

1 Pilot Study Revealed Association of DRD4 Promoter Variants 2 with ADHD Associated Functional Deficit in Indian Probands

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7

8 **Abstract**

9 Background: Attention Deficit Hyperactivity Disorder (ADHD) is often associated with
10 cognitive deficit. Since brain regions regulating cognition has higher expression of Dopamine
11 receptor 4 (DRD4), we explored association between functional DRD4 promoter variants and
12 cognition of ADHD probands. Methods: Subjects recruited following DSM-IV-TR were
13 assessed for Short Attention Span (SAS) and Erratic Organization Capability (EOC), based
14 on scores obtained through Conner's Parent Rating Scale and DSM-IV-TR as well as
15 computerized games. Functional variants were analyzed in ADHD probands, their parents and
16 age-matched controls. Results: Probands exhibited significant impairment in SAS and EOC.
17 rs10902180, rs747303, rs936462, showed association with cognitive deficit. Probands with
18 co-morbid learning disability showed higher cognitive impairment. Significant interactive
19 effects were evident between the markers.

20

21 **Index terms**— ADHD; molecular genetics; cognitive impairment; learning difficulties.

22 **1 I. Introduction**

23 The current theory on Attention Deficit Hyperactivity Disorder (ADHD) emphasizes on delayed maturation of
24 brain regions involved in controlling executive function (EF), 1,2 thus leading to ageinappropriate impulsivity,
25 hyperactivity and inattention. 3 Though deficit in inhibitory control mechanisms was earlier hypothesized as
26 the major cause for improper EF, 4 recent studies revealed that this is primarily moderated by deficits in basic
27 information processing. 5 Apart from the core symptoms, individuals with ADHD frequently suffer from co-
28 morbid learning difficulty (LD), oppositional defiant disorder, and conduct disorder, 3 which also could be due
29 to improper information management.

30 Image analysis revealed significant reduction in the prefrontal cortex (PFC) volume of ADHD probands. 6
31 As PFC is interconnected with other brain regions like the neocortical regions, amygdala, limbic circuit and
32 cerebellum, it was proposed to have vital role in memory encoding and retrieval as well as decision making, 7
33 emotion related arousal, 8 and motor movements. 9 PFC microcircuits are supposed to play key roles in perception
34 of action cycle while dealing with different types of environmental and social stimuli thereby executing a particular
35 behavioral response. 10 Thus sustained attention and information processing, mediators of executive processes,
36 may also be regulated by PFC.

37 As proposed by Dr. Barkley, EF involves six sets of self regulatory activities, such as self-inhibition, selfdirected
38 sensory-motor action, self-directed private speech, self-directed emotion/motivation, self-directed play, and self-
39 monitoring which eventually affect future consequences. 11 He also concluded that these six functions form the
40 Instrumental-Self-directed level of EF that is most proximal to PFC development and functioning. Self inhibition,
41 spatial management and sustenance of self-motivation form part of these selfregulatory behaviors and injuries / or
42 developmental anomalies of the PFC were found to disturb these functions. Dopamine (DA) is one of the major
43 neurotransmitter involved in movement, motivation and other executive processes 12 and the PFC is enriched

5 C) GENETIC ANALYSIS

44 with DA receptors, both type I and II. While bioavailability of DA in the PFC and striatum is regulated by DA
45 receptor 2 (DRD2), receptor 4 (DRD4) and DA transporter, 13 PFC is preferentially enriched with DRD4. 14 A
46 dual role of DRD4 on 7-amino-3-hydroxy-5-methyl-4isoxazolepropionic acid (AMPA) receptor, hypothesized to
47 underlie the mechanisms of evoke related response, inhibitory control and other cognitive processes, has also been
48 documented; during the hyper-activated state of the PFC, DRD4 was found to reduce glutamatergic transmission
49 while at the hypoactive state PFC was reported to trigger AMPA response via the same pathway. 15 Genetic
50 polymorphisms in the DRD4 have been explored widely. The most frequently investigated site is a variable number
51 of tandem repeat in the exon3 and meta-analysis revealed association of higher repeats (>6R) with ADHD in
52 the Caucasoid 16 as well as Indo-Caucasoid probands. 17 Individuals homozygous for the common 4R variant
53 showed reduction in the PFC gray matter volume 18 while being less efficient in a measure of executive attention.
54 19 Based on these findings, we speculated that DRD4 may have a contributory role in the EF of ADHD probands
55 and for the first time investigated association of functional DRD4 promoter variants with Erratic Organizational
56 Capability (EOC) and Short Attention sustainability (SAS), as part of selfregulatory trajectories under EF, in
57 eastern Indian probands with or without co-morbid LD.

