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## Association Study of Serotonin 3 Receptor subunit Gene Variants in Antipsychotic-induced Weight Gain

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### Abstract

**Background**—Schizophrenia is a chronic, severe neuropsychiatric disorder where pharmacological treatment has been hindered by adverse effects, including antipsychotic-induced weight gain (AIWG) and related complications. Genetic studies have been exploring the appetite-

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### STATEMENT OF INTEREST:

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regulation and energy homeostasis pathways in AIWG with some promising leads. The serotonin system has been shown to participate in these pathways.

**Methods**—In the current study, we examined single nucleotide polymorphisms across the serotonin receptor genes *HTR3A* and *HTR3B*. Prospective weight change was assessed for a total of 149 schizophrenia patients of European ancestry.

**Results**—We did not find the tested *HTR3A* or *HTR3B* gene markers to be associated with AIWG in our sample.

**Conclusion**—Our preliminary findings suggest that these receptors may not play a major role in predicting AIWG.

### Keywords

Serotonin 3A and 3B receptor genes (*HTR3A*, *HTR3B*); schizophrenia; antipsychotic-induced weight gain; pharmacogenetics

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## INTRODUCTION

Treatment of schizophrenia (SCZ) symptoms with second-generation antipsychotics, such as clozapine and olanzapine, is often accompanied by significant weight gain experienced in up to 30% of treated patients. While the underlying mechanisms of antipsychotic response and side effects remain uncertain, genetic factors appear to play a prominent role [1–6].

There is evidence for a role of the serotonin system in the regulation of food intake [7]. The serotonin-2C receptor has been previously genetically associated with AIWG [8]; however the role of the serotonin-3 receptor (5-HT<sub>3</sub>) has not been explored. Ondansetron, a 5-HT<sub>3</sub> antagonist that is used to treat chemotherapy-induced emesis [9], has been shown to block the suppression of food intake by serotonin [7] or methamphetamine administration [10]. Another 5-HT<sub>3</sub> antagonist, tropisetron, blocks glucose-induced weight gain in mice [11]. More specifically, the 5-HT<sub>3</sub> receptor may mediate the insulin secretion from pancreatic beta cells in response to glucose during pregnancy [12]. Mice deficient in 5-HT<sub>3</sub> receptor also appeared to lessen high fat-diet induced weight gain [13].

The serotonin 3 receptor is a pentameric ligand-gated cation-selective ion channel that, through its presynaptic and postsynaptic localization, regulates the release of neurotransmitters [14]. It has been shown to be antagonized by clozapine [15], an antipsychotic with high propensity for significant weight gain. The 15.4-kb *HTR3A* gene (HGNC:5297), which is mapped to chromosomal region 11q23.2, codes for the 5-HT<sub>3</sub> receptor, alpha subunit, while the adjacent 47.6-kb *HTR3B* gene (HGNC:5296), mapped to 11q23.1, codes for the beta subunit. In the present study, we aim to investigate the possible association between the *HTR3A* and *HTR3B* gene and antipsychotic-associated weight gain (AIWG).

## METHODS

### Clinical Diagnostic Criteria

We included 149 participants of self-reported European ancestry from three independent clinical studies (Clinical and demographic information included in Table 1). Diagnosis of SCZ was based on the Structured Diagnostic Interviews for DSM-III-R and/or DSM-IV diagnoses (SCID, American Psychiatric Association, 1994, [16]) for Samples US1 and US2, or an interview for both DSM and ICD diagnoses as in Sample GER. Two trained and experienced investigators reviewed the interview scoring, medical records, and clinical summary to reach a best-estimate consensus diagnosis [17]. In case of incongruities, another psychiatrist performed reviews to provide the final decision on the diagnosis. Adult probands with DSM-III-R/IV diagnosis of SCZ or schizoaffective disorder were included. Exclusion criteria include a history of drug dependence (substance and severe alcohol use disorders), drug-induced psychosis, major neurological disorder including epilepsy, or cranial injury with significant loss of consciousness. The study has been approved by our local Research Ethics Board, and each participant gave written informed consent for participating in the study after they were given the complete study description. All 149 subjects were self-reported as of European ancestry, and 86 of them received clozapine or olanzapine during the study period.

