

# Neurobiological Bases of Digital Behavior: Associations of DRD2, COMT, and BDNF Polymorphisms with Constructive and Destructive Internet Use Strategies among Young People

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## Abstract

**Introduction.** In the context of the rapid development of digital technologies, the study of both psychological aspects of constructive and destructive forms of digital behavior and their neurobiological underpinnings has become increasingly relevant. These underpinnings include genetic factors that determine individual differences in motivation for Internet use. **Objective.** To analyze the frequency of allelic variants of genes of the dopaminergic system (DRD2, COMT) and the neurotrophic factor gene (BDNF) in young people with different digital behavior strategies. **Methods.** The study involved 193 respondents aged 18–25 years ( $M = 19.37$ ;  $SD = 2.1$ ; 85% female), students enrolled in humanities programs. Digital behavior was assessed using the Digital Behavior Strategies questionnaire (Abakumova et al., 2021). Genotyping was performed using allele-specific real-time PCR for the BDNF (rs6265), COMT (rs4680), and DRD2 (rs1800497) genes. Statistical analysis included k-means cluster analysis, the Kruskal–Wallis nonparametric test and Dunn’s post hoc pairwise comparisons. **Results.** Carriers of different genotypes demonstrated significant differences in the expression of specific motives for Internet use. The BDNF Val/Val genotype was associated with higher

scores on information-seeking motives; the COMT Val/Val genotype was linked to increased expression of radical ideas; and carriers of the DRD2 CT variant showed higher levels of self-presentation and community participation. Cluster analysis identified three behavioral profiles—passive users, constructively engaged users, and destructively engaged users—which differed in the frequency of allelic variants of the studied genes. **Discussion.** The findings confirm the presence of associations between polymorphisms of dopaminergic system genes and BDNF and different strategies of digital behavior among young people, indicating the important role of genetic factors in the formation of constructive and destructive patterns of Internet use.

### Keywords

digital behavior, internet addiction, psychological predictors, genetic predictors, gene polymorphisms, COMT, DRD2, BDNF

### Funding

This study was supported by a grant from the Russian Science Foundation, project no. 22-78-10107, project topic: "Transformations of constructive and destructive strategies of youth information behavior in the context of increasing geopolitical risks: psychological, psychophysiological, and psychogenetic predictors," <https://rscf.ru/project/22-78-10107/>

### For citation

Ermakov, P. N., Denisova, E. G., Grishina, A. V., Sylka, N. V., Sahakyan, O. S., Belousova, E.E. (2025). Neurobiological Bases of Digital Behavior: Associations of DRD2, COMT, and BDNF Polymorphisms with Constructive and Destructive Internet Use Strategies among Young People. *Russian Psychological Journal*, 22(4), 158–184. <https://doi.org/10.21702/rpj.2025.4.8>

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### Introduction

In the context of the rapid development of digital technologies leading to increased Internet use, a number of advantages (such as access to information and communication opportunities) coexist with several negative consequences, including the risk of developing Internet addiction. Research indicates that the number of digital devices used and the frequency of Internet use are associated with the level of digital health literacy, which may play a key role in the effective and safe use of online resources (Zhao et al., 2024). At the same time, the risk of developing destructive forms of digital behavior may be linked not only to psychosocial factors (Gaidamashko, Lenkov, & Rubtsova, 2024), but also to biological determinants, including brain functioning characteristics and genetic predisposition (Long et al., 2016).

Internet addiction represents a global problem and is structurally similar to both substance-related and non-substance-related addictions (Kolesnikov, Melnik, & Teplova, 2019). Problematic Internet use in adolescents may be characterized by loss of control, compulsive behavior, irritability, and depressive symptoms (Singh, Kumar, & Reddy, 2025; Sun, Wang, & Liu, 2025). Among the significant risk factors for Internet gaming disorder, low self-regulation and anxiety have been identified (Rho et al., 2018), while depression is considered a key mediator in the development of addictive gaming behavior (Kircaburun et al., 2019; Cimino & Cerniglia, 2025).

Molecular genetic studies indicate that the development of Internet addiction involves a genetic component. In particular, most authors focus on genes involved in the regulation of neurotransmitter and neuropeptide systems (Sindermann et al., 2021; Annunzi et al., 2023). Recent review studies suggest that the risk of addictive behaviors is most likely associated with polymorphisms in the DRD2/ANKK1 (rs1800497, Taq1A), COMT (rs4680, Val158Met), DAT1 (rs28364027), 5-HTT (SLC6A4, rs25531), CHRNA4 (rs1044396), OPRM1 (rs1799971), BDNF (rs6265), HTR2A (rs6313), GRIN2B (rs2268498), and other genes (Tereshchenko & Smolnikova, 2020; Tereshchenko, 2023). For example, individuals demonstrating problematic or risky online behavior show a higher frequency of the minor A1 (T) allele in the polymorphic locus (C2137T) of the ANKK1 gene, which is associated with reduced expression of dopamine D2 receptors and altered levels of behavior-regulating hormones (Rył et al., 2024). In addition, the Val66Met polymorphism (rs6265) of the BDNF gene is known to be associated with reduced brain-derived neurotrophic factor activity, leading to impaired synaptic plasticity in the prefrontal cortex and hippocampus, which may increase vulnerability to compulsive behaviors and addictions through dysfunctions in cognitive control (Demirci et al., 2023). Another polymorphic locus, rs6313 in the HTR2A gene encoding the serotonin 2A receptor, has been associated with increased impulsivity and emotional lability, which, in turn, correlates with Internet addiction and maladaptive social media use (Dai et al., 2024).