58 2 II. Methods

59 3 a) Participants and study design

60 Nuclear families with ADHD probands (N=200; mean age 7.7 yrs; sex ratio M:F 9.5:1) were enrolled based on
61 the Diagnostic and Statistical Manual for Mental Disorders-IV-text revised (DSM-IV-TR) criteria. 3 ADHD
62 index, hyperactivity level and cognitive attributes/ inattentiveness of probands were measured by the Conners'
63 Parent Rating Scale-Revised (CPRS). 20 Intelligence/developmental quotient were assessed by the Wechsler's
64 Intelligence Scale for children 21 for proband above five years and Developmental Screening Test for children
65 below 5 years. 22 Out of 200 probands, 160 were complete parent-proband trios, 22 had only one parent while
66 18 were affected probands only. Majority of the probands belonged to the combined subtype (72.5%) while
67 hyperactive/impulsive (12.5%) and inattentive (15%) subtypes were only few. 60% probands showed cognitive
68 deficit while 63% exhibited hyperactivity. Co-morbid conditions assessed using the DSM-IV-TR criteria 3 showed
69 LD in 29% of probands. Subjects with only psychiatric problems including pervasive developmental disorders,
70 any form of mental retardation (IQ < 70) and fragile-X syndrome, were excluded.

71 Ethnically matched control subjects were evaluated for the DSM-IV-TR criteria for ADHD 3 , hypothyroidism,
72 intelligence/developmental quotient (>80) as well as for any psychiatric disorder running in the family and those
73 without any abnormality (N=200; Mean age 13.45 yrs; sex ratio 1.4:1) were recruited. Informed written consent
74 was obtained for participation in the study and the protocol was approved by the Institutional Human Ethics
75 Committee.

76 4 b) Assessment of traits

77 SAS and EOC were measured through questions selected from the DSM-IV-TR and CPRS scale (Table ??),
78 scores (0-3) were given based on the responses received, and the total score was converted to percentage. CPRS
79 score percentage for each trait was cross validated with the DSM-IV-TR score and an individual exhibiting more
80 than 5% deviation was excluded. Based on the CPRS score percentage, individuals having less than 30% were
81 considered to have low deficit (1), whereas those with 30-60% were identified as having medium deficit (2) and
82 more than 60% were coined as having maximum deficit (3).

83 Computerized games were used to measure the cognitive function of ADHD probands (N=25, 6-12 yrs, 23
84 male / 2 female) and controls (N=10, 7-12 yrs, 6 male / 4 female). Participants were tested for working memory
85 (Game 1), speed (Game 2) and spatial (Game 3) information processing, , and dual N back test (Game 4) for 5
86 minutes. For each game, there were 3 levels with increasing complexity followed by automatic recording of score.
87 Wrong entry in any round iterated the same level and thus score increased with delay/error in response.

88 Probands (N=80; mean age 12.67 ±3.95 years) were reassessed after 3 years using the same questionnaire
89 (Table ??) to follow their performance.

90 5 c) Genetic analysis

91 Online programs F-SNP (compbio.cs.queensu.ca/F-SNP/), Brain-array (<http://brainarray.mbnl.med.umich.edu/brainarray/database/searchsnp/snfunc.asp> x), and SNPInfo (<http://snpinfo.niehs.nih.gov/cgi-bin/snpinfo/snfunc.cgi>) were used to analyze functional roles of seven upstream variants. Peripheral blood
92 leukocytes were processed for extraction of genomic DNA. 23 Oligonucleotides designed using the Primer3
93 (www.bioinformatics.nl/primer3plus/) program were used for PCR amplification in ABI Gene Amplifier #9700
94 PCR system. rs 916455 was genotyped by restriction fragment length polymorphism analysis of PCR amplicon
95 using RsaI restriction enzyme (New England Biolab); in presence of the "T" allele, two fragments of 58 and 163
96 bp were generated. The other SNPs were analyzed by sequencing of the PCR amplicon in Applied Biosystems
97 3130 Genetic analyzer using Big Dye v 3.1 chemistry and Sequencing Analysis Software, v 5.2.

