

The role of a mineralocorticoid receptor gene functional polymorphism in the symptom dimensions of persistent ADHD

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Abstract Attention-deficit/hyperactivity disorder (ADHD) affects approximately 5 % of school-aged children and 2.5 % of adults. Genetic studies in ADHD have pointed to genes in different neurobiological systems, with relatively small individual effects. The mineralocorticoid receptor is the main receptor involved in the initial triggering of stress response. Therefore, its encoding gene (*NR3C2*) is a candidate for psychiatric disorder studies, including ADHD, and behavioral phenotypes. There is evidence that the Val allele of the MRI180V polymorphism (rs5522) increases the risk of depression, attention and cognitive deficits. We investigated the possible role of the mineralocorticoid receptor gene in the symptom dimensions and susceptibility to persistent ADHD. We compared genotype and allele frequencies in 478 adult patients with ADHD and 597 controls and symptom dimensions in 449 patients

and 132 controls. Diagnoses were based on the DSM-IV criteria. ADHD symptom dimensions were investigated with SNAP-IV for ADHD severity and Barkley scales for severity and impairment. Carriers of the Val allele presented higher inattention, hyperactivity/impulsivity and impairment scores, while genotype and allele frequencies did not differ between patients and controls. These results are consistent with a possible link between genetic variations in the HPA axis and inattention and hyperactivity measures.

Keywords ADHD · Cortisol · Stress · Mineralocorticoid receptor · MRI180V · Severity

Introduction

The main symptoms of attention-deficit hyperactivity disorder (ADHD) are inattention, impulsivity and hyperactivity. Its prevalence was estimated at approximately 5 % of school-aged children [1–3], persisting in 2.5 % of adults [4]. Meta-analyses of candidate gene investigations have suggested that a few frequently studied genes, mainly from neurotransmitter systems, present small but significant effects [5]. On the other hand, genome-wide association studies (GWAS) in ADHD have suggested the potential involvement of other genes related to basic cellular processes like cell division, adhesion, neuronal migration and neuronal plasticity [6].

There is evidence that neurotrophins, in concert to hypothalamic–pituitary–adrenal (HPA) axis, play a key role in modulating brain plasticity and behavioral coping, especially during ontogenetic critical periods, when the developing brain is particularly sensitive to external stimulations [7]. Stress-induced alterations in the fetal

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environment can modify brain development, predisposing individuals to develop psychopathologies in childhood, adolescence or even at adulthood, such as attentional and cognitive deficits, anxiety, disturbed social behavior, vulnerability to alcohol and drug consumption, sleep disturbance, schizophrenia and depressive symptoms [8–12].

The relationships between ADHD, cortisol levels and cortisol reactivity are far from clear. Some studies have reported reduced cortisol reactivity in patients with ADHD [13, 14]. Others, however, have found this effect only in ADHD patients with high rates of aggression [15] or did not detect any change in cortisol response [16]. Additionally, it was suggested that ADHD patients may differ in cortisol reactivity according to the ADHD subtype [17]. There is some evidence that the relationship between cortisol levels and disruptive and attention problems may also be modulated by the origin of the sample [14, 18, 19]. For example, these traits might be associated with lower cortisol levels in severe clinical samples [14, 18, 19] or slightly higher levels in a general population sample [20].

The mineralocorticoid receptor (MR) is involved in the onset of stress response [21]. MR is present in the kidney cells, where it is aldosterone selective and controls the salt homeostasis [22], and also in the brain, especially in the hippocampus, where it regulates the basal activity of the HPA and sets the activation threshold of stress responsiveness [21, 23]. Although MR binds cortisol and aldosterone with similar affinity [24, 25], brain MR is mainly exposed to cortisol, which circulates at up to 1000-fold excess compared to aldosterone [23]. MR is involved in anxiety and cognitive function [26]. The blockade of MR by spironolactone (a MR antagonist) in healthy men impairs several aspects of cognition, including selective attention [27].

