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HUMAN GENETICS

Role of Dopamine Transporter Gene (*DAT1*) Polymorphisms in Personality Traits Variation[1]

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Abstract—According to psychobiological model of personality proposed by Cloninger, personality traits characterizing enhanced tendency to novel stimuli, impulsivity and sociability are influenced by dopaminergic system functioning. The present study considered both the main effect of two polymorphic loci (*VNTR* and *2319G>A*) in dopamine transporter gene (*DAT1*) and the role of distinct *DAT1* gene haplotypes in personality traits variation in 592 healthy individuals belonging to different ethnicities (men and women). The results of the study revealed the involvement of *VNTR* and *2319G>A* polymorphisms in Novelty Seeking variation and the main effect of *2319G>A* polymorphism on Reward Dependence (TCI) observed in Russian females. Moreover, *DAT1* gene haplotype effect on Novelty Seeking in Russian females and on Persistence (TCI) in Tatar females was demonstrated. Reported in the current study results pointed to the involvement of dopaminergic system (*DAT1* gene in particular) in variation of personality traits characterizing the tendency to novel stimuli, purposefulness, and sociability specifically in women.

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INTRODUCTION

According to the twin and family studies, the heritable component in personality traits accounts for 30 to 60%. Moreover, it has been assumed that personality traits might be considered as intermediate phenotypes predisposing to psychopathologies and as factors influencing on psychotherapy effectiveness [1]. Psychobiological model of personality proposed by Cloninger and designed inventories – Tridimensional Personality Questionnaire (TPQ) and Temperament and Character Inventory (TCI) – did allow to correlate heritable component with distinct personality traits [2]. Variations in personality traits assessed by this model were thought to be influenced by neurotransmitter system functioning: variation in such temperament trait as Harm Avoidance (HA) is primarily related to serotoninergic system, in Novelty Seeking (NS) - to dopaminergic system, and in Reward Dependence (RD) - to noradrenergic system functioning [2].

Dopaminergic system is known to be involved into regulation of motor function, mood and reward. Molecular-genetic studies of personality traits pointed to the influence of genes involved in dopamine metabolism on exploratory behavior and communicative traits forming [1]. Dopamine transporter (DAT) plays the major role in the regulation of dopaminergic neurotransmission by dopamine reuptake from synapse and its transport to the presynaptic terminal.

Published findings demonstrated an association of *VNTR* loci in dopamine transporter gene (*DAT1*) (5p15.3) with attention deficit and hyperactivity disorder (ADHD) [3, 4], bipolar disorders [5], nicotine addiction [6]. Contradictory results were reported in relation to personality traits. It was shown that attention deficit and hyperactivity disorder and addiction are characterized by increased Novelty Seeking - personality trait related to impulsive and excited behavior [7, 8]. Sabol et al. revealed that decreased Novelty Seeking scores were associated with *DAT1*9R*-allele in nicotine dependent individuals [6]. Van Gestel et al. reported statistically significant increase in the frequency of *DAT1*10R/*10R*-genotype in healthy women demonstrated enhanced Novelty Seeking [9]. While studying healthy individuals from the Polish population, Samochowiec et al. observed that *DAT1*9R/*9R*-genotype carriers were characterized by decreased scores on one of Reward Dependence subscales (TCI) compared to *DAT1*10R/*10R*-genotype carriers [10].

Some of the published findings demonstrated the involvement of *2319G>A (rs27072)* (rs27072) polymorphic marker located in the 3'-untranslated gene region in predisposition to attention deficit and hyperactivity disorder [3], bipolar personality disorder [5], and nicotine dependence [11]. To date there are no stud-

[1] The article was translated by the authors.

ies indicating the role of this locus in personality traits variation.

Contradictory findings reported by different scientific groups might be caused by the great number of factors including gender, age, ethnical and environmental differences.