100 **6 d) Data analysis i. Association analysis**

101 Unphased verion 3.1.7 24 was used for populationand family-based analysis. Hardy-Weinberg equilibrium (HWE)
102 was analyzed using the online software (<http://ihg.gsf.de/cgi-bin/hw/hwa1.pl-hwe>) and Piface version 1.72 25 was
103 used to quantify the strength of statistically significant results ($P<=0.05$). The Odd's ratio (OR) was calculated
104 by online program (<http://www.hutchon.net/ConfidOR.htm>).

105 **7 ii. Analysis of interaction between the sites**

106 Interaction between haplotypes was analyzed by the Cocaphase program. Linkage Disequilibrium was calculated
107 using the Haplovview program. 26 SNP-SNP interaction was analyzed by the Multifactor dimensionality reduction
108 (MDR) program. 27 Volume XVI Issue II Version IYear 2016 (D D D D) A iii.

109 **8 Genotype-phenotype correlation analysis**

110 Association between each phenotypic trait and the gene variants were analyzed by Mann-Whitney test
111 (<http://elegans.som.vcu.edu/~leon/stats/utest.html>).

112 Association between genotypes and co-morbid LD was analyzed using the Cocaphase program.

113 ADHD probands were grouped into three categories, all cases, ADHD with co-morbid LD (ADHD+LD) and
114 without LD (ADHD-LD) for analyzing the level of SAS and EOC. Frequency of probands having various levels
115 of SAS and EOC, calculated through CPRS, were analyzed using the excel work book. Correlation between pair
116 of traits was obtained through online Pearson's calculator (<http://www.socscistatistics.com/tests/pearson/>)
117 and regression analysis software (<http://www.alcula.com/calculators/statistics/linear-regression/>) was used for
118 calculating the interdependence of these traits.

119 **9 iv. Measurement of cognitive function**

120 Mean scores obtained for ADHD probands and controls through computerized assessment were analyzed by the
121 1 tailed unpaired T test using online software (<http://studentsttest.com/>).

122 **10 III. Results**

123 **11 a) Analysis of variants**

124 Sequence analysis showed presence of a novel G>T substitution (Table 2, NSNP) 45 bases before rs747302. All
125 the seven SNPs are binding sites for transcription factors and four revealed moderate regulatory potential (Suppl
126 Table S1). rs916455 is located in the CpG island (ratio=0.99).

127 Genotypes of rs747303 deviated from the HWE in the probands ($P=0.0009$). rs10902180 genotypes deviated
128 for the proband ($P=0.0001$) as well their parents. Genotypes of all other variants followed the HWE. Population
129 based analysis showed significant bias for rs10902180 "C" allele (Suppl Table S1; $P=0.01$, Power=71, OR=1.57)
130 with a trend of association ($P= 0.08$) for the "CC" genotype (Table 2). rs916455 "CC" and rs936462 "AA"
131 genotypes showed significantly higher frequencies in the ADHD+LD probands as compared to control as well as
132 ADHD-LD (Table 2, $P<0.04$). rs10902180 showed higher frequency of the "GG" genotype in the ADHD+LD
133 compared to ADHD-LD individuals ($P=0.001$).

134 Family-based analysis revealed biased transmission of rs936462 "A", rs747303 "T", rs1800955 "T" and NSNP
135 "G" alleles (Table 3). For rs1800955 "T", a paternal bias was noticed ($\chi^2 = 6.32$, $P=0.01$). Analysis of
136 haplotypes failed to show any significant difference.

137 Linkage Disequilibrium pattern was different in the control individuals, probands and their parents, but
138 coefficient of correlation was insignificant (Suppl Fig. 1).

139 **12 b) Analysis of phenotypic traits**

140 EOC and SAS showed linear correlation in both ADHD-LD ($R=0.73$) and ADHD+LD ($R=0.88$). Regression
141 analysis validated EOC score as a function of SAS for these subgroups ($Y= 2.31+0.86X$ & $y= 1.08X-10.30$
142 respectively). Analysis between different subgroups exhibited higher number of ADHD+LD probands with high
143 SAS score ($\chi^2 =21$; $p>0.0001$) as compared to ADHD-LD group (Suppl Fig. 2). No significant difference was
144 noticed for the EOC score (Suppl Fig. 2). rs747303 "TT" showed association with higher EOC score (Suppl
145 Table S2, $P=0.05$), while the NSNP "GG" showed association with both high EOC and SAS scores ($P=0.02$ &
146 0.04 respectively).

147 Performance of ADHD probands was poor, more strikingly for Game 1 and 2, as compared to agematched
148 control children (Fig. 1).