The MR gene (*NR3C2*) is located on chromosome 4q31.1, with its coding region being formed by exons 2–9 [28]. Common gene variants, including *NR3C2*-2G/C (rs2070951) and the MRI180V (rs5522), have been associated with changes in the HPA axis reactivity [29]. There is evidence that MRI180V is involved in the vulnerability for psychiatric disorders [30] and cognitive functions [31]. This SNP is a missense mutation, notably an A-G transition in the second exon of the gene, at codon 180, resulting in an Isoleucine to Valine change [29]. In vitro studies demonstrated that the Val allele implies a loss of function using cortisol as ligand, but not aldosterone [23, 32]. This allele has also been associated with increased endocrine and autonomic responses to acute stress [23], diminished cortisol-induced *NR3C2* gene expression [23, 32], geriatric depressive symptoms [30], neuroticism [33] and reward learning deficits [31]. The Val allele has also been shown to be a moderator of parenting and infant attachment security, suggesting that the interaction between genetic

and environmental factors may help explain developmental outcomes [34].

In sum, there is evidence that the MRI180V polymorphism may be involved in the modulation of cortisol levels [23], which in turn have a complex association with attention deficits [13–19], cognitive performance [27] and depressive symptoms [30]. Despite the heterogeneity of stress response in ADHD studies, and the central role of the MR in HPA axis function, *NR3C2* has not been investigated in an ADHD candidate gene approach yet. This study tests the possible role of MRI180V in ADHD susceptibility and symptom dimensions among adult patients with ADHD and healthy volunteers.

Materials and methods

Sample

The ADHD sample included 478 adult patients that were recruited consecutively in the ADHD outpatient Program of the Hospital de Clínicas de Porto Alegre (HCPA). The mean age of the ADHD sample was 34 years (± 11.2). The inclusion criteria were as follows: (a) native Brazilians of European descent (b) age 18 years or older and (c) fulfillment of DSM-IV diagnostic criteria for ADHD [35], both currently and during childhood. The exclusion criteria were as follows: (a) evidence of clinically significant neurologic diseases that might affect cognition (e.g., delirium, dementia, epilepsy, head trauma and multiple sclerosis), (b) current or past history of psychosis and (c) intelligence quotient (IQ) ≤ 70 [36]. Data on symptom dimensions were available for 449 patients.

The control sample was composed of blood donors ($n = 597$ for genotype frequencies; $n = 132$ for symptom dimensions). Volunteers were recruited in the same hospital where patients were ascertained. The inclusion criteria were being both native Brazilians of European descent and 18 years of age or older. The control sample was matched to the ADHD patients on age, sex, years of formal schooling and socioeconomic status (Table 1). The exclusion criteria for controls were the same used for the patients (as mentioned above) added to the fulfillment of DSM-IV ADHD diagnosis [35].

In order to deal with a putative cultural bias toward claiming European ancestry, we used morphological classification based on skin color and morphological traits combined with self-classification for ethnicity. That is, cases and controls were included in the study if, in addition to morphological characteristics of European ancestry, they informed to have grandparents of European origin. The population from Southern Brazil, where this study was performed, is mainly of European descent [37], and no

Table 1 Demographic and comorbidity profiles in adult subjects with ADHD and controls

	ADHD (<i>n</i> = 449)* Mean ± SD	Controls (<i>n</i> = 132)* Mean ± SD
Age	33.98 ± 11.13	30.58 ± 9.97
Years of schooling	13.90 ± 3.72	13.90 ± 2.96
Income (minimum wages/month)	14.38 ± 27.25	11.41 ± 11.25
IQ	101.50 ± 9.16	106.72 ± 9.69
	<i>n</i> (%)	<i>n</i> (%)
Gender (% male)	235 (52.3)	61 (46.2)
School failure	287 (63.9)	41 (31.1)
Mood disorders	267 (59.3)	41 (31.1)
Anxiety disorders	190 (43.5)	33 (27.3)
Nicotine dependence	196 (43.7)	28 (21.2)
Other substance use disorders	87 (19.4)	4 (3.0)