Furthermore, evidence suggests that epigenetic mechanisms—particularly differential DNA methylation in genes regulating neurotransmitter systems—may modulate behavioral phenotypes associated with excessive use of digital technologies. Annunzi et al. (2023) demonstrated that individuals with subclinical manifestations of Internet addiction (Internet Addiction Test scores of 30–49) exhibit significant alterations in methylation levels in the promoter regions of the OXTR gene, encoding the oxytocin receptor, as well as in dopamine and serotonin transporter genes (SLC6A4 and SLC6A3).

Thus, despite the evident benefits of contemporary digital technologies, their development is accompanied by substantial risks, among which Internet addiction and destructive Internet use strategies occupy a prominent place. This phenomenon has a complex etiology involving both psychosocial and biological factors. However, despite the growing body of research on the genetic foundations of Internet addiction, data for Russian populations on how polymorphisms in genes of neurotransmitter and neuropeptide systems (including DRD2, BDNF, COMT, among others) are associated with

Internet use strategies remain scarce. In this context, the aim of the present study is to conduct a comparative analysis of the frequencies of allelic variants of genes involved in the regulation of the dopaminergic system and neurotrophic factors in individuals exhibiting different digital behavior strategies within a Russian sample.

## Methods

The sample consisted of 193 participants aged 18–25 years (mean age = 19.37; 85% female), all students enrolled in humanities-related academic programs. To assess features of digital behavior, the Digital Behavior Strategies questionnaire was employed (Abakumova et al., 2021).

To examine genetic predictors, a molecular genetic analysis was conducted. The following candidate genes were selected for analysis: the dopamine receptor gene DRD2 (rs1800497), the catechol-O-methyltransferase gene COMT (rs4680), and the brain-derived neurotrophic factor gene BDNF (rs6265).

Participants were surveyed in person using an electronic testing format. Collection of genetic material (buccal epithelial cells) for genomic DNA extraction was performed immediately after completion of the psychological assessment, predominantly during the first half of the day. DNA analysis was carried out using allele-specific polymerase chain reaction (PCR) with real-time detection.

Statistical analyses included the Shapiro–Wilk test to assess the normality of empirical distributions. Cluster analysis (k-means method) was used to divide the sample into groups according to digital behavior characteristics. Differences between the identified subgroups were examined using the nonparametric Kruskal–Wallis test, followed by Dunn’s pairwise post hoc comparisons.

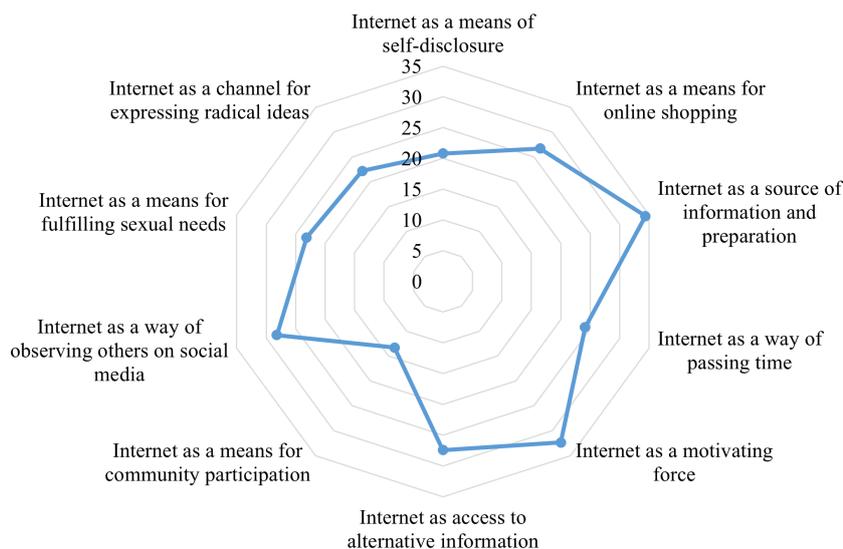
All statistical analyses were performed using the JASP software package (version 0.16)

## Results

The analysis of digital behavior revealed that the most strongly expressed motives for Internet use were Internet as an informational resource (mean score = 34.34 out of a possible 50) and Internet as a motivating force (mean score = 32.35) (Figure 1). The lowest scores were observed on the Internet for community participation scale (mean = 13.31).

**Figure1**

*Results of the assessment of digital behavior characteristics in the sample (mean values)*



A quantitative analysis of the questionnaire results for all digital behavior scales was conducted for each participant to identify the predominant motives for Internet use, determined by the highest score (Table 1). The number and percentage of individuals exhibiting predominant constructive strategies (according to the questionnaire key, corresponding to the first five scales) and destructive strategies (scales 6–10) were calculated. Additionally, comparisons were made based on participants’ total scores for constructive versus destructive strategies. Overall, the analysis confirmed that constructive digital behavior strategies were predominant in the sample. The most frequently identified leading motives were Internet as a source of information and preparation and Internet as a motivating force.