149 Association of higher scores for Game 1 and 2 with rs916455 "CC" was observed. rs936462 "AA" and rs747303
150 "TT" revealed nominal differences, while rs10902180 "GC" showed distinct difference in Game 2 score with a
151 mild difference for Game 1 (Suppl Fig. ??). Higher mean score was also noticed for rs1800955 "CC" in case of
152 Game4. No difference could be observed for rs747302 and data for NSNP could not be shown due to the presence
153 of only one heterozygote (Suppl Fig. ??).

13 IV. DISCUSSION

154 Interaction analysis revealed major independent effects of both SAS and EOC (Fig. 2 A & B respectively) in
155 ADHD individuals exhibiting higher scores (score>1) against those having low score (score=1). With EOC as a
156 phenotypic co-variate, interaction between rs916455-rs747302 and rs1800955-NSNP was also noticed (Fig. 2B).
157 Stratification based on the presence of co-morbid LD revealed major independent effects of phenotypic traits and
158 gene variants in ADHD-LD probands as compared to the control individuals (Fig. 2C), while in ADHD+LD
159 individuals, strong interactive effect was observed between SAS-rs1800955 and EOC-rs747303 in absence of any
160 major independent effect (Fig. 2 D), as compared to ADHD-LD individuals. Mild positive interaction was also
161 noticed between SAS-rs747302, SAS-rs747303, and EOC-rs1800955 (Fig. 2D).

162 Follow up after three years showed that while the number of probands with high EOC gradually reduced
163 with time (Suppl Fig. ??, Low T0/T3=2/24, High T0/T3= 44/15, ?2=32.5, P=0.0001), SAS score improved
164 in a number of probands (Suppl Fig. ??, Low T0/T3= 0/11, High T0/T3= 56/48, ?2=11.5, P=0.003). ADHD
165 subjects harboring rs916455CC, rs747303TT and NSNPGG genotypes had higher EOC scores after three years,
166 while NSNP also showed association with high EOC score (Suppl Table S3). Follow up study also revealed
167 strikingly low scholastic improvement in ADHD+LD (58%) probands as compared to ADHD-LD (79%).

168 13 IV. Discussion

169 Earlier investigators reported delayed maturation of brain regions controlling EF, affecting self regulation,
170 attention and working memory. 2 Since these regions are enriched with DRD4 receptor, we investigated
171 association between DRD4 promoter variants and EF of ADHD probands. LD is a major comorbid condition
172 and may result from low attention sustainability, memory retrieval, working memory, and poor comprehension.
173 We compared the genotypic pattern of ADHD+LD individuals with that of ADHD-LD individuals as well as
174 controls to find out if any particular genotype is affecting the trait.

175 Based on the data obtained, we for the first time report significant association of DRD4 promoter variants with
176 EF deficit of Indo-Caucasoid ADHD probands. F-SNP analysis revealed that rs916455, an upstream variant,
177 may regulate binding of transcription factor, though the mechanism is yet to be understood. The rs916455 "C"
178 allele showed association with persistence of symptoms in Chinese ADHD subjects. 28 Follow up of ADHD
179 probands during the present study also revealed association of "CC" with high EOC score. Higher occurrence
180 of the "CC" genotype was earlier reported in ADHD+LD probands 29 and further analysis in extended samples
181 also revealed association of the "CC" genotype with ADHD+LD as compared to controls (P=0.05) as well as
182 ADHD-LD (P=0.04). MDR analysis exhibited additive effect of rs916455 and rs747302 on EOC. In ADHD+LD
183 individuals, this site showed strong independent effect. "CC" was also associated with Game 1 and 2, depicting
184 its role in working memory impairment as well as poor cognitive flexibility while follow up revealed link between
185 the "CC" genotype and poor attention.

186 rs747302, presented as a trimorphic variant (C/A/G) in the dbSNP database (build 86/142), showed only two
187 alleles (C/G) in the present study as well as previous investigations. 30, 31 F-SNP analysis suggested that the C
188 allele affects binding of transcription factor E2F. Comparative analysis failed to show any significant association
189 of rs747302 with ADHD in the Indo-Caucasoid population and further investigation in other ethnic population
190 is warranted to understand the actual role.