* Individuals with information available on ADHD severity and impairment scores

significant population structure was found in the European-derived population of Rio Grande do Sul [38]. The inter-ethnic admixture estimates show that individuals from Southern Brazil present a predominantly European ancestry (94 %) [39], making population stratification unlikely to occur in this situation [40]. The MRI180V Val allele frequency in our control sample (12.1 %) was similar to those reported in other European-derived control groups, varying from 12 % [23] to 14 % [30].

All subjects (patients and controls) signed an informed consent form approved by the Ethics Committee of the HCPA.

Diagnostic procedures

The presence of ADHD and comorbid diagnoses were evaluated through the following semi-structured interviews: (a) K-SADS-E (Schedule for Affective Disorders and Schizophrenia for School-Age Children-Epidemiologic Version), adapted to adults, for ADHD and oppositional defiant disorder (ODD) [41, 42]; (b) SCID-IV-R (Structured Clinical Interview for DSM-IV) for the Axis I psychiatric comorbidities [43] and (c) M.I.N.I (Mini-international Psychiatric Interview) for the diagnoses of conduct and antisocial personality disorder [44]. The estimated IQ scores were obtained from the vocabulary and block design subtests of the Wechsler Adult Intelligence Scale-Revised (WAIS-R) [45] administered by a trained psychologist.

The Portuguese version of the Swanson, Nolan and Pelham Rating Scale-version IV (SNAP-IV) addressed the severity of current ADHD and ODD symptoms [46]. Barkley's scales were used to evaluate both DSM-IV ADHD symptoms (Barkley severity scores) and impairment (how often their symptoms interfere in 10 areas of life

activities—Barkley problem areas). They are all self-report forms that include current (last 6 months) and childhood evaluations [47]. A more detailed description of the ascertainment methods and psychiatric profile of the ADHD sample is described elsewhere [48–51].

Laboratory methods

DNA was extracted from peripheral blood with the salting out procedure [52] and standardized (1:10). The SNP rs5522 in the *NR3C2* gene was genotyped applying the TaqMan technology on an ABI7500 system (Applied Biosystems, Foster City, CA, USA) with the following assay-ID: C_12007869_20. The standard PCR was carried out using TaqMan Genotyping PCR Master Mix reagent kit according to the manufacturer's instructions. Reference sequences and SNP rs-number were obtained from the National Center for Biotechnology Information (NCBI) database (<http://www.ncbi.nlm.nih.gov/>).

Ten percent of the total sample was randomly re-genotyped by a different researcher. The overall genotyping successful rate (considering genotyping and re-genotyping) was 99.1 %, and the reproducibility accuracy was 98.2 %. For those samples with divergence between first and second genotypes, a third round of genotyping was carried out by a third researcher in order to assure data confidence and the correct genotype was assumed as that with two coincidences.

Statistical analysis

Genotype and allele frequencies were compared between cases and controls by Pearson chi-square tests. ADHD symptom and impairment dimensions (SNAP and Barkley scores) were analyzed by ANCOVA, comparing carriers

and non-carriers of the Val allele. Val carriers (homozygous and heterozygous) were grouped due to the small frequency of Val/Val homozygotes (~1 %).

The dimensional analysis was performed using the entire sample (cases and controls), adjusting for the ADHD diagnosis, which was always included as a covariate (except for Barkley severity scores, which were available only for patients). This approach was chosen because the direction of the association is the same in cases and controls, consistently with a possible dimensional nature of the effect of MRI180V SNP. The direction of the findings was also checked in an analysis restricted to patients with ADHD. Sex, age, IQ, socioeconomic status, educational level and frequent comorbidities (major depressive disorder, bipolar disorder, generalized anxiety disorder, obsessive–compulsive disorder, antisocial personality disorder, nicotine dependence, alcohol dependence and drug dependence) were considered for inclusion as covariates. Since none of these variables were associated with both the MRI180V and severity scores with $P < 0.20$, they were not included in the final analyses. In addition, none of these variables was associated with MRI180V with $P < 0.05$.