**Table1**

*Results of the analysis of predominant motives and strategies of Internet use*

Motives and Strategies of Internet Use	Number of Participants	% of the Sample
Internet as a means of self-disclosure	7	3,63
Internet as a means for online shopping	8	4,15

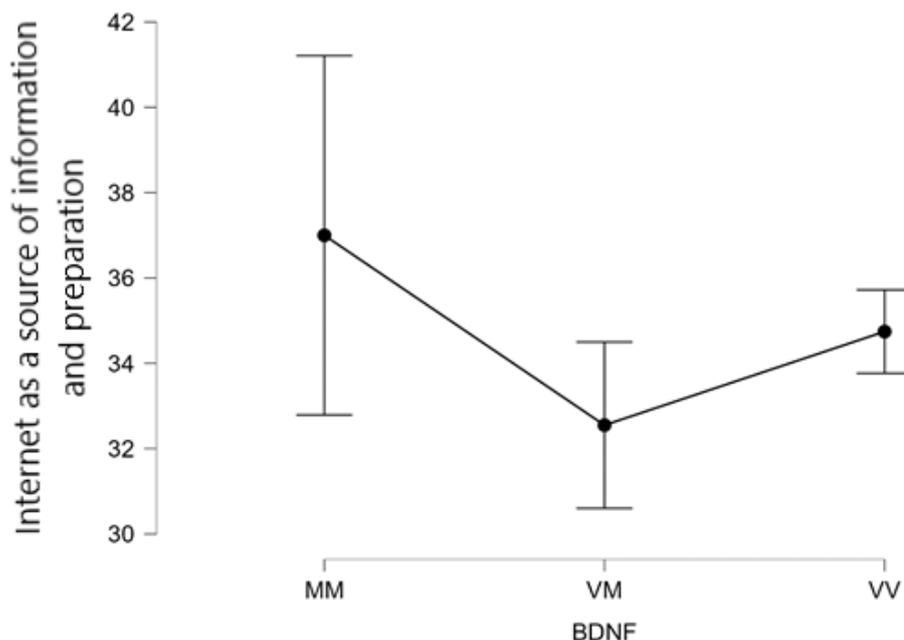
Motives and Strategies of Internet Use	Number of Participants	% of the Sample
Internet as a source of information and preparation	56	29,02
Internet as a way of passing time	4	2,07
Internet as a motivating force	36	18,65
Internet as access to alternative information	13	6,74
Internet as a means for community participation	0	0,00
Internet as a way of observing others on social media	22	11,40
Internet as a means for fulfilling sexual needs	4	2,07
Internet as a channel for expressing radical ideas	1	0,52
Mixed motives	42	21,76
Total with predominant constructive strategy	147	76,17
Total with predominant destructive strategy	46	23,83
Constructive strategies predominate (by total score)	166	86,01
Destructive strategies predominate (by total score)	27	13,99

To test the hypothesis that carriers of different genotypes in the studied genes may exhibit differences in the expression of digital behavior strategies, a comparative analysis was conducted. The significance of differences was assessed using the Kruskal–Wallis test, with Dunn’s post hoc pairwise comparisons applied for post hoc analysis (Appendix 1).

Regarding genotypes of the brain-derived neurotrophic factor gene BDNF (rs6265), it was found that carriers of the Val/Val (VV) allele variant had significantly higher scores on the scale measuring Internet use for information seeking, including academic purposes, compared to Val/Met (VM) carriers (Dunn post hoc test, VV vs. VM,  $p = 0.034$ ; Figure 2). Met/Met (MM) carriers showed the highest mean scores compared to the other groups, but also exhibited a substantial variability in this scale (as well as across most other scales) within the subgroup.

**Figure2**

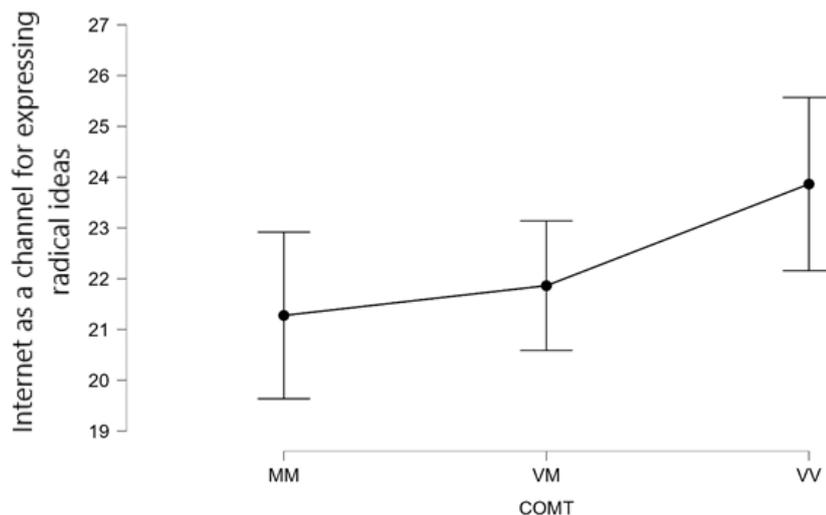
*Differences in the expression of specific Internet use motives among carriers of different BDNF (rs6265) genotypes*



Regarding the catechol-O-methyltransferase gene COMT (rs4680), carriers of the Val/Val (VV) allele exhibited significantly higher scores on the scale measuring Internet use for expressing radical ideas compared to carriers of other genotypes (Dunn post hoc test, VV vs. VM,  $p = 0.046$ ; VV vs. MM,  $p = 0.046$ ; Figure 3).