### Samples

**Sample GER** (N = 86) was collected at the Charité University Medicine, Berlin, Germany (DJ Müller). Patients 18–60 years old diagnosed with SCZ or schizoaffective disorder according to DSM-IV and ICD-10 criteria were included (more details have been described elsewhere; [18]). Briefly, these patients were started on antipsychotic medications and followed for up to six weeks for weight change in a naturalistic study. The antipsychotics included haloperidol, olanzapine, risperidone, aripiprazole, quetiapine, and amisulpride. Patients from **Sample US1** (N = 52) were recruited from Case Western Reserve University in Cleveland, Ohio (HY Meltzer) or Hillside Hospital in Glen Oaks, New York (JA Lieberman) [19]. These SCZ patients under DSM-III-R diagnosis were treatment-refractory or intolerant to typical antipsychotic therapy [20]. After a two to four-week wash-out period without medication (unless clinically necessary), clozapine was administered, and weight change from baseline was assessed after 6 weeks. Clozapine serum levels were monitored during the course of the treatment to ascertain compliance. **Sample US2** (N = 11) [21] consists of inpatients who had not responded adequately to previous treatment [22]. Patients with a history of non-response to clozapine, olanzapine, or risperidone, and those who were not tolerant to clozapine, haloperidol, olanzapine, or risperidone were excluded. The US2 participants came from four psychiatric state hospitals (two in New York and two in North Carolina) and were assigned randomly to either clozapine or olanzapine in a 14-week, double-blinded study. Weight change was assessed for up to 14 weeks.

### Genotyping

Venous blood was drawn from the participants, and genomic DNA was extracted from blood lymphocytes using a high salt method as described previously [23]. Overall, we tested 21 single-nucleotide polymorphisms (SNPs); eight in *HTR3A* and 13 in *HTR3B* based on the

minimum minor allele frequency of 0.20 using HapMap genotypes (Rel 28 Phase II+III, August 10, on NCBI B36 assembly, dbSNP b126; URL: <http://hapmap.ncbi.nlm.nih.gov>). Specific SNPs were force-included based on previous studies or functional implications [24]. Genotyping of these SNPs were performed on 149 participants using a custom Illumina GoldenGate platform (Illumina, Inc. San Diego, CA, USA) (Hodgkinson et al, 2008). Genotyping rate was above 97% for all markers. Genotyping was repeated for 5% of the sample for quality control purposes, and the repeated genotypes were 100% concordant. The location of the analyzed markers in these two juxtaposing genes is shown in Figure 1.

### Statistical Analyses

Statistical analyses of demographic variables, which included sex, age at recruitment, and duration of treatment, were performed across samples using Fisher's Exact tests, analysis of variance, or Kruskal-Wallis tests (Table 1). The percentage weight change is not significantly different between male and female patients ( $p=0.774$ ). In terms of genetic analyses, the quantitative variable percent weight change was analyzed using ANCOVA, with sex, treatment duration, baseline weight, and clozapine/olanzapine (yes/no) being included as covariates (SPSS v21, IBM Corp). Analyses were done with all patients with available clinical/weight data ( $n = 149$ ), as well as secondarily with the 86 patients receiving clozapine or olanzapine, the two antipsychotics with the highest risk for significant weight gain. Linkage disequilibrium and  $r$ -squared between marker pairs as determined by Haploview 4.1 [25] is shown in Figure 1. We also performed haplotype analysis with covariates using UNPHASED version 3.1.5 [26]. Furthermore, we used the program mbmdr to detect gene-gene interaction between *HTR3A* and *HTR3B*, with significance estimated by permutation testing [27]. Based on genotypic correlation among the tested SNPs, the effective number of independent (uncorrelated) markers was determined to be 13.48; thus, we adjusted the significance threshold for multiple testing in the present study to 0.0038 [28].

