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Escitalopram reduces attentional performance in anxious older adults with high-expression genetic variants at serotonin 2A and 1B receptors

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Abstract

Older adults are among the most vulnerable to adverse cognitive effects of psychotropic medications and, therefore, the personalization of psychotropic treatment based on adverse drug reactions in this demographic is of great importance. We examined changes on neuropsychological tests of attention attributable to selective serotonin reuptake inhibitor (SSRI) treatment in anxious older adults. We also examined whether variation in serotonin receptor genes was associated with reduced attentional performance with SSRIs. We examined change from preto post-treatment in two attention measures – digit span and coding – in 133 adults aged 60 yr with generalized anxiety disorder in a 12-wk trial of escitalopram vs. placebo. We also examined attentional change in relation to genetic variability in four central serotonin receptors: the serotonin transporter and serotonin 1A, 2A and 1B receptors. Digit span scores were significantly lowered in patients receiving escitalopram relative to placebo, indicating reduced attentional performance attributable to the SSRI. Individuals with high-transcription variants in the receptors 5-HTR_{2A} rs6311 and 5-HTR_{1B} rs11568817 had greater reductions in attention with SSRI treatment compared to placebo. We conclude that SSRIs reduce attention in older adults, particularly in those with high-expression genetic variants at the serotonin 2A and 1B receptors. Analysing neuropsychological changes with SSRIs in relation to genetic variation in the serotonin system may be a useful strategy for detecting subgroups of older adults who are more susceptible to side-effects of SSRIs. These results, if confirmed, could lead to the personalization of SSRI use to reduce adverse neurocognitive effects.

Keywords

Anxiety; antidepressant; elderly; neuropsychological functioning; pharmacogenomics

Introduction

Roughly one in seven older adults in the US is taking an antidepressant and the most commonly prescribed are serotonin specific reuptake inhibitors (SSRIs; Chung, 2005;

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Olfson & Marcus, 2009; Pagura et al. 2011). Yet little research has examined in a controlled or experimental fashion the neurocognitive effects of SSRIs in this demographic. A placebocontrolled study of the serotonin-norepinephrine reuptake inhibitor duloxetine in late-life depression (LLD) showed significant improvement in verbal learning and memory but also a seeming trend towards worse attention (Raskin et al. 2007). Other research has been mixed regarding improvement of cognitive impairment in LLD with SSRIs, with one report showing significant improvement in memory with escitalopram (Savaskan et al. 2008) and others showing a lack of significant improvement (Butters *et al.* 2000; Nebes *et al.* 2003). Similarly, in young adults with depression, there have been mixed findings, with some evidence of improved cognitive functioning in SSRI responders but not non-responders (Mandelli et al. 2006) and in post-menopausal women, potentially modulated by oestradiol levels (Pae et al. 2008). We recently demonstrated in late-life generalized anxiety disorder (LLGAD) that the SSRI escitalopram produced no memory or other cognitive improvements aside from a single executive task (Butters et al. 2011). Given that LLD and LLGAD cause neurocognitive impairment in older adults (Bhalla et al. 2006; Butters et al. 2000), the failure of SSRIs to improve neurocognitive function in these disorders raises the possibility that SSRIs, while helping neurocognition in some ways (for example, by reducing the effects of depression and anxiety on certain cognitive biases; Mogg et al. 2004; Savaskan et al. 2008) may be impairing other aspects of neurocognition. SSRIs have been implicated in sedation, cognitive impairment, increased body sway and falls (Drueke et al. 2009; Dumont et al. 2005; Fava et al. 2006; Gagne et al. 2011; Joo et al. 2002; Laghrissi-Thode et al. 1995; Pollock, 1999; Wroolie et al. 2006), suggesting that they may cause neurocognitive impairment at least in some older adults.