**Figure 3**

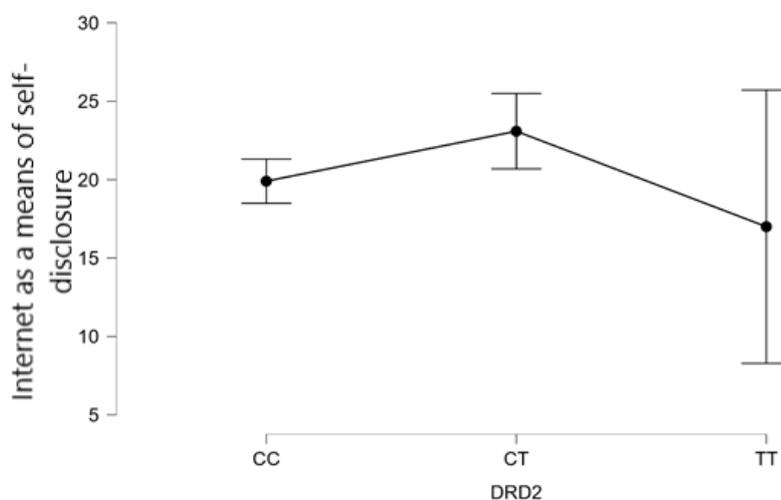
*Differences in the expression of specific Internet use motives among carriers of different COMT (rs4680) genotypes*



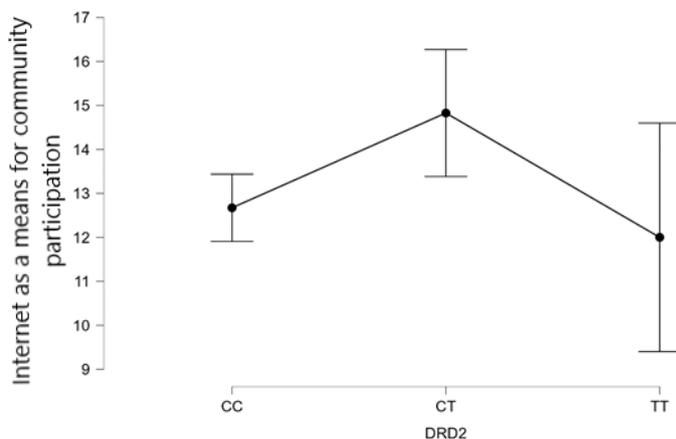
For the dopamine receptor gene DRD2 (rs1800497), it was shown that carriers of the CT allele variant scored significantly higher than CC carriers on the scales measuring Internet use for self-disclosure (Dunn post hoc test, CC vs. CT,  $p = 0.018$ ) and community participation (Dunn post hoc test, CC vs. CT,  $p = 0.001$ ; Figure 4). TT carriers had the lowest mean scores compared to the other groups, but also exhibited substantial variability on these scales (as well as most other scales) within the subgroup.

**Figure 4**

*Differences in the expression of specific Internet use motives among carriers of different DRD2 (rs1800497) genotypes*



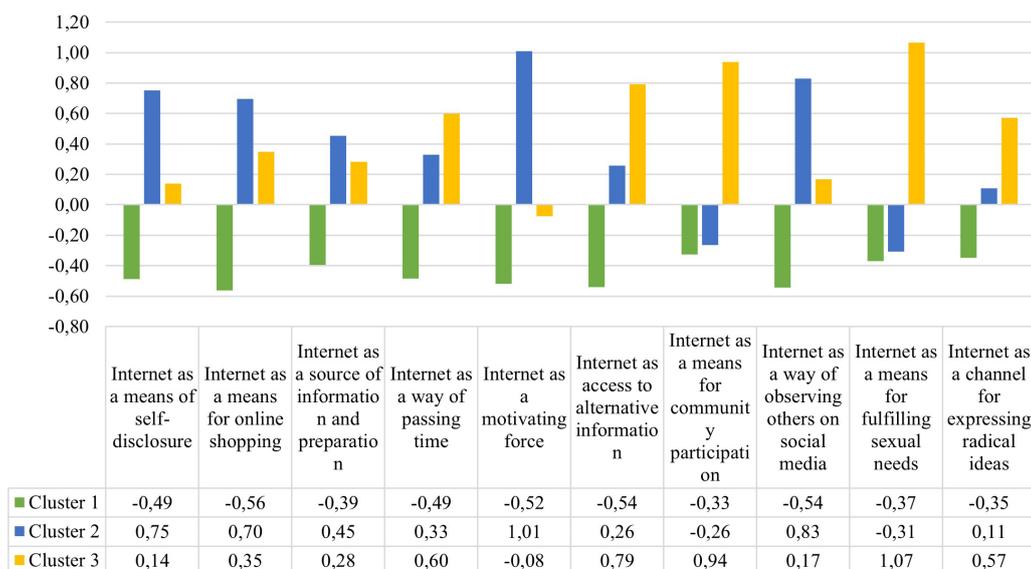
PSYCHOPHYSIOLOGY



The mean total scores for constructive and destructive strategies did not significantly differ among carriers of the studied genotypes. However, analysis of the structure of Internet use motives, both in the current sample and in our previous studies (Abakumova et al., 2021; Ermakov et al., 2022), revealed substantial within-group variability, indicating heterogeneity in behavioral profiles. To identify latent patterns beyond the initially proposed dichotomy of constructive and destructive strategies, cluster analysis (k-means) was applied. Based on sample size, preliminary calculations, and inter-cluster differences, three clusters were identified (Figure 5, Table 2).