## RESULTS

Table 2 presents the results from analyses of the percent weight change in antipsychotic-treated SCZ patients of European ancestry. There were no significant deviations of genotype distributions from Hardy-Weinberg Equilibrium ( $p>0.05$ ).

The *HTR3B* rs2011249 marker was nominally associated with percent weight gain from the ANCOVA ( $p<0.05$ ) in the overall sample. More specifically, the TT genotype (mean weight change  $-0.40\pm 2.20\%$ ) was associated with lower weight gain than C allele-carrying genotypes ( $4.36\pm 5.28\%$ ) (ANCOVA  $p=0.014$ ). The *HTR3B* rs1176744 marker was nominally associated with percent weight gain from the ANCOVA ( $p<0.05$ ) in the subgroup of patients treated with clozapine or olanzapine. More specifically, the TG genotype (mean weight change =  $6.21 \pm 5.31\%$ ) were associated with higher percent weight change than the GG carrying genotype ( $1.33 \pm 3.54\%$ ) (ANCOVA  $p=0.036$ ). These findings did not survive correction for multiple testing. Results from the haplotypic analyses were not significant ( $p>0.05$ ). Results from the pairwise interaction analyses between *HTR3A* SNPs and *HTR3B* SNPs did not yield significant findings after multiple-testing correction. The top

findings from the interaction analysis was observed between rs10789980 and rs6589400 ( $p=0.031$ ), where double heterozygotes were associated with significantly lower weight gain ( $1.10\pm 5.34\%$ ) than the other genotype combinations ( $4.76\pm 5.08\%$ ).

## DISCUSSION

This study is the first to focus on the *HTR3A* and *HTR3B* genes in AIWG in SCZ patients of European ancestry. Previously, the serotonin 2C receptor gene has been implicated in AIWG [8]. Given preclinical evidence of the 5-HT<sub>3</sub> receptors in weight regulation, we investigated common polymorphisms across the *HTR3A* and *HTR3B* genes. We observed nominal associations of *HTR3B* SNPs rs1176744 and rs2011249 with AIWG, as well as a possible interaction between the *HTR3A* rs10789980 and *HTR3B* rs6589400 SNPs. These findings did not survive correction for multiple-testing, thus our findings did not support a major role for these receptors in AIWG.

The present study could have been influenced by a number of limitations in addition to the limited sample size. These include heterogeneity within our sample in terms of clinical and medication history, as well as confounding by co-medication and substance use. Future studies investigating both common and rare variants across these genes in larger samples are needed before the role of these genes in AIWG can be dismissed conclusively (Matosin et al, 2014).

Additional 5-HT<sub>3</sub> receptor subunits (5-HT<sub>3C</sub>, 5-HT<sub>3D</sub>, and 5-HT<sub>3E</sub>) have been described recently. The genes coding for these subunits may be of interest for future AIWG studies when more evidence on their role in the regulation of 5-HT<sub>3</sub> receptor signaling (Holbrook et al, 2009) and their interaction with antipsychotics become available. A number of candidate genes have been identified by our group as well as others (e.g., [18; 29–32]) and replicated for AIWG. Given the reported synergistic effect of 5-HT<sub>3</sub> and cholecystokinin on the regulation of food intake [7] and that our group previously reported an association of the cholecystokinin B receptor gene with AIWG, additional gene-gene interaction (e.g., [33]) and pathway analyses (e.g., [34]) using larger samples may lead to more fruitful research findings that can be translated to better antipsychotic treatment outcome for patients.