191 Frequency of rs936462 "A" allele was 50% less in the studied Indo-Caucasoid population as compared to the
192 Hungarian population. ??1 We have noticed preferential transmission of the "A" allele by familybased analysis
193 (Odds ratio 4.73). Individuals harboring "AA" showed higher score for Game 1, 3 and 4. While Game 1 is a test
194 for working memory, Game 3 and 4 requires sustained attention and organizational efficiency. Therefore, the "A"
195 allele may be considered as a risk allele in this population. A previous report showed that absence of the "G"
196 allele caused a significant difference in the genotype of -521 C/T, i.e. rs1800955, 31 though in the studied Indian
197 population no such difference was noticed. On the basis of the present study, rs936462 merits further analysis to
198 understand the role of the site in the disease etiology.

199 rs747303 was rarely investigated in ADHD patients and the present study revealed biased transmission of the
200 "T" allele (OR 2.81). F-SNP analyses suggested regulation of transcriptional activity; the GC box disappears
201 in presence of the T allele thus affecting transcription initiation. ADHD probands with the "TT" genotype had
202 poorer information processing capability as compared to probands harboring the "GG" genotype. This is also
203 indicated by scores for Game 3 & 4. MDR analysis showed positive effect of this site on poor attention span in
204 ADHD+LD subjects. On the basis of these findings, rs747303 "T" allele could be considered as a risk variant for
205 ADHD which merits further in depth analysis.

206 This first association analysis on rs10902180 identified the site as a transcriptional regulator. Marginally
207 higher frequency of the "C" allele and "CC" genotype was noticed in the ADHD probands as compared to
208 control. Individuals with the "CC" genotype obtained higher scores for Game 1 and 2. On the other hand,
209 analysis among the subgroups showed significantly higher frequency of the "GG" genotype in ADHD+LD. This
210 contradictory finding may suggest a different mechanism of DRD4 expression in the ADHD+LD subgroup since
211 the gene not only interferes with NMDA receptor or other D2 type receptors, but also interacts with D1 type
212 D5 receptors which work by upstream regulation of gene (analyzed by KEGG pathway). MDR analysis showed
213 strong independent effect of this site on the phenotypic traits. Since our study involves only limited number of
214 ADHD+LD probands, we conclude that this site may have a role in the learning problem of ADHD probands
215 which merits further analysis in higher number of subjects.

216 rs1800955 is a transcriptional regulator widely investigated in ADHD as well as other psychiatric disorders.
217 ??2 Transcription factor CAP is functional in presence of the "T" allele; transcriptional activity was reduced
218 by 40% in presence of the "T" allele 33 though the finding could not be reproduced. ??4 Earlier studies on
219 the Indo-Caucasoid population revealed biased parental transmission of haplotype 7R-T of DRD4 Exon3 VNTR
220 and rs1800955. ??5 The present study also revealed parental over transmission of "T" to the probands, which is
221 basically paternal in nature. "CC" was associated with higher scores for SAS and EOC measured through CRS
222 as well as Game 2 and 4 suggesting its role in cognitive impairment as a whole. MDR showed strong independent
223 effect of rs1800955 in ADHD. In ADHD+LD both attention sustainability and information processing was found
224 to be affected in presence of this variant. The novel substitution NSNP detected in the 5' upstream region
225 showed a parental bias in transmission of the wild type allele and interaction with rs1800955. The heterozygous
226 form showed association with both SAS and EOC. However the site failed to show any significant functional
227 contribution thus making it difficult to interpret its role.

228 Linkage Disequilibrium between rs747302-rs1800955 and rs916455-rs1800955 in the Indo-Caucasoid control
229 population was similar to that observed in the Japanese population. ??6 However, in the Hungarian population,
230 a strong bond was noticed between rs936462-rs1800955 30 which was absent in the Indian population. Further,
231 in families with ADHD probands, the pattern was totally different as compared to the ethnically matched control
232 population. From the observed pattern, we may interpret that the DRD4 promoter region harbors recombination
233 hotspots which culminates in a break in the Indo-Caucasoid population.