**Рисунок 5**

*Results of cluster analysis of the sample based on digital behavior strategy scores (z-scores)*



To assess differences in Internet use strategies between the identified clusters, a one-way analysis of variance (ANOVA) was conducted. The results revealed statistically significant intergroup differences across all examined measures ( $p < 0.001$ ). The largest effect size was observed for the motive Internet as a motivating force (examples of others) ( $F = 132.26$ ), while the smallest was for Internet for expressing radical ideas ( $F = 31.87$ ).

**Table 2**

*Results of the ANOVA assessing the significance of differences between identified clusters*

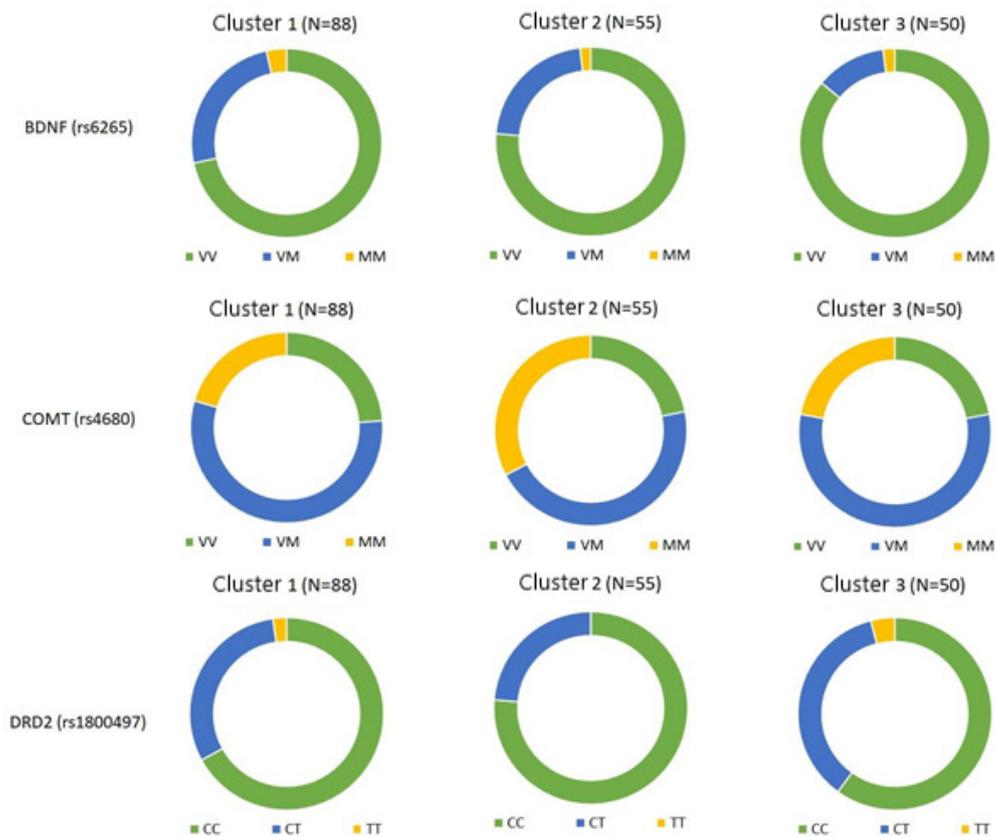
	Between-group variance	Within-group variance	F-value (Fisher's F)	Significance level (p-value)
Internet as a means of self-disclosure	105,42	280,58	72,14	< 0,001
Internet as a means for online shopping	121,12	264,88	87,79	< 0,001
Internet as a source of information and preparation	58,01	327,99	33,96	< 0,001
Internet as a way of passing time	89,81	296,19	58,22	< 0,001
Internet as a motivating force	157,44	228,56	132,26	< 0,001
Internet as access to alternative information	121,61	264,39	88,32	< 0,001
Internet as a means for community participation	110,90	275,10	77,40	< 0,001
Internet as a way of observing others on social media	129,63	256,37	97,08	< 0,001
Internet as a means for fulfilling sexual needs	143,37	242,63	113,45	< 0,001
Internet as a channel for expressing radical ideas	54,96	331,04	31,87	< 0,001

Participants in the first cluster exhibited the lowest mean scores across all scales and can be characterized as the least engaged or relatively passive users. The second cluster was characterized by the predominance of constructive and social motives (self-presentation and observing others) and can be described as users oriented toward building online identity and gaining social approval. The third cluster primarily included participants with predominant destructive motives, although these were combined with certain constructive (pragmatic) motives.

Subsequently, to analyze the frequencies of allelic variants in genes associated with regulation of the dopaminergic system and neurotrophic factors among individuals with different digital behavior strategies, absolute numbers and percentages of carriers for each allelic variant were calculated within each cluster (Figure 6, Appendix 2).

**Figure 6**

*Frequencies of different genotypes for BDNF (rs6265), COMT (rs4680), and DRD2 (rs1800497) across identified clusters*



The analysis showed that the frequency of the VV variant of BDNF (rs6265) was higher in Cluster 3. For COMT, there was a relative decrease in the frequency of the VM variant and an increase in MM carriers in Cluster 2. Cluster 2 also demonstrated an increased proportion of CC carriers for DRD2 (rs1800497).