The proximal target of all SSRIs is the serotonin transporter, with consequent altered serotonergic transmission at the serotonin 1A, 2A, 1B and other receptors (Lotrich & Pollock, 2005). These serotonin receptors are found throughout cortical areas involved in cognition, with significant inter-individual variation (Saulin *et al.* 2011). There is known functional genetic variability in these receptors, leading to genetic variants in which higher or lower numbers of the receptors are expressed (Lotrich & Pollock, 2005). This generates the hypothesis that genetic variability leading to functional genetic effects – that is, differential expression of these serotonin receptors and thus greater or fewer serotonin receptors – may predict an individual's risk of neurocognitive side effects.

We completed a placebo-controlled evaluation of escitalopram, a first-line treatment for GAD (Baldwin *et al.* 2011), in LLGAD (Lenze *et al.* 2009). The study included pre- and post-treatment assessment with a neuropsychological test battery and also genetic and pharmacokinetic (drug level) tests. Therefore, we were able to examine neurocognitive changes attributable to escitalopram and their genetic and pharmacokinetic predictors. We hypothesized that patients receiving SSRI would exhibit a reduction in attentional performance compared to those receiving placebo. Further, we examined the relationship of attentional change with functional genetic polymorphisms in key central serotonin receptors and with drug concentration.

Method

The study was a 12-wk, double-blind, randomized controlled trial comparing escitalopram and placebo (Lenze *et al.* 2009). Subjects were aged 60 yr, with a principal diagnosis of GAD (according to the Structured Diagnostic Interview for DSM-IV axis I diagnoses; First *et al.* 1996) and a score of 17 on the Hamilton Anxiety Rating Scale (Hamilton, 1959) Subjects were randomized to 10 mg escitalopram (increased to 20 mg after 4 wk if tolerated and as needed) or placebo. The University of Pittsburgh Institutional Review Board approved the study. Recruitment sources included primary care sites, speciality mental

health practices and advertisements. Co-morbid unipolar depression and other anxiety disorders were allowed as was mild cognitive impairment (i.e. not dementia). Exclusion criteria included lifetime psychosis or bipolar disorder, dementia, medical instability, exogenous steroid use (including inhaled steroids) and antidepressant or anxiolytic co-prescription (with the exception of continuing low-dose benzodiazepines if already in use for at least 2 months). Severity of symptoms was assessed using the Hamilton scales for depression and anxiety (Hamilton, 1959, 1960) and the Penn State Worry Questionnaire, which measures worry severity (Meyer *et al.* 1990).

Neuropsychological assessment included pre- and post-treatment testing with the Repeatable Battery for the Assessment of Neuropsychological Status (Randolph, 1998). Forms A and B were administered in a counterbalanced manner. The present analysis focused on the two tests of attention: digit span and coding. The digit span is a test of basic attention that requires the subject to repeat sequences of single-digit numbers in the same order as read aloud by the examiner. The length of the sequences increases progressively, to a maximum of nine digits. An individual's ability to register a sequence of numbers in immediate memory depends greatly on his or her degree of focused attention. The coding test is a more multi-factorial visuoperceptual-motor decoding task that requires the subject to associate single-digit numbers with unfamiliar symbols. A stimulus set of nine printed digit-symbol pairs is presented above rows of numbers without the appropriate symbols. The subject is instructed to draw the correct symbol below each of the numbers using the digit-symbol code presented above. The score is based on the number of substitutions completed within a 90-s time limit.

DNA was extracted from blood using standard procedures. For all serotonin receptor polymorphisms other than the serotonin transporter, we used the SequenomTM (USA) technology. For the serotonin transporter polymorphisms we followed a protocol that genotypes the *SLC6A4* promoter haplotype (Wendland *et al.* 2006). In short, it is a triplex polymerase chain reaction protocol followed by double restriction endonuclease digestion, determining the phase-certain 5-HTTLPR and rs25531 genotypes, which are then combined as Sa, Sg, La and Lg haplotypes. All haplotypes other than La are considered low-expressing, consistent with other research (Beevers *et al.* 2011; Dombrovski *et al.* 2010; Frodl *et al.* 2008; Steiger *et al.* 2007; Thakur *et al.* 2010; Wankerl *et al.* 2010). For genetic analyses, we initially examined only Caucasian subjects, although we re-ran results with the entire sample, which included 20 African–Americans; results did not change in effect size or significance when the entire sample was used. No genotypes violated Hardy–Weinberg equilibrium (HWE) in the Caucasian-only sample, although rs25531 violated HWE in the entire sample because of a greater-than-expected number of g/g homozygotes (*n* = 3) among African–Americans.