The present study aimed to assess the role of *VNTR* and *2319G>A (rs27072)* polymorphic markers located in 3'-untranslated region of *DAT1* gene as well as the possible *DAT1* gene haplotype effect on personality traits variation in healthy individuals considering gender and ethnical differences. It was shown that genotyping of few functional polymorphic markers and the possibility to construct haplotypes possesses the larger statistical power and self-descriptiveness compared to the use of the single gene polymorphism [5].

MATERIALS AND METHODS

We recruited 592 healthy individuals from Bashkortostan (mean age ± SD, 19.5 ± 2.4 years): 210 Russians (155 women, 55 men) and 382 Tatars (234 women, 148 men). All enrolled individuals were students at the Universities without any familial history of psychopathologies. Written inform consent was obtained from all the participants after they were acquainted with all the procedures.

Personality traits were assessed using the Russian version of psychological inventories EPI (Eysenck Personality Inventory) (consists of 57 items) and TCI (Temperament and Character Inventory) (contains 125 items) [2]. TCI was translated and adapted by researchers from Laboratory of Developmental Psychogenetics of Psychological Institute of Russian Academy of Education (Moscow).

Genomic DNA was isolated from the whole blood using standard phenol-chlorophorm techniques. Fifteen mkl of reaction mixture for amplification consisting of 0.1–1 μg of genomic DNA, 10 pmol of each oligoprimer, 250 μM of each desoxynucleotidetriphosphate, 0.05 units of *Taq*-polymerase were added to 15 μl of 1× PCR buffer containing 67 mM Tris–HCl, pH 8.8, 6.7 mM magnesium chloride, 16.6 mM ammonium sulfate, 0.01% Tween-20.

DAT1 VNTR locus was detected using PCR technique with the following oligonucleotide primers: 5'-TGTGGTGTAGGGAACGGCCTGAG-3' and 5'-CTTCCTGGAGGTCACGGCTCAAGG-3'. After initial denaturation (94°C, 4 min), 31 amplification cycle consisting of denaturation (94°C – 30 s), annealing (68°C – 30 s), elongation (72°C – 1 min 30 s) and final extension step on 72°C – 7 min were performed. Subsequently, PCR products were resolved in 7% polyacrylamide gel (PAAG) and DNA fragments differing in 40 bp with the maximal size 523 bp (11 repeats) were detected.

In order to detect *2319G>A (rs27072)* polymorphism in *DAT1* gene, we conducted PCR analysis with the following primers: 5'-CCGTGTCTTGTGTTGCTGTA-3' and 5'-ACGGGGATTCTCAGCAGGTG-3'. After initial denaturation (95°C, 5 min), 35 amplification cycles consisting of denaturation (95°C – 30 s), annealing (62°C – 30 s), elongation (72°C – 30 s) were performed. Consequently, probes were subjected to the final extension step on 72°C – 7 min and cooled. Allele detection consisted of PCR products treatment with 3U of *Msp*I restriction endonuclease during 16 hours under 37°C. As a result of restriction, *DAT1*A*-allele (217 bp) and *G*-allele (consisting of 135 and 82 bp) were observed.

In order to demonstrate association between mean scores of personality traits and genotypes (alleles), statistical analyses were conducted using one-way (ANOVA) and multivariate analyses of variance (MANOVA) performing Bonferroni correction for multiple comparisons (statistical package SPSS 13.0). A measure of linkage disequilibrium (*D'*) between two markers (*VNTR* and *2319G>A*) was obtained with 2LD software package (http://www.iop.kcl.ac.uk/IoP/Departments/PsychMed/GEpiBSt/software.shtml). To test haplotype effects of the *DAT1* gene on personality traits we performed haplotype trend regression analyses [13] (http://statgen.ncsu.edu/zaykin/htr.zip).