## Discussion

This study demonstrated that carriers of different genotypes in the investigated genes show distinct patterns in specific motives for digital behavior. Val/Val (VV) carriers of the BDNF gene (rs6265) scored higher on the scale measuring Internet use as a source of information, including for academic purposes, compared with Val/Met (VM) carriers. This may reflect higher neurotrophic activity and enhanced neuroplasticity. Previous studies have linked the Val (G) allele with more efficient secretion of mature BDNF, which supports cognitive functions, synaptic plasticity, and learning (Egan et al., 2003; Demirci et al., 2023). Such neurobiological characteristics may facilitate engagement in structured learning and information-seeking online. At the same time, increased neuroplasticity in Val carriers may heighten sensitivity to external stimuli, including social and informational cues. This could explain their tendency to actively use the Internet as a source of information not only for learning but also as a means of regulating emotions and maintaining a sense of control. In this way, educational and informational digital content may serve both practical and compensatory-regulatory functions, helping reduce stress through predictability and perceived efficacy.

For the COMT gene (rs4680), carriers of the Val/Val (VV) allele scored significantly higher on the scale measuring Internet use for expressing radical ideas compared to carriers of other genotypes. The COMT gene encodes an enzyme responsible for dopamine degradation, and Val/Val carriers exhibit the highest enzymatic activity, resulting in faster dopamine breakdown in the prefrontal cortex. Studies on the functional significance of the Val158Met polymorphism have produced somewhat mixed findings. Within the "warrior/worrier" framework (Madsen et al., 2024; Serrano et al., 2019), Val/Val is associated with greater stress resilience due to lower emotional reactivity, whereas Met carriers tend to show increased anxiety and physiological sensitivity to stressors. Under moderate stress, Val/Val carriers demonstrate better executive functioning compared to baseline, whereas VM and MM carriers show a decline in performance under stress (Zareyan et al., 2021). At the same time, data on cognitive efficiency often follow an inverted-U pattern, in which homozygous carriers—whether with the highest or lowest enzymatic activity—exhibit lower cognitive performance compared with VM carriers; moreover, when interactions with other genes are taken into account, this relationship is not always consistently observed (Pizzonia et al., 2023). In the context of our findings, the elevated expression of radical ideas in Val/Val carriers may reflect particular features of emotional reactivity. Individuals with lower prefrontal dopamine levels are likely to respond less intensely to negative environmental cues, including social criticism. In this

case, reduced emotional reactivity may not only confer greater calmness and resilience but also influence emotional and cognitive processing in a way that allows these individuals to express their opinions more directly or promptly, without hesitation or fear of negative evaluation.

It was also found that carriers of the CT genotype of the DRD2 gene (rs1800497) scored significantly higher than CC carriers on scales measuring Internet use for self-disclosure and participation in online communities. The rs1800497 polymorphism involves a single nucleotide substitution (thymine to cytosine), which does not directly alter the protein structure but may affect the expression levels of dopamine D2 receptors. T allele carriers are thought to have reduced D2 receptor density. Psychologically, this variant has been associated with increased impulsivity, lower self-control, and heightened vulnerability to stress (Zhang et al., 2012). In the context of our findings, the lower density of D2 receptors in T allele carriers appears to correspond with greater sensitivity to external sources of reward, including social approval, likes, comments, and engagement in group-based online interactions.

Regarding the cluster analysis results, this study was able to refine the initially proposed dichotomy of constructive and destructive strategies. The sample naturally divided into three groups: minimally engaged users (passive-constructive strategy), constructively engaged users (active-constructive strategy), and destructively engaged users (active-destructive strategy). Consistent with previous research (Abakumova et al., 2021; Ermakov et al., 2022), no passive-destructive type emerged, indicating the need for both sample expansion and potential refinement of the measurement instrument.

Differences in genotype distribution indicate that the second cluster, characterized by self-presentation and social approval motives, showed an increased frequency of MM carriers for COMT and CC carriers for DRD2. These genetic features may contribute to enhanced prefrontal dopamine activity, both through reduced dopamine degradation (MM carriers) and higher D2 receptor density (CC carriers). This dopaminergic profile may support improved executive functioning, planning, self-regulation, and social-cognitive sensitivity, collectively promoting behavior oriented toward social interaction, impression management, and approval-seeking. Such individuals are likely to manage their digital presence more effectively, adjusting it finely to social context and audience feedback.

The third cluster, representing a destructive-pragmatic profile, included a higher proportion of VV carriers of BDNF, suggesting increased neuroplasticity and heightened sensitivity to external stimuli, including social and digital cues. When combined with adverse environmental conditions (e.g., digital overload or stress), this heightened sensitivity may promote reactive and potentially maladaptive behavioral patterns, including the expression of destructive motives.

Internet addiction is influenced by multiple polymorphisms in dopaminergic and serotonergic genes, which modulate the relationship between environmental factors and addictive behaviors (Cerniglia et al., 2020). For example, the T allele of rs6277 in DRD2 is

associated with reduced D2 receptor density in extrastriatal regions and represents a risk factor for video game addiction in adolescents (Tereshchenko et al., 2024; He et al., 2020). At the psychological level, genetic variations regulate impulsivity and decision-making tendencies: homozygous Met carriers of COMT exhibit higher risk-related impulsivity, increasing vulnerability to addictive behaviors (Malloy-Diniz et al., 2013; Wu et al., 2024).