Plasma samples for escitalopram levels were obtained at weeks 2, 8 and 12. We assessed escitalopram concentrations using high performance liquid chromatography with ultraviolet detection (Foglia *et al.* 1997). Nonlinear mixed effects modelling was used for the population pharmacokinetic analysis using the NONMEM computer program (version 5, level 1.1; University of California at San Francisco, USA; Beal & Sheiner, 1992) to calculate normalized average daily exposure for each subject at a given dose. From this model, the variable utilized in this study was average escitalopram concentration at the post-treatment time-point (Jin *et al.* 2009). We used only parent compound levels, as metabolites appear to have little to no pharmacological effect *in vivo*.

Statistical analysis

We examined the relationship between treatment group and attentional change in 133 GAD subjects for whom both pre- and post-treatment neuropsychological data were available. We

tested the hypothesis that change in escitalopram-treated subjects was more negative (deleterious) than placebo-treated subjects, using mixed effect models (PROC MIXED in SAS). We also examined the same models divided by genetic group. The focus in these mixed effect analyses was the treatment group \times time interaction, which showed the relative degree of change in attention in the escitalopram and placebo groups in the overall sample and in each genetic subgroup. We retested the significant results with alternative, equally appropriate statistical techniques (repeated measures analysis of variance, analysis of covariance on the change controlling for baseline and Wilcoxon); all provided the same findings and level of significance. To maximize power, we dichotomized subjects within each genotype into 'high transcription' or 'low transcription' groups based on the presence or absence of at least one high-transcription allele (Conner *et al.* 2010; Lemonde *et al.* 2004; McMahon *et al.* 2006; Villafuerte *et al.* 2009; Wilkie *et al.* 2008). We also examined the same models with haplotypes composed of the three serotonin 1B polymorphisms. Finally, we also examined pharmacokinetic effects by testing the correlation between average escitalopram concentration (derived from the NONMEM model) with change in attention.

Results

From 2005–2007, we randomized 177 subjects to escitalopram or placebo. Of these, 44 dropped out of the study or did not provide pre- and post-treatment neuropsychological data, leaving 133 subjects for the present analysis. Table 1 shows demographic and clinical features of these 133 subjects. Because the table shows a small over-representation of males in the placebo group, all analyses below were re-run controlling for gender; results did not change in significance.

Figure 1 shows the effects of escitalopram *vs.* placebo on the two tests of attention over the 12-wk clinical trial. We found a significant reduction in the score of one – digit span – with escitalopram, compared to placebo. The effect size of this reduction was Cohen's d = 0.33 (between a small and medium effect size). The other test – coding – showed no different between escitalopram *vs.* placebo. All subsequent analyses focused on digit span score as an outcome. We re-ran this test controlling for possible confounds: baseline Hamilton or Penn State Worry Questionnaire scores, demographics and co-morbidities. The significance of the effect on digit span did not change.

We chose six polymorphisms in the serotonin system - in the serotonin transporter and 1A, 2A and 1B receptors – based on biological plausibility and published data demonstrating their functional effects on transcription, as well as sufficiently high minor allele frequency (see Table 2). Because of the multiple genotypes, we used Bonferroni's corrected *p*-value of 0.008 (=0.05/6). Table 3 shows associations of the six genetic polymorphisms with digit span changes from pre-to post-treatment [Supplementary Table S1 (online) contains full treatment group, time and group \times time interaction statistics]. As Table 3 shows, two polymorphisms were significant with a corrected p < 0.008: rs6311 (serotonin receptor 2A G-1438A, where A is the high-transcribing allele) and rs11568817 (serotonin receptor 1B T-161G, where G is the high-transcribing allele). In both cases, the high-transcription group (A/A + A/G for rs6311, G/G + G/T for rs11568817) showed the significant decrease in the digit span test with escitalopram vs. placebo, while the low-transcription homozygote group did not. These contrasts are displayed in Fig. 2. The effect sizes of these decreases were d=0.64 for rs6311 and d =0.55 for rs11568817, indicating that, within these specific genotype groups, the magnitude of attention change was in the medium to medium-large effect size range.