RESULTS

Genotyping of two polymorphic markers (*VNTR* and *2319G>A*) located in 3'-untranslated region of *DAT1* gene and psychological assessment were performed in 592 unrelated healthy individuals. Since personality traits are assumed to be relatively stable during 11–27 years [14] and in order to minimize the influence of environmental factors, the present study was comprised of individuals less than 25 years with already obtained master degree or studying at the universities at the current moment. Since our study included healthy individuals both from Russian population (belonging to Slavic group of the Indo-European language family) and Tatar population (belonging to Turkic group of the Altaic language family), it was necessary to take ethnical differences into account.

DAT1 VNTR loci consisting of 3–11 repeats of 40 bp region is located in 3'-untranslated region of the gene, 425 bp upstream from *2319G>A* polymorphic marker. Allele frequencies for both loci for individuals from Russian and Tatar population (men and women) are demonstrated in Table 1. Distribution of allele and genotype frequencies was not differ from Hardy–Weinberg equilibrium. According to the results of psychological assessment, mean scores for all scales did not differ from the normal distribution.

Multivariate analysis of variance revealed statistically significant influence of gender on such personality traits as Neuroticism ($P = 0.000$; $F = 48.734$), Novelty Seeking ($P = 0.000$; $F = 14.697$), Harm Avoidance ($P = 0.025$; $F = 5.019$), Reward Dependence ($P =$

Table 1. Allele frequencies of two polymorphic loci in *DAT1* gene (*VNTR* and *2319G>A*) and linkage disequilibrium coefficient (D') between them in individuals from Tatar and Russian populations (women and men)

Marker, coefficient	Allele	Tatars		Russians	
		Women $N = 234$	Men $N = 148$	Women $N = 155$	Men $N = 55$
VNTR	**9R*	87/0.186	65/0.220	71/0.229	17/0.155
	**10R*	381/0.814	231/0.780	239/0.771	93/0.845
2319G>A	**A*	99/0.212	65/0.220	64/0.206	15/0.136
	**G*	369/0.788	231/0.780	246/0.794	93/0.844
D'	*VNTR* and *2319G>A*	0.749	0.435	0.996	0.947
D		0.030	0.021	0.048	0.021
D_{max}		0.040	0.048	0.048	0.022

Note: *N* – sample size. The number of observations/allele frequency are demonstrated.

0.000; $F = 13.275$); while the influence of ethnicity on Extraversion ($P = 0.001$; $F = 10.220$), Neuroticism ($P = 0.006$; $F = 7.738$), Novelty Seeking ($P = 0.001$; $F = 11.394$), Harm Avoidance ($P = 0.044$; $F = 4.077$), Self-transcendence ($P = 0.007$; $F = 7.395$) was established. Assuming these data, the following analyses were conducted considering gender and ethnical differences.

Published data point to the increase in gene expression associated with the presence of *DAT1*10R*-repeat allele in *VNTR* loci [15, 16]. Considering this fact and the rare frequency of *DAT1 VNTR* alleles consisting of 6–8 and 11 repeats in all studied groups (less than 2%), analysis of variance was performed in order to detect differences between *VNTR* 9-repeat allele carriers (*DAT1*9R*-allele) and *DAT1*10R*/**10R*-genotype carriers. According to ANOVA results, *DAT1*10R*/**10R*-genotype was associated with increased Novelty Seeking (TCI) ($P = 0.048$, $F = 3.986$) (Table 2) in Russian females. No statistically significant differences in personality traits scores in other investigated groups between carriers of various *DAT1 VNTR* genotypes were observed.

In order to detect correlation between *2319G>A* (*rs27072*) marker and personality traits, analysis of variance was performed between: 1) carriers of different genotypes; 2) *DAT1*A*-allele and *DAT1*G*/**G*-genotype carriers. Since the small number of individuals bearing *DAT1*G*-allele was observed in all investigated groups, in order to avoid type I error no analysis between *DAT1*G*-allele carriers and *DAT1*A*/**A*-genotype carriers with respect to personality traits was carried out. While using the second variant of grouping, association of *DAT1*A*-allele with the higher Novelty Seeking (TCI) in Russian female group was revealed ($P = 0.018$, $F = 5.737$) (Table 2). Moreover, significant influence of *DAT1*A*-allele on increased Reward Dependence (TCI) in Russian female group was observed ($P = 0.047$, $F = 4.011$) (Table 2).