Results

Genotype and allele frequencies of the MRI180V polymorphism in ADHD patients and controls are presented in Table 2. In both samples, the MRI180V polymorphism is in Hardy–Weinberg equilibrium (patients: $\chi^2 = 0.13$; $P = 0.934$; control subjects: $\chi^2 = 0.06$; $P = 0.969$). Patients and controls did not differ in allele ($\chi^2 = 2.46$; $P = 0.117$) and genotype frequencies, using different genetic models (Ile/Ile \times Ile/Val \times Val/Val: $\chi^2 = 2.71$, $P = 0.258$; Ile/Ile + Ile/Val \times Val/Val: $\chi^2 = 0.24$, $P = 0.625$; Val/Val + Ile/Val \times Ile/Ile: $\chi^2 = 2.27$, $P = 0.132$).

SNAP severity scores and Barkley problem areas were analyzed as dimensional variables (Table 3). Both cases and controls were included, using ADHD diagnosis as a covariate (the footnote of Table 3 presents results restricted to the ADHD sample). The results for Barkley severity scores were based only on the ADHD sample, since this data are not available for controls.

Carriers of the Val allele of the MRI180V polymorphism presented higher SNAP scores of inattention ($P = 0.045$), hyperactivity/impulsivity ($P = 0.010$) and the total sum of symptoms ($P = 0.014$), but the presence of this allele was not associated with ODD scores ($P = 0.304$).

The analysis of self-reported Barkley scores in the last 6 months did not reveal differences between carriers and non-carriers of the Val allele for inattention, but carriers presented higher scores in hyperactivity ($P = 0.045$) and a

Table 2 Genotype and allele frequencies of the MRI180V polymorphism in adult subjects with ADHD and controls

MRI180V genotype	ADHD		Controls		Analysis	
	<i>n</i>	%	<i>n</i>	%	$\chi^2 = 2.71$	$P = 0.258$
Ile/Ile	388	81.2	461	77.2		
Ile/Val	86	18.0	128	21.5		
Val/Val	4	0.8	8	1.3		
Total	478		597			
Allele frequencies	<i>n</i>	%	<i>n</i>	%	$\chi^2 = 2.46$	$P = 0.117$
Ile	862	90.2	1,050	87.9		
Val	94	9.8	144	12.1		

Continuity correction was applied for the tests. The number of missing values may differ for each analysis

Ile/Ile + Ile/Val \times Val/Val: $\chi^2 = 0.24$, $P = 0.625$

Val/Val + Ile/Val \times Ile/Ile: $\chi^2 = 2.27$, $P = 0.132$

trend in the total scores ($P = 0.063$). The analysis on childhood symptoms showed that carriers of the Val allele presented higher scores for inattention ($P = 0.011$), hyperactivity ($P = 0.002$) and total scores ($P = 0.001$). Carriers of the Val allele presented more impairment according to the Barkley problem areas scales, both in childhood ($P = 0.011$) and in the last 6 months ($P = 0.012$).

Discussion

Carriers of the Val allele of the MRI180V polymorphism presented higher inattention and hyperactivity/impulsivity scores and higher impairment, with findings coming from two different assessment instruments. The direction of the association was the same among patients with ADHD and healthy volunteers.

Although there are a very small number of previous genetic association studies considering the *NR3C2* gene, some patterns start to emerge. An interesting point is that the Val allele has consistently been reported as the risk allele. That is, some phenotypes that include putative maladaptive behavioral symptoms [30, 31] have been suggested to be associated with the Val allele. Interestingly, these findings are in agreement with those obtained with the spironolactone blockade of MR, which impairs several aspects of cognition, including selective attention [27]. Several phenotypes related to the Val allele are also related to ADHD dimensions. These include smoking behavior [53], depression [54] and emotional instability [55, 56], which are associated with inattention and hyperactivity.