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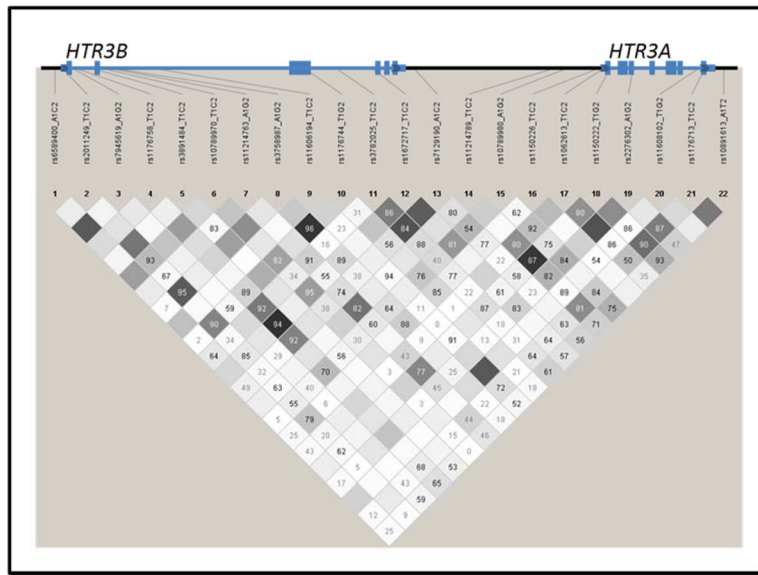
We are grateful to the patients who agreed to participate in our studies.

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**Figure 1.** A schematic diagram of the *HTR3B* and *HTR3A* genes with positions of the tested markers and linkage equilibrium structure based on our genotypes. The values in the figure indicate D-prime values, while the color intensity indicates the strength of correlation between marker pairs.



**Table 1**

Demographic information for the study sample of European ancestry (n = 149).

Samples	GER(N=86)	US1(N=52)	US2(N=11)	<i>p</i> -value
Age (Mean±St Dev) <sup>a</sup>	35.49±12.19	33.73±7.51	41.25±5.37	0.055
Males: Females <sup>d</sup>	50:36	32:20	11:0	0.015
Clozapine or Olanzapine/Others <sup>d</sup>	26/60	52/0	8/3	<0.001
Study duration (weeks) <sup>a</sup>	5.12±1.55	6.00±0.00	10.55±4.18	<0.001
Weight change (kg ± Standard Deviation) <sup>c</sup>	3.27±3.95	2.83±4.03	3.88±4.15	0.681
Percentage weight change (Mean ± Standard Deviation) <sup>c</sup>	3.96±4.79	4.09±5.78	5.58±6.64	0.636

<sup>c</sup> *p*-value from ANOVA.<sup>a</sup> *p*-value from Kruskal-Wallis tests.<sup>d</sup> *p*-values from Fisher's Exact Tests.

Table 2

Results from analysis of the (a) eight *HTR3A* and (b) 13 *HTR3B* single-nucleotide polymorphisms (SNPs) in antipsychotic-associated weight gain in schizophrenia patients of European ancestry.

(a)	SNP	Genotypes	Number of patients	Mean percentage weight change	Standard Deviation of percentage weight change	Genotype <i>P</i> (all antipsychotics/clozapine or olanzapine only)
	rs10789980_A1G2	A/A	29	4.83	5.77	0.099/0.651
		A/G	72	3.32	5.15	
		G/G	44	5.13	5.01	
	rs1150226_T1C2	T/T	1	3.56		0.970/0.801
		T/C	24	4.17	5.57	
		C/C	124	4.12	5.27	
	rs1062613_T1C2	T/T	6	3.27	6.56	0.759/0.948
		T/C	54	4.01	5.24	
		C/C	89	4.25	5.28	
	rs1150222_T1G2	T/T	2	6.79	12.03	0.829/0.817
		T/G	43	3.87	4.79	
		G/G	104	4.18	5.40	
	rs2276302_A1G2	A/A	70	3.88	5.25	0.699/0.621
		A/G	69	4.38	5.31	
		G/G	10	4.09	5.72	
	rs11214789_T1C2	T/T	102	4.09	5.37	0.957/0.932
		T/C	43	4.19	4.96	
		C/C	3	4.53	9.37	
	rs10891613_A1T2	A/A	61	4.23	5.60	0.978/0.467
		A/T	74	4.05	4.91	
		T/T	15	3.82	5.91	
	rs11608102_T1G2	T/T	134	4.06	5.29	0.402/0.574