Overall, these results support the view that individual differences in digital behavior motivation may be partly explained by neurobiological mechanisms and align with findings from contemporary behavioral genetics research. However, these effects should be interpreted cautiously, as this study did not examine potential environmental or psychological moderators, representing a key limitation. Furthermore, the differentiation between constructive and destructive strategies requires further theoretical and methodological refinement, including potential adjustments to the measurement instrument.

## Conclusions

The present study aimed to analyze the frequency of allele variants in genes associated with the regulation of the dopaminergic system and neurotrophic factors among individuals with different digital behavior strategies in a Russian sample. The results indicate that polymorphisms in DRD2, COMT, and BDNF are associated both with the intensity of specific motives and, more broadly, with constructive and destructive strategies of digital behavior.

The Val/Val genotype of BDNF (rs6265) is associated with more pronounced pragmatic Internet use, including for educational purposes, but may also relate to destructive strategies. The Val/Val genotype of COMT (rs4680) is linked to more frequent expression of radical ideas, which may reflect reduced emotional sensitivity and a more direct, straightforward approach in social behavior, whereas Met/Met carriers tend to demonstrate more constructive engagement. Carriers of the CT genotype of DRD2 (rs1800497) scored significantly higher than CC carriers on scales measuring Internet use for self-disclosure and participation in communities. Notably, the CT allele was also more frequent among individuals with predominating destructive-pragmatic motives.

Future research directions include refining the methodology for assessing digital behavior strategies, incorporating additional socio-psychological factors that shape digital behavior, and comparing identified behavioral profiles with the concept of Reward Deficiency Syndrome (Blum et al., 2022), particularly regarding reduced reward sensitivity and increased need for external stimulation, which may explain certain forms of excessive or maladaptive online activity.

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## Appendix 1

### *Results of the comparative analysis of the intensity of specific motives for Internet use among carriers of different genotypes of BDNF (rs6265), COMT (rs4680), and DRD2 (rs1800497)*

	Mean scores on the "SIB" questionnaire (Abakumova et al., 2015) for carriers of different genotypes of BDNF, COMT, DRD2			Significance of differences			
	VV	VM	MM	Kruskal-Wallis test	Dunn's pairwise post hoc tests	p-value	
	H	p-value	comparisons				z
BDNF	21	20,825	20,784	0,137	MM - VM	0,224	
						MM - VV	0,318
						VM - VV	0,215
Internet as a means of self-disclosure	VV	VM	MM	0,568	MM - VM	0,629	
	21,702	20,52	20,477			MM - VV	0,702
						VM - VV	0,201
COMT	CC	CT	TT	6,319	CC - CT	-2,368	
	19,901	23,086	17			CC - TT	0,613
						CT - TT	1,324
DRD2				0,042	CC - CT	0,018	
						CC - TT	0,54
						CT - TT	0,185

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Mean scores on the "SIB" questionnaire (Abakumova et al., 2015) for carriers of different genotypes of BDNF, COMT, DRD2		Significance of differences				
		Kruskal–Wallis test		Dunn's pairwise post hoc tests		
		H	p-value	comparisons	z	p-value
BDNF	VV	VM	MM	MM - VM	-0,625	0,532
	23,6	25,65	27,054	MM - VV	-1,248	0,212
				VM - VV	-1,521	0,128
COMT	VV	VM	MM	MM - VM	0,049	0,961
	26,83	27	25,75	MM - VV	0,846	0,398
				VM - VV	0,936	0,349
DRD2	CC	CT	TT	CC - CT	0,245	0,807
	26,824	26,586	23	CC - TT	1,304	0,192
				CT - TT	1,206	0,228

Internet as a means for online shopping

Mean scores on the "SIB" questionnaire (Abakumova et al., 2015) for carriers of different genotypes of BDNF, COMT, DRD2		Significance of differences				
		Kruskal–Wallis test		Dunn's pairwise post hoc tests		
		H	p-value	comparisons	z	p-value
BDNF	VV	VM	MM	MM - VM	1,742	0,081
	37	32,55	34,743	MM - VV	0,985	0,325
				VM - VV	-2,125	0,034
COMT	VV	VM	MM	MM - VM	1,27	0,204
	35,255	34,167	33,795	MM - VV	1,379	0,168
				VM - VV	0,362	0,717
Internet as a source of information and preparation	CC	CT	TT	CC - CT	0,023	0,982
	34,527	34,017	33,25	CC - TT	0,11	0,912
				CT - TT	0,101	0,919

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Mean scores on the "SIB" questionnaire (Abakumova et al., 2015) for carriers of different genotypes of BDNF, COMT, DRD2	Significance of differences					
	Kruskal–Wallis test			Dunn's pairwise post hoc tests		
	H	p-value	comparisons	z	p-value	
BDNF	VV	VM	MM			
	25,2	23,5	24,264	0,521	0,771	MM - VM 0,573 0,566
						MM - VV 0,368 0,713
						VM - VV -0,588 0,557
Internet as a way of passing time	VV	VM	MM			
	25	24,186	23,068	1,348	0,51	MM - VM 0,745 0,456
						MM - VV 1,157 0,247
						VM - VV 0,617 0,537
	CC	CT	TT			
	24,13	24,052	25,25	0,107	0,948	CC - CT 0,112 0,911
						CC - TT -0,296 0,767
						CT - TT -0,325 0,745