In the present study, we found associations between the presence of the Val allele and higher inattention,

Table 3 Severity and the presence of Val allele of the MRI180V polymorphism in adults with ADHD and controls

	ADHD		Controls		Total		<i>F</i>	<i>P</i> ^a
	Carriers	Non-carriers	Carriers	Non-carriers	Carriers	Non-carriers		
<i>SNAP severity scores</i>	(<i>n</i> = 83)	(<i>n</i> = 366)	(<i>n</i> = 35)	(<i>n</i> = 97)	(<i>n</i> = 118)	(<i>n</i> = 463)		
Inattention	1.97 ± 0.57	1.83 ± 0.55	0.39 ± 0.31	0.38 ± 0.33	1.50 ± 0.88	1.52 ± 0.78	4.03	0.045
Hyperactivity/impulsivity	1.69 ± 0.71	1.47 ± 0.72	0.46 ± 0.40	0.39 ± 0.34	1.32 ± 0.85	1.25 ± 0.80	6.62	0.010
Oppositional defiant disorder ^b	0.96 ± 0.61	0.92 ± 0.59	0.28 ± 0.25	0.15 ± 0.21	0.79 ± 0.62	0.81 ± 0.61	1.06	0.304
Total ^b	1.55 ± 0.51	1.43 ± 0.49	0.34 ± 0.21	0.24 ± 0.21	1.25 ± 0.69	1.25 ± 0.62	6.12	0.014
<i>Barkley severity scores</i> ^c	(<i>n</i> = 82)	(<i>n</i> = 354)	(<i>n</i> = 31)	(<i>n</i> = 80)	(<i>n</i> = 113)	(<i>n</i> = 434)		
Last 6 months								
Inattention	2.01 ± 0.59	1.92 ± 0.57	–	–	–	–	1.35	0.246
Hyperactivity	1.79 ± 0.68	1.60 ± 0.74	–	–	–	–	4.05	0.045
Total	1.89 ± 0.52	1.77 ± 0.54	–	–	–	–	3.47	0.063
Childhood								
Inattention	2.19 ± 0.59	2.00 ± 0.62	–	–	–	–	6.57	0.011
Hyperactivity	1.94 ± 0.79	1.63 ± 0.83	–	–	–	–	9.68	0.002
Total	2.07 ± 0.61	1.81 ± 0.62	–	–	–	–	11.41	0.001
<i>Barkley problem areas</i>								
Last 6 months								
	1.88 ± 0.58	1.70 ± 0.57	0.31 ± 0.29	0.27 ± 0.28	1.44 ± 0.87	1.44 ± 0.77	6.29	0.012
Childhood								
	1.36 ± 0.61	1.18 ± 0.56	0.22 ± 0.22	0.18 ± 0.22	1.05 ± 0.74	0.99 ± 0.65	6.59	0.011

Data are presented as mean ± SD

Because of the very low frequency of the homozygote Val/Val genotype (~1%), it was analyzed in combination with the heterozygous Ile/Val genotype

Analyses restricted to the ADHD sample: SNAP severity scores—inattention (*P* = 0.033); hyperactivity/impulsivity (*P* = 0.016); oppositional defiant disorder (*P* = 0.589); total (*P* = 0.032)/Barkley problem areas—last 6 months (*P* = 0.013)/Barkley problem areas—childhood (*P* = 0.013)

^a ANCOVA—ADHD diagnostic status (cases/controls) was included as covariate (except for Barkley severity scores, available only for patients)

^b The sample size for the SNAP ODD and total dimensions in the control group is smaller (27 carriers and 65 non-carriers of the Val allele)

^c All Barkley variables are self-reported. Barkley severity measures were not investigated in the control sample

hyperactivity/impulsivity and impairment scores, which might indicate that Val carriers are predisposed to a variety of psychopathological symptoms whose exact nature remains to be clarified. Taken together, there are potential interrelationships between the Val allele, inattention and hyperactivity symptoms and other psychiatric phenotypes. Future research should address how the physiologic consequences of Val allele relate to these behavioral phenotypes. We should have in mind that multiple genes are regulated by the MR as a transcription factor, with putative pleiotropic consequences [57].