Linkage disequilibrium coefficient (*D*') for individuals from Russian population and for women from Tatar population was sufficiently high (Table 1), which might be explained by the close location of two markers (425 bp). However, decreased *D*' was detected in Tatar male group that might be due to the small ratio of deviation between estimated and observed haplotype frequencies (*D*) to multiplication between the rare allele frequencies of both loci (D_{max}) (Table 1).

Since linkage disequilibrium coefficient between two loci is equal to:

$$D' = D/D_{max} = (p_{A9}p_{G10} - p_{A10}p_{G9})/D_{max},$$

where $p_{A9}, p_{G10}, p_{A10}, p_{G9}$ – observed frequencies of *DAT1* haplotypes *A*9R, G*10R, A*10R, G*9R* correspondingly, then *D*' might be larger in the case of increased D for distinct haplotype and in the case of decreased D_{max}. Moreover, accuracy of linkage disequilibrium coefficient *D'* estimation is related to the rare allele frequency of each loci [13], since D_{max} is calculated as multiplication of rare allele frequencies of each loci.

However, in Tatar female group *D* coefficient (hence *D*') was increased due to the lower frequency of observed rare *DAT1*9R*A*-haplotype [13]. For its turn, decrease in the frequency of the rare *DAT1*9R*A*-haplotype was shown to correlate with the lower frequencies of *DAT1*A*/**A*-genotype and *DAT1*9R*/**9R*-genotype at the major extent (that was demonstrated in Tatar female group).

Accordingly, differences in *D*' coefficient revealed in Tatar male and female groups might be caused by the differences in rare allele frequencies in both loci and by the frequency of the rare *DAT1*9R*/**9R*-genotype resulting in variability in the rarest *DAT1*A*9R*-haplotype.

The frequencies of *DAT1* gene haplotypes and mean scores for all personality scales with respect to *DAT1* gene haplotypes assessed via EM-algorithm (expectation-maximization algorithm) for 4 groups are demon-

Table 2. Mean scores of personality traits assessed by EPI and TCI questionnaires and one-way analysis of variance performed for *DAT1* gene *2319G>A* and *VNTR* polymorphisms in individuals from Tatar and Russian populations (women and men)