234 ADHD associated EF deficit was hypothesized to occur from poor flexibility, self motivation and working
235 memory, ultimately giving rise to altered behavioral response. 11, ??7 Uncontrolled inhibition with triggered
236 impulsivity and error prone behavior was also noticed. ??7 Further investigation showed improper information
237 processing as the major reason for ADHD associated symptoms. 5 These domains are supposed to be affected in
238 children with LD too. As In the present study, we have noticed aberrant information processing along with short
239 attention sustainability. Higher scores for Game 1 and 2 in ADHD probands indicate poor working memory and
240 cognitive flexibility as a result of improper information processing. Scores for Game 3 and 4 were moderately
241 high in the ADHD probands as well as healthy individuals which may indicate that these traits involve a more
242 complicated network of information processing which develops during adolescence. MDR analysis also revealed
243 strong major effects of these two phenotypic traits in addition to independent effect of the studied sites and an
244 additive effect of rs916455-rs747302 on EOC. Comparative analysis between subgroups showed that phenotypic
245 traits of ADHD+LD subjects are affected more severely by interactive effect of the markers; while in ADHD-
246 LD both SAS and EOC showed strong independent effects, interactive effects were pronounced in ADHD+LD.
247 Follow up revealed a constant deficit in attention sustainability with a gradual improvement in EOC and academic
248 achievement was worse for ADHD+LD patients. rs916455 "CC", rs747302CC, rs936462 "AA", rs747303 "TT",
249 rs1800955 "CT/TT" and NSNP "GG" were found to be more frequent in subjects with high and medium score
250 for SAS and EOC indicating significant impact of these genotypes in the cognitive function. Follow up study also
251 confirmed role of rs747303 "TT", rs1800955 "TT" and NSNP "GG" in ADHD.

252 Since ADHD probands are believed to have an altered function of the frontal lobe 38 and DRD4 density is high
253 in this region, we speculated that the promoter variants may alter transcriptional activity leading to a reduction
254 in DRD4 receptor density, thereby causing altered behavioral and cognitive outcome. The data obtained indicate
255 that failure in information processing, leading to reduction in attention span, may lead to the symptoms of ADHD
256 which is more evident in subjects with co-morbid LD. Further analysis involving additional functional variants
257 is warranted in large cohort of subjects to validate our observation. Supplementary Figure 1 : LD analysis for
258 all ADHD probands (A), Father of the probands (B), Mother of the probands (C), ethnically matched healthy
259 individuals (D).

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261 15 Legend to Figures

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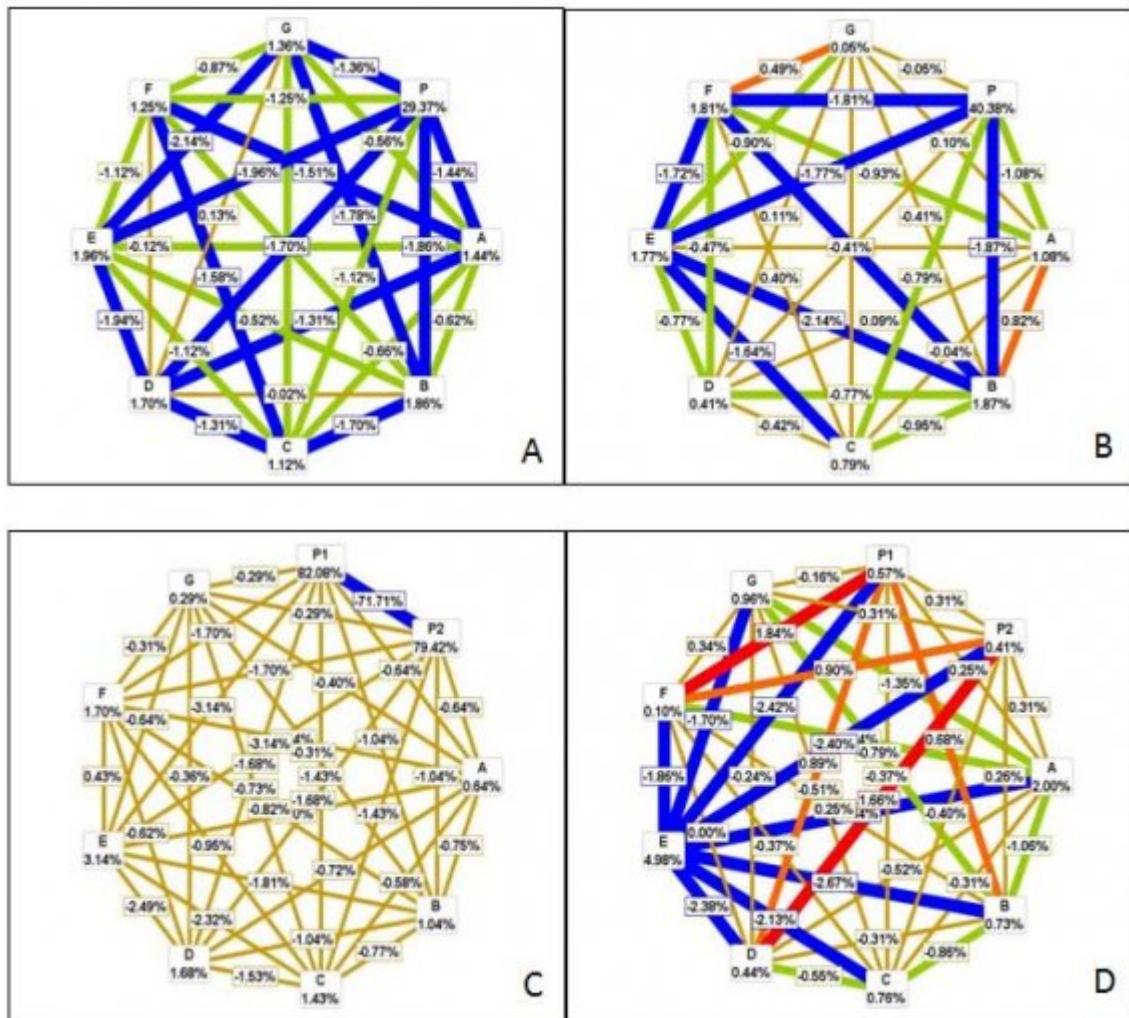