Further analyses of these two genotypes suggest that the effect of escitalopram vs. placebo on attentional change was similar in both the high-transcription homozygote subjects and the

heterozygote subjects (Supplementary Figs S1 and S2). For rs6311, the A/A group estimate for the group × time interaction was 0.16 (s.E. 0.09) and the A/G estimate was 0.11 (s.E. 0.05), *vs*. 0.01 (s.E. 0.05) for the low-transcription homozygotes (G/G). Similarly for rs11568817, the G/G estimate was 0.08 (s.E. 0.08) and the G/C estimate was 0.13 (0.04), *vs*. -0.02 (s.E. 0.08) for the low-transcription homozygotes (T/T). Formal statistical tests were not run because of the small sample sizes; estimates are provided here only to portray the extent of similarity between the genotype subgroups.

As Table 3 also shows, in all of other genotypes, the high-transcription subgroup also showed a decrease in the digit span test in the escitalopram group compared to the placebo group, although the trend was in the same direction, the significance levels only reached p < 0.05 and did not survive correction for multiple testing. Therefore, no further analyses were carried out with these genetic subgroups.

We tested linkage disequilibrium between the three serotonin 1B receptor polymorphisms using PLINK software (http://pngu.mgh.harvard.edu/purcell/plink/; Purcell *et al.* 2007). The three genotypes were in linkage disequilibrium (D'=1 for all three associations), with R^2 =0.54 between rs11568817 and rs130058; R^2 = 0.36 between rs11568817 and rs6296 and R^2 =0.20 between rs130058 and rs6296. These values are similar to what is observed in HapMap data (www.hapmag.org). We also carried out haplotype analyses on the three serotonin 1B genotypes. The data are included in Supplementary Table S2, which sorts all diplotypes (haplotype pairs) in order of 'risk', defined as the treatment group × time estimate for digit span within that diplotype. Given the small sample size for many of the diplotypes, we cannot draw strong conclusions about the potential for multiple genotypic effects from the linked single nucleotide polymorphisms (SNPs). However, individuals who are 'risk' homozygotes at rs130058 (i.e. A allele), and rs6296 (i.e. G allele) have the lowest risk when they also have the low-expressing allele at rs11568817 (i.e. the T allele). This suggests that the rs11568817 locus is either the only genetic effect of these three serotonin 1B SNPs or it dominates other effects.

To ensure that differences in digit span change were not due to different treatment outcomes, we examined the correlations of change in Penn State Worry Questionnaire and in Hamilton Anxiety score with change in digit span. There was a small though significant relationship (r=0.18, p=0.045) of Hamilton Anxiety change with digit span change: those with a greater drop in anxiety symptoms also had a greater drop in digit span. This relationship was not seen with Penn State Worry Questionnaire change. The correlation was no different in the escitalopram and placebo groups and was no different among genotypes (data not shown). Therefore, treatment outcome did not appear to account for the digit span findings. Additionally, to ensure that differences in digit span change were not due to differential benzodiazepine use, we examined proportions of each genotype who were taking benzodiazepines; the proportion was small (<20% in all groups) and did not significantly differ between any genotype on exact tests (exact p range 0.25–0.80).

We also carried out pharmacokinetic analyses in the escitalopram group. Escitalopram average drug concentration was not correlated with digit span changes in the overall group nor in any subgroup at rs6311 or rs11568817 (see Supplementary Table S3).

Discussion

Antidepressant medications are widely and increasingly prescribed in older adults, the demographic at highest risk for adverse neurocognitive changes from psychotropic medications, owing to pharmacokinetic changes and reduced physiologic and cognitive homeostatic capacity (Pollock, 1999). In this study we found that the SSRI escitalopram

resulted in reductions in attention as measured by the digit span in older adults during acute treatment for anxiety. This effect appeared isolated to subjects with high-transcription serotonin receptor genotypes. The randomized design with placebo control is a strength of this study, because it allows us to control for expectancy, practice and time effects.

