

# A candidate gene investigation of methylphenidate response in adult attention-deficit/hyperactivity disorder patients: results from a naturalistic study

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Supplementary table 1. Description of the analysed genetic variants

Gene	SNP	Reference and reason for inclusion in this study
<i>GRM7</i>	rs3792452	One of the top SNPs in a GWAS on MPH effect in children where the G allele was associated with better a response to MPH (Mick et al. 2008). The SNP is located in a gene expressed in brain areas associated with ADHD and was therefore judged to be relevant by the authors of the study.
<i>DRD5</i>	18.5 kb 5-prime VNTR	148bp allele is over-transmitted in Turkish children who are MPH responders (Tahir et al. 2000) .
<i>LPHN3</i>	rs6551665	G allele has been associated with increased stimulant response in children (Arcos-Burgos et al. 2010), though in a later study in children it was associated with a worse MPH response (Labbe et al. 2012)
<i>LPHN3</i>	rs6858066	G allele has been associated with a good MPH response in children (Labbe et al. 2012)
<i>LPHN3</i>	rs2345039	G allele has been associated with a poor MPH response in children (Labbe et al. 2012)
<i>SLC6A3/DAT1</i>	rs2963238	A allele has been associated with a good response to the antipsychotic clozapine in schizophrenia patients (Xu et al. 2010).
<i>SLC6A3/DAT1</i>	rs2652511	C allele has been associated with both child and adult ADHD (de Azeredo et al. 2014).
<i>SLC6A3/DAT1</i>	3'UTR VNTR	A meta-analysis including both children and adults indicates that there are no, or possibly a minor effect from the 10-repeat allele (10R). The minor effect was noted in naturalistic studies where 10R homozygosity predicted a reduced effect from MPH on ADHD symptoms (Kambeitz et al. 2014).
<i>ADRA2A</i>	rs1800544 (MspI)	The G allele has been associated with increased improvement in inattentiveness in children and adolescents using MPH (da Silva et al. 2008) and symptomatically good response to MPH in children (Cheon et al. 2009). Though the results from both children and adults are conflicting (Contini et al. 2011; Kim et al. 2011; Park et al. 2013).
<i>ADRA2A</i>	rs553668 (DraI)	The variant has been shown to interact with the <i>DRD4</i> VNTR and affect the MPH response in children (Hong et al. 2012). However, the SNP alone has not been associated with changes in the MPH response in neither children or adults (Contini et al. 2011; Kim et al. 2011; Park et al. 2013)
<i>DRD4</i>	Exon 3 VNTR	4-repeat allele has been associated with more favourable MPH dose-response curve in children (Froehlich et al. 2011) and conversely the 7-repeat allele has been shown to predict higher doses of MPH necessary for satisfactory response in children (Hamarman et al. 2004). The 4-repeat allele has also been associated with a good response to MPH in Korean children (Cheon et al. 2007). A study in adults has not shown any effect (Contini et al. 2012).

<i>BDNF</i>	rs6265	The G allele has been associated with a better response to MPH in Korean children (Kim et al. 2011).
<i>BDNF</i>	rs61888800	The G allele has been associated with antidepressant response in adults (Licinio et al. 2009) and the SNP is located in a gene affected by MPH administration (Amiri et al. 2013).
<i>SLC6A2/NET</i>	rs28386840	T allele has been associated with a better MPH response in Korean children (Kim et al. 2010)
<i>SLC6A2/NET</i>	rs192303	The SNP was nominally associated with MPH effect in a GWAS conducted in children (Mick et al. 2008) and is located in a key pharmacological target of MPH.
<i>CES1</i>	rs2244613	CES1 is the main metabolizing enzyme of MPH (Sun et al. 2004) and the SNP has been associated with changes in serum concentrations of the anticoagulant dabigatran also metabolized by CES1 (Pare et al. 2013).
<i>SNAP25</i>	rs363020	A candidate SNP that has not been shown to be associated with MPH response in adult ADHD, but was still labeled as a strong candidate in the same article (Contini et al. 2012).
<i>SNAP25</i>	rs3746544	The T allele has been associated with better MPH dose-response in children (McGough et al. 2006). A study in adults has not shown any effect (Contini et al. 2012)
<i>SNAP25</i>	rs1051312	The T allele has been associated with worse MPH response in children (McGough et al. 2006)
<i>COMT</i>	rs4680 (Val158Met)	The G allele (Val) has been associated with a better response to MPH in children (Cheon et al. 2008; Kereszturi et al. 2008), though not in adults (Contini et al. 2012).
SNP = Single nucleotide polymorphism, GWAS = Genome-wide association study, MPH = Methylphenidate, UTR = Untranslated region , VNTR = Variable number tandem repeat		