Figure 1:

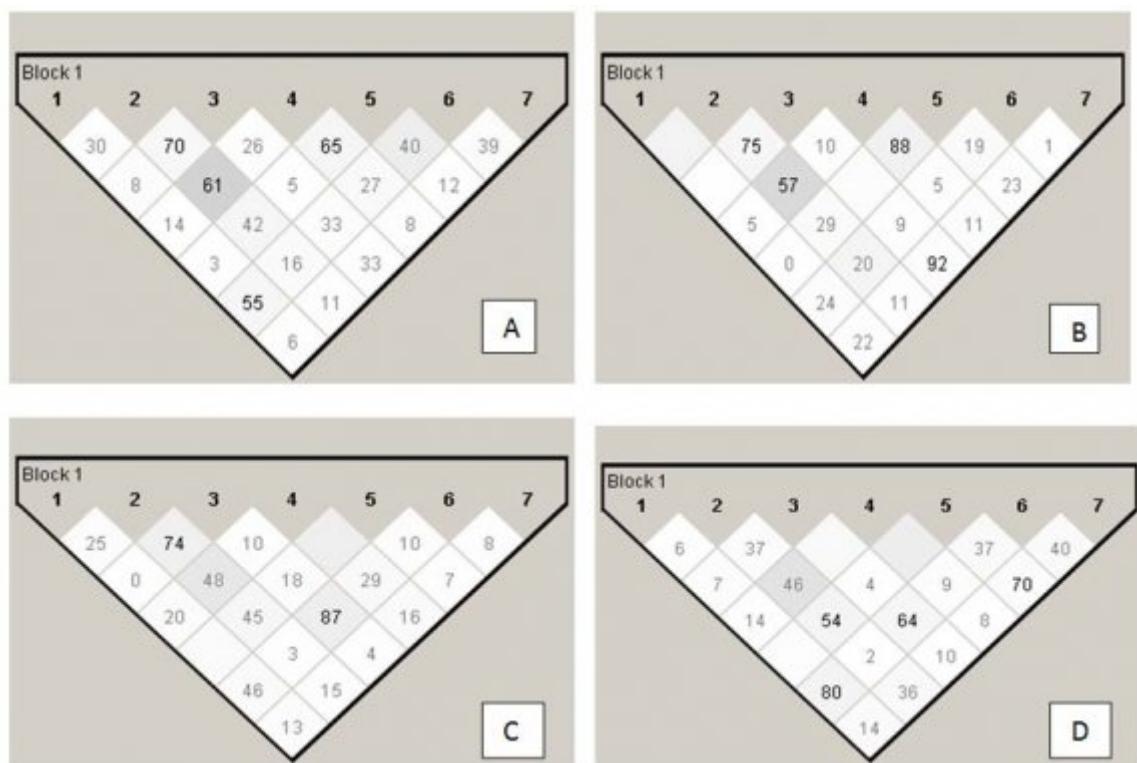


Figure 2: Figure 1 :