Previous GWAS findings in ADHD have not detected a signal in the *NR3C2* region [6, 58]. A meta-analysis of GWAS in ADHD children [58] found no association between MRI180V and ADHD (*P* = 0.308). Consistent with these previous studies, we found no association between MRI180V and ADHD. However, GWAS for IQ scores [59] and tobacco use [60] detected signals in the *NR3C2* gene. Considering the small effect sizes and heterogeneity effects detected in meta-analyses for ADHD-related genes [5], it is plausible that some findings may

appear only in a dimensional analysis. This is especially true for ADHD, where the nature of the disorder is indeed dimensional [61–63].

Some limitations have to be considered in the interpretation of these findings. The modulation of the HPA axis and stress response is influenced by many genetic and environmental factors [64, 65]. For example, the cortisol level is also influenced by other polymorphisms in the mineralocorticoid and glucocorticoid receptor genes [29, 66]. MRI180V is a functional SNP [23, 32] and is the most frequently studied polymorphism in *NR3C2*. However, a more detailed analysis of this gene, including other polymorphisms and haplotype structure could potentially provide additional information. In the CEU population of HapMap database, the MRI180V is in strong linkage disequilibrium with several other SNPs forming a haplotype block into the *NR3C2* gene. There are evidences that the MRI180V is in strong linkage disequilibrium with the downstream rs5525 SNP, also in exon 2, and with the functional upstream -2 G/C SNP (rs2070951) [28], which affects transactivation in vitro [67]. Another limitation is

the fact that we did not perform an evaluation of cortisol levels in our sample. Future studies might explore the relationships between genetic polymorphisms, physiologic response and dimensional or categorical definitions of ADHD. These studies might be designed for an in-depth analysis of stress response factors in ADHD. Statistical power is certainly an issue in this study, as usual in this field, considering either disorders or dimensional approaches [68]. Even considering the highest OR for a gene with significant association in a meta-analysis with ADHD in children—OR of 1.33 for the Exon 3 VNTR of DRD4 [5], our sample size would still allow for a power of approximately 50 %. Indeed, our sample size would allow for a power of 80 % only with an OR of 1.48. However, it is more difficult to predict the statistical power for a dimensional analysis as the one that we performed. Lack of statistical power might explain, for example, the lack of association between MRI180V SNP and SNAP ODD and Barkley inattention scores in the last 6 months. We think that a cautious interpretation is the best approach, and this data should be used in future meta-analytic studies aiming to evaluate the relationships between HPA-related genes and ADHD.

In conclusion, there is increasing evidence of the implications of stress response variations in mental disorders. Our findings support the consideration of stress response genes, especially *NR3C2*, as candidate gene in future genetic studies of attention symptoms and disorders.

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Conflict of interest Dr Rohde was on the speaker's bureau and/or acted as consultant for Eli-Lilly, Janssen-Cilag and Novartis in the last 3 years. Currently, his only industry-related activity is taking part in the advisory board/speaker's bureau for Eli-Lilly and Novartis (less than US\$ 10,000 per year and reflecting less than 5 % of his gross income per year). The ADHD Program chaired by him received unrestricted educational and research support from the following pharmaceutical companies in the last 3 years: Abbott, Bristol-Myers Squibb, Eli-Lilly, Janssen-Cilag and Novartis. Dr Belmonte-de-Abreu is on the speaker's bureau or is a consultant for Janssen-Cilag and Bristol-Myers Squibb. Dr Grevet is on the speaker's bureau or is a consultant for Novartis, Janssen-Cilag and Shire.

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