Reduction in attentional performance from SSRIs is not surprising. SSRIs affect cortical and subcortical regions involved in attention and other aspects of neurocognition (Lotrich & Pollock, 2005; Smith *et al.* 2011). In geriatric depression, SSRI administration has been shown to alter cerebral glucose metabolism in many of these areas, although the behavioural or clinical significance of these changes remains unclear (Diaconescu *et al.* 2010).

There are some caveats to this finding of reduced attentional performance with SSRI use. First, escitalopram reduced performance in the digit span, which measures the basic ability to pay attention for a few seconds, but it did not reduce performance on the more multifactorial coding task. The effect size of this reduction in the overall group was in the small-medium range, although it was higher (medium to medium-large) in the two significant genotype-defined subgroups. It is unclear whether this reduction represents a clinically relevant impairment or a subclinical change. We are not aware of any study that has determined the clinical significance of changes on the digit span. However, digit span measures a very basic cognitive function (the ability to maintain focus for a few seconds), upon which most other cognitive and everyday functions depend. For example, the ability to learn new information is highly dependent upon the amount of information one is able to encode, which, in turn, is highly dependent upon how well one is able to focus his/her attention. It is also important for understanding long sentences and performing everyday tasks. As such, it would seem the decrement in attention that we detected (which was about 0.5 for the overall escitalopram group and around 1 point drop, meaning an entire digit lost, in the 'at risk' genotypes) would be clinically important. Second, it is unclear whether this effect is specific to older adults. A similar study in young women with depression found no effects of citalopram on the digit span test, although some reduction in verbal fluency performance was noted (Wroolie et al. 2006). Finally, our finding should not be taken to suggest that SSRIs not be used in older adults. Instead, the findings suggest that there is room for drug development or personalization to provide a more beneficial neurocognitive profile.

For two serotonin receptors – 2A and 1B – we found evidence that high-expression genetic variants placed individuals at risk for significantly reduced attention with escitalopram, while the low-expression genetic variants did not. It is not surprising that we found that these receptor types are influential in the attentional effects of SSRIs. The serotonin 2A receptor (5-HTR_{2A}) is an excitatory G protein coupled receptor (GPCR; Cook *et al.* 1994) and is expressed widely throughout the central nervous system, particularly in neocortical areas; it may also have an inhibitory effect in some of these brain regions (Martin *et al.* 1998). High concentrations of 5-HTR_{2A} in cortical layer 5 pyramidal neurons demonstrate that this receptor is a key modulator of aspects of neurocognition (Aghajanian & Marek, 1999). The serotonin 1B receptor (5-HTR_{1B}) is an inhibitory GPCR expressed widely across cortical and subcortical brain regions involved in neurocognition, including attention and motivation (Sari, 2004). Like 5-HTR_{2A}, it is responsive to SSRI exposure and therefore is of interest as a moderator of antidepressant effects (Carr & Lucki, 2011; Murrough & Neumeister, 2011). Studies examining the neurocognitive effects of these antidepressants ought to model for functional genetic variability at these receptors.

Escitalopram drug level was not associated with change in attention performance in the overall sample or any genetic subgroup. Thus, although it has been posited that psychotropic adverse effects in older adults are related to higher and more variable drug concentrations

(Pollock, 2005), we were unable to detect a pharmacokinetic effect in this study. We used a medication with simple pharmacokinetics and a fairly restricted dose range (10–20 mg daily); perhaps larger samples or antidepressants with more variable drug levels would show such an effect.

The main limitation of our study is a relatively small sample size, which may have led to some negative results due to lack of power. Additionally, our sample was not sufficiently powered to test group × genotype × time interactions (i.e. a statistical test of whether attentional performance is significantly worse in a high-transcription genotype group than a low transcription group). Sample size requirements for such a study would be daunting (Leon, 2008), but future confirmatory research could utilize larger open-label treatment or possibly pharmaco-epidemiological studies that include genetic and neuropsychological measures. Such research could identify genetic subgroups of individuals more likely to suffer neurocognitive side-effects of serotonergic antidepressants, leading to personalization of treatment for the growing number of older adults taking these medications (Olfson & Marcus, 2009; Pagura *et al.* 2011).