2

ID	Genotype	Control	All	? 2 (P)	Probands (N=146)	(N=54)	ADHD-LD	ADHD+LD	?
		(N=200)	(N=200)						
rs916455	CC	0.88	0.89	1.53	0.85	0.94			6
	CT	0.12	0.10	(0.47)	0.14	0.04			(
	TT	0.0	0.01		0.01	0.02)
rs747302	CC	0.34	0.39	0.95	0.37	0.41			1
	GC	0.46	0.43	(0.62)	0.46	0.37			(
	GG	0.20	0.18		0.17	0.22)
	AA	0.90	0.93	3.22	0.91	1.0			7
rs936462	GA	0.09	0.07	(0.20)	0.09	0.0			(
	GG	0.01	0.0		0.0	0.0)
	GG	0.09	0.10	3.97	0.10	0.12			4
rs747303	GT	0.36	0.26	(0.14)	0.28	0.20			(
	TT	0.55	0.64		0.62	0.68)
	GG	0.77	0.66	5.02	0.61	0.83			1
rs10902180	CC	0.17	0.24	(0.08)	0.26	0.14			(
	CC	0.06	0.10		0.13	0.03)
	CT	0.19	0.16	0.93	0.16	0.15			2
rs1800955	CT	0.51	0.50	(0.62)	0.49	0.44			(
	TT	0.30	0.34		0.35	0.41)
	GG	0.82	0.80	0.10	0.81	0.77			0
NSNP	GT	0.18	0.20	(0.74)	0.19	0.23			(
	TT	0.0	0.0		0.00	0.00)

[Note: *Compared to controls; ! Compared to ADHD-LD. © 2016 Global Journals Inc. (US)]

Figure 3: Table 2 :

3

SNP	Allele	Transmitted	Not transmitted	? 2 (P)	Power (%)	Odds Ratio
rs916455	C	0.96	0.94	1.47	—	—
	T	0.04	0.06	(0.23)		
rs747302	C	0.63	0.59	0.64	—	—
	G	0.37	0.41	(0.42)		
rs936462	A	0.99	0.93	9.01	85	4.73
	G	0.01	0.07	(0.003)		(1.15-19.41)
rs747303	G	0.10	0.25	17.7	99	2.81
	T	0.90	0.75	(2.59e-005)		(1.36-5.82)
rs10902180	G	0.83	0.82	0.07	—	—
	C	0.17	0.18	(0.79)		
rs1800955	C	0.37	0.48	5.54	65	1.52
	T	0.63	0.52	(0.02)		(0.89-2.74)
NSNP	G	0.97	0.82	27.15	99	4.89
	T	0.03	0.18	(1.89e-007)		(1.94 -12.06)

Supplementary

[Note: N.B. Statistically significant differences are presented in bold.]

Figure 4: Table 3 :

S1

Supplementary

Figure 5: Table S1 :

S2

ID	Genotypes	Score for phenotypic traits			
		SAS		Med	High
		Low	High		
rs916455	CC	100	0	100	
	CT			0	
	CC	13		64	
rs747302	GC	62		29	
	GG	25		7	
	AA	89	11	100	
rs936462	GA			0	
	GG	22		0	
	AA			22	
Year	GT	22	56	78	22
	TT			92	
	GG			50	
2016	GC			29	
	CC	0		21	
	CC	12		7	
Volum	ID	Predicted functional score			
XVI	rs916455	Allele	F-SNP	SNPinfo	0.109
Is-	rs747302				0.148029
sue	rs936462				C
II	rs747303				T
Ver-	rs1800955				0.208
sion	NSNP				0.086621
I					C G C G T G C C T G T
D	rs10902180	0.05	0.163562	T	
D				G	
D					
D					
)					
(C	
A					
	rs1800955	0.176	0.181188	C	
				T	
NSNP	None detected	—		G	
				T	
ID	Genotype	EOC			
		Mean± SE	P value	Mean± SE	
rs916455	CC	65.38 2.06	—		
	CT	65.19 5.34			
rs747302	CC	66.72 3.13			
	GC	66.41 2.77	—		
rs936462	GG	60.99 5.08			
	AA	65.17 2.02	—		
rs747303	GA	69.67 6.96			
	GG	58.78±4.43	—		
rs10902180	GT	64.90±3.90			
	TT	67.10±2.53	0.05		
rs1800955	GG	67.21±2.20	—		
	GC	61.91± 4.83			
	CC	61.46±6.51 ¹⁰			
	TT	68.40±3.11	0.09		
	CT	62.51±2.73			
	GG	63.28±5.31			

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[Note: © 2016 Global Journals Inc. (US)]

Figure 7:

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