Group			*N*	Extraversion	Neuroticism	NS	HA	RD	PS
Tatars	Women	**A*	90	14.1 ± 3.5	14.5 ± 4.1	11.5 ± 3.3	9.7 ± 3.8	8.2 ± 2.2	2.5 ± 1.3
		**G/*G*	144	13.4 ± 3.8	14.8 ± 3.9	11.2 ± 2.9	9.7 ± 3.6	8.6 ± 2.5	2.9 ± 1.2
		**9R*	78	13.4 ± 3.8	14.2 ± 4.1	11.0 ± 3.1	9.4 ± 3.6	8.6 ± 2.6	2.6 ± 1.3
		**10R/*10R*	156	13.9 ± 3.6	14.9 ± 3.9	11.5 ± 3.1	10.0 ± 3.7	8.4 ± 2.2	2.8 ± 1.2
	Men	**A*	58	13.2 ± 3.8	12.3 ± 4.7	9.9 ± 3.0	8.8 ± 3.6	7.0 ± 2.4	2.5 ± 1.2
		**G/*G*	90	13.4 ± 3.8	12.3 ± 4.5	9.6 ± 3.1	8.3 ± 4.2	7.2 ± 2.4	2.7 ± 1.2
		**9R*	53	13.4 ± 3.9	12.6 ± 4.6	9.8 ± 2.6	8.8 ± 4.1	7.6 ± 2.1	2.5 ± 1.2
		**10R/*10R*	95	13.3 ± 3.7	12.2 ± 4.5	9.6 ± 3.2	8.2 ± 4.0	6.9 ± 2.4	2.7 ± 1.2
Russian	Women	**A*	57	15.2 ± 3.9	14.5 ± 4.1	**12.6 ± 2.7**[a]	8.1 ± 3.6	**8.3 ± 2.5**[c]	2.4 ± 1.3
		**G/*G*	98	14.3 ± 3.9	13.7 ± 4.7	**11.5 ± 2.9**[a]	8.7 ± 3.8	**7.6 ± 2.3**[c]	2.6 ± 1.3
		**9R*	59	14.5 ± 3.9	13.7 ± 4.1	**11.3 ± 3.1**[b]	8.3 ± 3.6	7.9 ± 2.3	2.6 ± 1.1
		**10R/*10R*	96	14.7 ± 3.9	14.1 ± 4.3	**12.2 ± 2.6**[b]	8.5 ± 3.8	7.8 ± 2.5	2.5 ± 1.4
	Men	**A*	14	14.2 ± 2.9	9.5 ± 4.4	12.0 ± 2.3	8.5 ± 2.7	7.2 ± 1.7	2.7 ± 1.3
		**G/*G*	41	14.6 ± 3.8	11.3 ± 4.2	10.8 ± 3.6	8.3 ± 3.9	7.7 ± 1.8	2.7 ± 1.3
		**9R*	16	15.5 ± 3.0	11 ± 3.2	12.5 ± 2.9	8.3 ± 4.3	7.7 ± 1.7	2.7 ± 1.2
		**10R/*10R*	39	14.5 ± 3.5	10.63 ± 4.6	11.0 ± 2.9	8.2 ± 3.5	7.6 ± 1.8	2.8 ± 1.3

Note: Mean and standard deviation are shown, *N* – the number of individuals in the group. Statistically significant differences ($P < 0.05$) are shown in bold: [a]$P = 0.018$, $F = 5.737$; [b]$P = 0.048$, $F = 3.986$; [c]$P = 0.047$, $F = 4.011$. NS – Novelty Seeking, HA – Harm Avoidance, RD – Reward Dependence, PS – Persistence.

strated in Table 3. Haplotype trend regression analysis conducted in Tatar female group revealed association between *DAT1*10R*G*-haplotype and increased Persistence (TCI) ($P = 0.014$). In Russian female group association of *DAT1*9R*G*-haplotype with decreased ($P = 0.036$) and *DAT1*10R*A*-haplotype – with increased Novelty Seeking scores (TCI) ($P = 0.038$) was demonstrated. The absence of any association in males from Russian and Tatar populations might be due to the small sample size. Moreover, no significant differences in character traits were revealed between either different *DAT1* haplotype carriers or individuals bearing various *2319G>A* and *VNTR* genotypes in all investigated groups.

DISCUSSION

The present study revealed the involvement of *DAT1* gene into variation of personality traits characterizing social activity (Novelty Seeking and Reward Dependence) and purposefulness (Persistence). Multivariate analysis of variance demonstrated the presence of statistically significant differences in personality traits between men and women. An increase in anxiety-related traits (Neuroticism, Harm Avoidance) was shown in women compared to men [17]. Contradictory findings were reported with respect to sociability-related traits (Extraversion, Novelty Seeking): both enhanced Extraversion [18] as well as its inhibition [19] in women compared to men was reported. Our sample was characterized by higher anxiety-related traits and extraversion in women compared to men. Personality traits variation between men and women might be explained with respect to biological theory (based on sex hormone differences) and psycho-social theory (model of social roles, in particular) [17]. According to the studies conducted on rats, increased dopaminergic activity in females might be caused by an estrogen (female sex hormone) action on dopamine transporter resulting in alteration of neurotransmitter affinity and dopamine accumulation in synapse [20].