In summary, we found that older adults have reduced attentional performance with SSRI treatment. Individuals with high-transcription genotypes at serotonin receptors appear to be at particularly high risk for this effect. Our findings urge further investigation of genetic predictors of neurocognitive changes with these commonly prescribed psychotropics in older adults.

Supplementary Material

Refer to Web version on PubMed Central for supplementary material.

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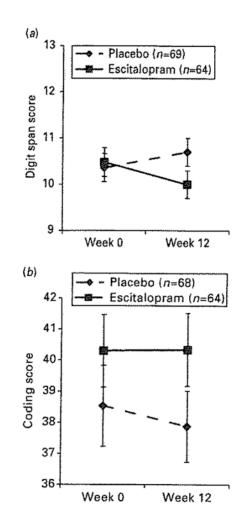
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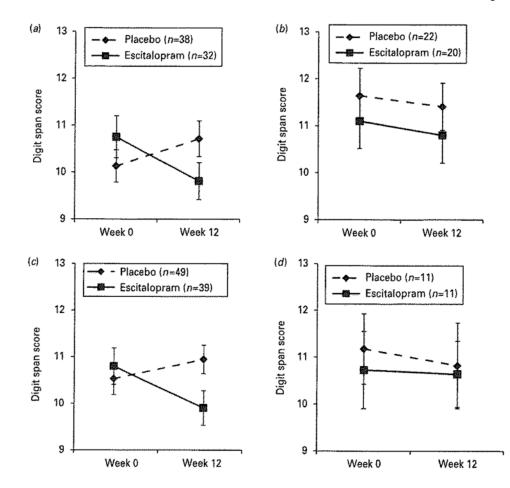
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Decrement in attention in escitalopram-treated vs. placebo-treated patients: effects seen with digit span task (a) but not with coding task (b).





Digit span decrement in genetic subgroups of the seroton in 2A receptor (5-HTR_{2A} rs6311) and the seroton in 1B receptor (5-HTR_{1B} rs11568817).

Baseline characteristics of the sample

	All patients $(n = 133)$	Placebo patients $(n = 69)$	Escitalopram patients $(n = 64)$	$\chi^2/t/$ Wilcoxon value	<i>p</i> value
Age	71.6 (s.d. =8.0)	72.4 (s.d. = 8.6)	70.7 (s.b. = 7.3)	1.19	0.2352
Gender					
Male	n = 46 (35%)	n = 28 (41%)	n = 18 (28%)	2.28	0.1313
Female	n =87 (65%)	$n = 41 \ (59\%)$	<i>n</i> = 46 (72%)		
Geographic ancestry					
White	$n = 113 \ (85\%)$	$n = 60 \; (87\%)$	n = 53 (83%)	0.45	0.5041
Black $(n = 19)$ or Asian Pacific $(n = 1)$	n = 20 (15%)	<i>n</i> =9 (13%)	n =11 (17%)		
Taking benzodiazepines					
Yes	$n = 19 \; (14\%)$	<i>n</i> =11 (16%)	n = 8 (12%)	0.32	0.5709
No	$n = 114 \ (86\%)$	$n = 58 \; (84\%)$	n = 56 (88%)		
Hamilton Anxiety Scale	22.7 (s.D. =4.3)	22.5 (s.D. = 4.5)	22.9 (s.D. =4.2)	-0.64	0.5255
Penn State Worry Questionnaire	56.3 (s.d. = 12.7)	57.9 (s.d. = 12.6)	54.6 (s.d. = 12.6)	1.48	0.1403
Hamilton Depression Scale	11.8 (s.d. = 3.8)	12.0 (s.d. = 4.2)	11.6 (s.d. = 3.4)	0.70	0.4863
RBANS total index score	94.7 (s.d. = 15.7)	93.7 (s.d. = 16.1)	95.8 (s.d. = 15.3)	-0.77	0.4422
RBANS digit span score	10.4 (s.d. = 2.5)	10.4 (s.d. = 2.5)	10.5 (s.d. = 2.5)	-0.28	0.7791
RBANS coding score	39.4 (s.d. = 10.1)	38.5 (s.D. = 10.7)	40.3 (s.d. = 9.3)	-1.01	0.3161
CIRSG (medical co-morbidity) score	9.0 (s.b. = 3.9)	8.6 (s.d. = 4.0)	9.6 (s.d. = 3.9)	-1.51	0.1330
Education, years	14.1 (s.d. $= 2.8$)	14.1 (s.d. = 3.1)	14.1 (s.d. $= 2.5$)	0.05	0.9599
Age of onset	38.7 (s.D. = 27.2)	35.9 (s.d. = 27.8)	41.7 (s.D. = 26.4)	-1.23	0.2215
Duration, months	383 (s.n. = 332)	426 (s.d. = 344)	337 (s.b. = 314)	1.55	0.1224

