADRA2A)	SNP C1291G rs1800544
Serotonergic	Serotonin 2A receptor (HTR2A)	SNP His452Tyr G>A rs6314
	Serotonin 1B receptor (HTR1B)	SNP rs6296
Dopaminergic	Dopamine D1 receptor (DRD1)	SNP A>G rs265981
	Dopamine transporter (DAT1)	VNTR
	Dopamine D4 receptor (DRD4)	VNTR
Growth factor	Brain-derived neurotrophic factor (BDNF)	SNP val66met rs6265
Immunologic	Complement component (3b/4b) receptor 1 (CR1)	SNP A>G rs6656401

Sample and Measures

493 children from 195 families who were recruited from an outpatient child psychiatry clinic to participate in the Vermont Family Study (47.2% female; mean age = 10.9 years; age range = 5-18 years). Participation was voluntary and was approved by the University of Vermont IRB.

Child Behavior Checklist (CBCL);³ 38 items from the Attention Problems (AP), Aggressive (AGG) and Anxious/Depressed (A/D) scales were used in the latent class analysis.

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Results

ad valid data for analysis of the BDNF genotype and ta for the HTR2A genotype.

del did not require family random effects (p > 0.1 when and demonstrated significant associations of being in class with BDNF and HTR2A ($p < 1 \times 10^{-5}$) and

eld when dysregulation class data was analyzed using deling. (Figure 1a,1b).

ulation showed Val homozygotes at BDNF have an ood of being in the dysregulation class [OR 2.602 (1.540-4.396)], G homozygotes at HTR2A were at increased risk [OR = 1.975 (1.080-3.611)], and having both risk genotypes also yielded a significantly increased risk [OR = 2.565 (1.579-4.165)] (Table 2).

Results (con't)

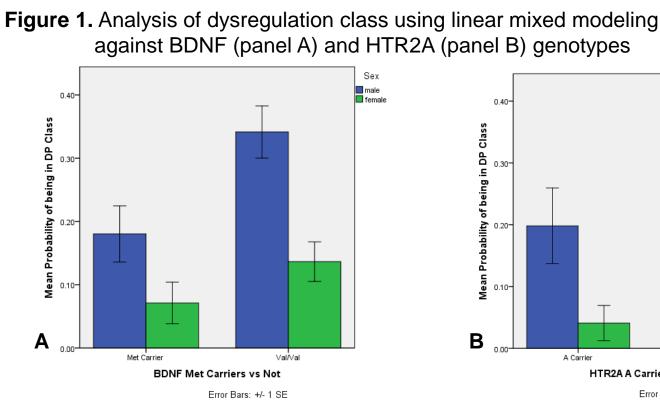


Table 2. Odds ratios from logistic regression

Gene	Genotype	OR	CI
BDNF	Val homozygotes	2.602	1.540-4.396
HTR2A	G homozygotes	1.975	1.080-3.611
BDNF/ HTR2A	BDNF Val homozygotes and HTR2A G homozygotes	2.565	1.579-4.165

Conclusions

In this family study, there are associations with the Dysregulation Profile of the CBCL (CBCL-DP) and both BDNF and HTR2A. This association holds when the data were analyzed as continuous and when family clustering was included. Future research should be conducted in order to examine whether these findings can be replicated using the same models with a larger sample size in a different population.

References

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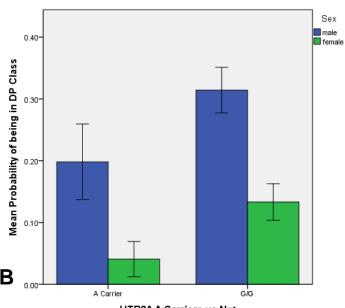
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No conflicts of interest or disclosures.



HTR2A A Carriers vs Not Error Bars: +/- 1 SE