As demonstrated in Table 1, distribution of allele frequencies in *DAT1 VNTR* marker in all groups corresponded to that reported in different European populations [10, 21] and was discrepant to that observed in Asian populations [21, 22]. The frequency of *DAT1* 10-repeat containing allele was shown to be significantly higher in Asian populations, especially in Chinese and Japanese (more than 90%) compared to European (Hispanic, in particular) and Afro-American (71.9, 70.9, and 72.9%, correspondingly) [21]. No differences in

Table 3. Haplotype trend regression analyses for *DAT1* gene polymorphisms in individuals from Tatar and Russian populations

Group		Haplotype	Frequency	Extraversion	Neuroticism	NS	HA	RD	PS
Tatars	Women	**9R*A*	0.010	14.192	15.579	12.087	9.737	7.535	2.125
		**9R*G*	0.176	13.267	14.431	10.912	9.654	8.760	2.639
		**10R*A*	0.206	14.044	14.590	11.338	10.034	8.287	2.523
		**10R*G*	0.608	13.791	14.812	11.423	9.704	8.408	2.856 ($P = 0.014$)
		Overall (*P*)	–	0.564	0.696	0.455	0.870	0.353	0.072
	Men	**9R*A*	0.027	13.372	12.234	10.710	9.155	7.094	2.381
		**9R*G*	0.191	13.527	12.959	9.542	8.884	7.754	2.432
		**10R*A*	0.194	13.094	12.482	9.808	8.683	7.115	2.571
		**10R*G*	0.588	13.387	12.102	9.607	8.247	7.052	2.673
		Overall (*P*)	–	0.950	0.630	0.582	0.729	0.244	0.627
Russian	Women	**9R*A*	0.000	14.368	13.631	11.894	7.526	8.157	2.894
		**9R*G*	0.234	14.561	13.602	11.219 ($P = 0.036$)	8.205	7.794	2.520
		**10R*A*	0.205	15.125	14.500	12.531 ($P = 0.038$)	7.843	8.265	2.359
		**10R*G*	0.561	14.462	13.937	11.902	8.794	7.702	2.645
		Overall (*P*)	–	0.551	0.570	0.063	0.369	0.478	0.071
	Men	**9R*A*	0.001	14.666	9.333	12.666	9.333	7.333	3.333
		**9R*G*	0.153	15.564	8.623	12.499	8.623	7.500	2.811
		**10R*A*	0.143	14.399	9.066	12.065	9.066	7.533	2.731
		**10R*G*	0.703	14.698	8.137	11.0833	8.137	7.766	2.794
		Overall (*P*)	–	0.765	0.603	0.315	0.806	0.943	0.813

Note: Statistically significant differences are shown in grey color. NS – Novelty Seeking, HA – Harm Avoidance, RD – Reward Dependence, PS – Persistence.

allele frequencies distribution of *2319G>A* polymorphic marker were demonstrated.

Despite the absence of data establishing functional significance of *DAT1* gene *2319G>A* polymorphism, probably, changes in nucleotide sequence in 3'-untranslated region of *DAT1* gene might influence on transcription effectiveness and stability of transcribed mRNA, and on changes in regulation of gene expression by specific microRNAs [23]. As a result of the present study, the main effect of *DAT1* gene *2319G>A* polymorphism on variation in personality traits (Novelty Seeking and Reward Dependence) was revealed: Russian females bearing *DAT1 DAT1*A*-allele demonstrated higher scores on these personality traits. To date there are no studies reporting an association of this loci in *DAT1* gene with personality traits; however, association of *DAT1 2319G>A*-allele with nicotine dependence, characterized by increased Novelty Seeking, was reported in male from Chinese population [11]. While investigating individuals from Israel and Canada with attention deficit and hyperactivity disorder, opposite findings were observed: preferential transmission of *DAT1*G*-allele in children with this disorder [3], characterized by higher Novelty Seeking [8], was detected.