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The RBANS total index has a mean of 100 (s. D. = 15) in healthy adults.

Table 2	Candidate genotypes for attention changes with escital opram vs . placebo

Chromosome	Chromosome Polymorphism	rs number	Alleles	u	High-expressing allele	<i>n</i> High-expressing allele High-expressing allele frequency
5	HTR1A (C-1019G)	rs6295	C, G	132 G	G	0.50
6	HTR1B (T-261G)	rs11568817	T, G	130	G	0.48
9	HTR1B (A-161T)	rs130058	А, Т	127	A	0.65
9	HTR1B (G861C)	rs6296	G, C	128	G	0.74
13	HTR2A (G-1438A)	rs6311	G, A	132	A	0.41
17	5-HTT triallelic haplotype 5-HTTLPR + $rs25531$ S or L + G, L + A 133 L + A	5-HTTLPR + rs25531	S or L + G, L + A	133	L + A	0.47

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			Escitalopram	opram		Placebo	0				
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г отупног ринзни	centrype	"	LIC	I USL	1	IIC	I USL	1	L	μ	ESUIIAUE (S.E.)
rs6295 (HTR _{IA})	G/G + G/C	86	10.64	9.93	-0.71	10.50	10.86	0.36	6.3	0.0143	0.09 (0.04)
	C/C	26	11.90	11.30	-0.60	11.19	11.25	0.06	0.43	0.5163	0.06 (0.08)
rs11568817 (HTR _{1B})	G/G + G/T	88	10.85	9.92	-0.93	10.57	11.00	0.43	9.3	0.0031^{*}	0.11 (0.04)
	T/T	22	10.73	10.64	-0.09	11.18	10.82	-0.36	0.08	0.7793	-0.02 (0.08)
rs130058 (HTR _{1B})	A/A + A/T	92	10.82	10.13	-0.69	10.74	10.94	0.20	4.17	0.0442	0.07 (0.04)
	T/T	15	10.50	10.30	-0.20	10.20	11.20	1.00	06.0	0.3610	0.10 (0.11)
rs6296 (HTR _{1B})	G/G + G/C	100	10.78	10.02	-0.76	10.67	10.95	0.28	5.98	0.0163	0.09 (0.04)
	C/C	×	10.80	11.20	0.40	11.33	11.00	-0.33	0.18	0.6873	-0.06 (0.14)
rs6311 (HTR _{2A})	A/A + A/G	70	10.75	9.81	-0.94	10.13	10.71	0.58	9.1	0.0035^{*}	0.13 (0.04)
	G/G	42	11.10	10.80	-0.30	11.64	11.41	-0.23	0.01	0.9107	0.01 (0.05)
5-HTTLPR +	LA +	78	11.06	10.36	-0.70	10.57	10.81	0.24	4.1	0.0455	0.08 (0.04)
rs25531	LA-	35	10.53	10.00	-0.53	10.94	11.28	0.34	1.3	0.2639	0.08 (0.06)

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Data are in Caucasians only. Within each genotype, treatment group × time interaction tests the relative change in digit span in the escitalopram and placebo groups. Full statistical data (group, time effects) can be found in Supplementary Table S1.