Supplementary table 2. Summary of the genotyping per genotyping method

Genotyping platform	MPH responders	MPH non-responders	Total
Sequenom MassARRAY iPLEX	423	66	489
Illumina HumanExome BeadChip 12v1_B	432	66	498
VNTR fragment analysis	476	77	553
<i>Unique patients</i>	487	77	564
VNTR = Variable number tandem repeat			

Supplementary table 3. Results from statistical analysis

Gene	SNP	Risk allele	Observed frequency of risk allele	Additive model		Dominant model	
				OR (95% CI)	p-value*	OR (95% CI)	p-value*
<i>GRM7</i>	rs3792452	A	0.144	0.814 (0.490 -1.354)	0.428	0.706 (0.403 - 1.236)	0.223
<i>DRD5</i>	18.5 kb 5-prime VNTR	148bp	0.521	0.971 (0.690 -1.365)	0.864	1.190 (0.682 -2.075)	0.540
<i>LPHN3</i>	rs6551665	G	0.397	1.037 (0.711 -1.511)	0.851	1.100 (0.641 - 1.888)	0.730
<i>LPHN3</i>	rs6858066	A	0.491	1.188 (0.820 -1.722)	0.363	1.187 (0.664 -2.124)	0.563
<i>LPHN3</i>	rs2345039	G	0.423	0.945 (0.650 -1.375)	0.768	0.813 (0.457 -1.444)	0.479
<i>SLC6A3/DAT1</i>	rs2963238	A	0.456	0.984 (0.671 - 1.441)	0.933	1.092 (0.617 -1.933)	0.763
<i>SLC6A3/DAT1</i>	rs2652511	T	0.454	1.039 (0.711 -1.518)	0.845	1.220 (0.698 -2.132)	0.485
<i>SLC6A3/DAT1</i>	3'UTR VNTR	10 repeat	0.706	1.077 (0.747 -1.554)	0.690	0.772 (0.315 -1.893)	0.572
<b><i>ADRA2A</i></b>	<b>rs1800544 (MspI)</b>	<b>G</b>	<b>0.274</b>	0.728 (0.482 -1.100)	0.131	<b>0.560 (0.329 -0.953)</b>	<b>0.033</b>
<i>ADRA2A</i>	rs553668 (DRAI)	T	0.181	0.719 (0.441 -1.173)	0.186	0.628 (0.368 -1.072)	0.088
<i>DRD4</i>	Exon 3 VNTR	7 repeat	0.193	0.983 (0.630 -1.534)	0.939	1.093 (0.652 -1.834)	0.736
<i>BDNF</i>	rs6265	A	0.194	1.159 (0.718 -1.872)	0.546	1.071 (0.615 -1.865)	0.808
<i>BDNF</i>	rs61888800	T	0.289	0.785 (0.530 -1.160)	0.224	0.876 (0.518 -1.482)	0.621
<i>SLC6A2/NET</i>	rs28386840	T	0.240	1.377 (0.861 -2.203)	0.181	1.402 (0.812 -2.420)	0.226
<i>SLC6A2/NET</i>	rs192303	C	0.309	0.988 (0.666 -1.466)	0.954	0.791 (0.466 -1.342)	0.384
<i>CES1</i>	rs2244613	C	0.188	0.970 (0.611 -1.539)	0.897	1.057 (0.603 - 1.855)	0.846
<i>SNAP25</i>	rs363020	T	0.129	1.565 (0.846 -2.897)	0.154	1.669 (0.837 -3.325)	0.146
<i>SNAP25</i>	rs3746544	C	0.338	0.934 (0.638 -1.368)	0.726	0.913 (0.536 -1.555)	0.738

<i>SNAP25</i>	rs1051312	C	0.306	0.946 (0.634 -1.412)	0.785	0.915 (0.542 -1.545)	0.740
<i>COMT</i>	rs4680	G	0.465	1.315 (0.906 -1.908)	0.150	1.072 (0.606 -1.896)	0.812
*p-values presented are uncorrected. The Bonferroni corrected significance threshold is $p = 0.00125$ .							
SNP = Single Nucleotide Polymorphism, OR = Odds ratio, VNTR = Variable Number Tandem Repeat, 95% CI = 95% confidence interval.							
OR > 1 means that the variant is associated with MPH response and OR < 1 that the variant is associated with MPH non-response.							

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