Association of *DAT1*9R/*9R VNTR*-genotype with lower scores on one of Reward Dependence subscales (TCI) was reported in polish population [10]. Since the presence of linkage disequilibrium between *DAT1*9R*-allele and *DAT1*G*-allele was observed [24], that is in agreement with our data (Table 3), probably, it might be supposed that *DAT1*G/*G*-genotype carriers might demonstrate tendency to Reward Dependence inhibition. Findings observed in the present study confirmed this effect: healthy women from Russian population were characterized by statistically significant decrease in Reward Dependence (TCI) in the case of the presence of *DAT1*G/*G*-genotype. Moreover, involvement of *DAT1* gene in Reward Dependence variation was established by Kim et al. [22].

Results observed in the current study that demonstrated association of *DAT1 VNTR 10R/10R*-genotype with higher Novelty Seeking (TCI) in Russian female group are in accordance with data revealed by Van Ges-

tel et al. who reported significant increase in *DAT1*10R/*10R*-genotype frequency in women [9]. Moreover, lower Novelty Seeking was shown to be associated with *DAT1*9R*-allele in individuals with nicotine dependence [6].

Earlier findings pointed to the presence of association between *DAT1*10R*A* and alcohol addiction in individuals from Japanese population [24]. Since individuals with one of alcohol addiction types were shown to demonstrate enhanced Novelty Seeking [7], results reported by Ueno et al. might be compared with our data demonstrating association of *DAT1*10R*A*-haplotype with increased and *DAT1*9R*G*-haplotype – with decreased Novelty Seeking in Russian female group. Moreover, published data evidence in the presence of association between *DAT1*10R*-allele and higher scores on mentioned personality trait [6, 9].

However, revealed association of *DAT1*10R*G*-haplotype with higher Persistence in Tatar female group is discrepant to the findings reported by some scientific groups that observed higher frequency of *DAT1*10R*G*-haplotype [4] and *DAT1*G*-allele [3] in children with attention deficit and hyperactivity disorder (ADHD) demonstrated decreased purposefulness [8]. Contradiction between data reported here and revealed by Brookes et al. [4] might be due to the presence of socio-cultural and ethnical differences. Since individuals bearing *DAT1*10R*G*-haplotype are prevalent in our sample, it might be assumed that Tatar females characterized by enhanced Persistence have higher adaptation ability.

Consequently, results revealed in the present study demonstrated haplotype effect of *DAT1* gene on such personality traits as Novelty Seeking and Persistence in Russian and Tatar female groups correspondingly. However, variations in Reward Dependence (TCI) were shown to be associated with *2319G>A* polymorphism in Russian females. Revealed findings are in agreement with hypothesis proposed by Cloninger assuming the involvement of dopaminergic system genes (*DAT1*, in particular) in Novelty Seeking variation. At the same time, association between *DAT1* gene haplotypes or *2319G>A* polymorphism and Reward Dependence or Persistence demonstrated in the present study is in accordance with theory proposed by Comings et al. considering the involvement of different neurotransmitter system genes into simultaneous variation of various personality traits [25]. Reported findings point to the presence of gender and ethnical differences in personality traits caused by the influence of sex hormones, environmental factors, society, culture and ethnicity.

Despite the advantages of the current study (the use of homogenous sample with respect to age and education level, analysis conduction considering gender and ethnical differences), some limitations might be discussed. Firstly, frequencies of some genotypes and haplotypes in Russian male group were rather lower that might result in type I and II errors. Secondly, the main effect of one gene on personality traits variation was assessed; however, the data regarding gene interaction on molecular level were reported earlier. Thirdly, we were not able to consider such environmental factors as style of parental rearing, socio-cultural and financial level – that were shown to influence personality traits. The future studies in that field might be conducted considering gene-gene and gene-environment interactions.

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