<b>(a)</b>						
SNP	Genotypes	Number of patients	Mean percentage weight change	Standard Deviation of percentage weight change	Genotype <i>P</i> (all antipsychotics/clozapine or olanzapine only)	
	T/G	15	4.71	5.35		
	G/G					
<b>(b)</b>						
SNP	Genotypes	Number of patients	Mean percentage weight change	Standard Deviation of percentage weight change	Genotype <i>P</i> (all antipsychotics/clozapine or olanzapine only)	
rs3891484_T1C2	T/T	112	4.18	5.36	0.125/0.317	
	T/C	33	4.61	4.96		
	C/C	4	-1.29	2.67		
rs10789970_T1C2	T/T	31	2.84	4.64	0.296/0.748	
	T/C	69	4.45	5.78		
	C/C	49	4.48	4.88		
rs11214763_A1G2	A/A	5	6.09	7.99	0.255/0.600	
	A/G	52	4.91	4.78		
	G/G	92	3.58	5.37		
rs3758987_A1G2	A/A	80	4.17	5.54	0.062/0.071	
	A/G	56	4.67	5.13		
	G/G	11	0.60	3.03		
rs1176744_T1G2	T/T	74	3.80	5.34	0.099/ <b>0.044</b>	
	T/G	61	5.03	5.40		
	G/G	13	1.76	3.70		
rs3782025_T1C2	T/T	46	4.11	5.64	0.962/0.834	
	T/C	78	4.19	5.29		
	C/C	25	3.97	4.74		
rs1672717_T1C2	T/T	62	3.54	4.82	0.431/0.410 <sup>L</sup>	
	T/C	66	4.70	6.00		

SNP	Genotypes	Number of patients	Mean percentage weight change	Standard Deviation of percentage weight change	Genotype <i>P</i> (all antipsychotics/clozapine or olanzapine only)
	C/C	21	4.03	3.99	
rs2011249_T1C2	T/T	8	-0.40	2.20	<b>0.047</b> /0.206
	T/C	45	4.56	4.94	
	C/C	96	4.30	5.47	
rs6589400_A1C2	A/A	93	4.37	4.81	0.477 <sup><i>F</i></sup> /0.663
	A/C	45	3.44	6.36	
	C/C	8	4.52	4.85	
rs11606194_T1C2	T/T	130	3.98	5.25	0.444/0.289
	T/C	18	4.98	5.65	
	C/C	1	7.42		
rs1176758_T1C2	T/T	62	3.80	5.00	0.614 <sup><i>F</i></sup> /0.439
	T/C	72	4.57	5.80	
	C/C	15	3.33	3.61	
rs7129190_A1C2	A/A	45	3.96	5.17	0.727/0.426
	A/C	74	4.36	5.50	
	C/C	30	3.81	5.03	
rs7945619_A1C2	A/A	4	2.82	5.58	0.313 <sup><i>F</i></sup> /0.607 <sup><i>F</i></sup>
	A/G	35	3.25	6.31	
	G/G	109	4.46	4.94	

<sup>c</sup> *p*-values from ANCOVA (comparison among the three genotype groups) of percent weight change with sex, treatment duration, baseline weight, and clozapine/olanzapine (yes/no) as covariates.

<sup>L</sup> significant Levene's Test.

<sup>F</sup> significant Lack of Fit Test.

*p*-values in bold font <0.05.