Mean scores on the "SIB" questionnaire (Abakumova et al., 2015) for carriers of different genotypes of BDNF, COMT, DRD2	Significance of differences					
	Kruskal–Wallis test			Dunn's pairwise post hoc tests		
	H	p-value	z	comparisons	z	p-value
BDNF	VV	VM	MM	MM - VM	-0,385	0,701
	30,4	31,35	32,689	MM - VV	-0,796	0,426
				VM - VV	-1,009	0,313
COMT	VV	VM	MM	MM - VM	1,557	0,12
	33,213	31,657	33,045	MM - VV	0,385	0,7
				VM - VV	-1,074	0,283
Internet as a motivating force	CC	CT	TT	CC - CT	-0,731	0,464
	32,038	33,207	30,25	CC - TT	0,629	0,529
				CT - TT	0,841	0,4

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		Mean scores on the "SIB" questionnaire (Abakumova et al., 2015) for carriers of different genotypes of BDNF, COMT, DRD2				Significance of differences			
						Kruskal–Wallis test		Dunn's pairwise post hoc tests	
		H	p-value	comparisons	z	p-value			
BDNF	VV	VM	MM						
	28	26,95	27,514		0,419	MM - VM	0,52	0,603	
						MM - VV	0,338	0,736	
COMT	VV	VM	MM						
	27,745	27,431	27		0,448	MM - VM	0,63	0,529	
						MM - VV	0,547	0,585	
DRD2	CC	CT	TT						
	27,679	26,621	30		0,912	VM - VV	0,02	0,984	
						CC - CT	0,887	0,375	
Internet as access to alternative information									
						CC - TT	-0,268	0,789	
						CT - TT	-0,534	0,594	
BDNF	VV	VM	MM						
	11,2	13,15	13,419		1,283	MM - VM	-0,625	0,532	
						MM - VV	-0,933	0,351	
COMT	VV	VM	MM						
	12,979	13,392	13,455		0,395	VM - VV	-0,717	0,473	
						MM - VM	-0,551	0,582	
DRD2	CC	CT	TT						
	12,672	14,828	12		11,124	MM - VV	-0,564	0,573	
						VM - VV	-0,118	0,906	
					CC - CT	-3,334	< ,001		
					CC - TT	-0,409	0,683		
					CT - TT	0,616	0,538		

Mean scores on the "SIB" questionnaire (Abakumova et al., 2015) for carriers of different genotypes of BDNF, COMT, DRD2		Significance of differences							
		Kruskal–Wallis test		Dunn's pairwise post hoc tests					
		H	p-value	comparisons	z	p-value			
BDNF	VV	VM	MM						
	25,2	27,15	28,595	1,602	0,449	MM - VM	-0,48	0,631	
						MM - VV	-0,883	0,377	
COMT	VV	VM	MM						
	28,979	26,961	30,273	4,013	0,134	VM - VV	-0,977	0,329	
						MM - VM	1,277	0,202	
DRD2	CC	CT	TT						
	28,214	28,552	23	1,533	0,465	MM - VV	-0,528	0,597	
						VM - VV	-1,862	0,063	
BDNF	VV	VM	MM						
	26,8	21,2	23,541	4,419	0,11	CC - CT	-0,05	0,96	
						CC - TT	1,227	0,22	
COMT	VV	VM	MM						
	22,638	23,471	22,909	0,33	0,848	CT - TT	1,22	0,223	
						MM - VM	1,771	0,076	
DRD2	CC	CT	TT						
	23,221	23	22,5	0,39	0,823	MM - VV	1,219	0,223	
						VM - VV	-1,605	0,108	
Internet as a means for fulfilling sexual needs	VV	VM	MM						
	22,638	23,471	22,909	0,33	0,848	MM - VM	-0,41	0,682	
						MM - VV	0,094	0,925	
Internet as a way of observing others on social media	VV	VM	MM						
	22,638	23,471	22,909	0,33	0,848	VM - VV	0,51	0,61	
						CC - CT	0,608	0,543	
Internet as a means for fulfilling sexual needs	CC	CT	TT						
	23,221	23	22,5	0,39	0,823	CC - TT	0,198	0,843	
						CT - TT	0,009	0,993	

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	Mean scores on the "SIB" questionnaire (Abakumova et al., 2015) for carriers of different genotypes of BDNF, COMT, DRD2				Significance of differences				
	Kruskal–Wallis test		Dunn's pairwise post hoc tests		H	p-value	comparisons	z	p-value
	VV	VM	MM	MM - VM					
BDNF	VV	VM	MM	MM - VM	3,923	0,141	MM - VM	-1,432	0,152
	17,2	21,3	22,581	MM - VV			MM - VV	-1,84	0,066
				VM - VV			VM - VV	-0,884	0,377
COMT	VV	VM	MM	MM - VM	5,165	0,076	MM - VM	-0,424	0,671
	21,277	21,863	23,864	MM - VV			MM - VV	-2,07	0,038
				VM - VV			VM - VV	-1,993	0,046
DRD2	CC	CT	TT	CC - CT	0,157	0,924	CC - CT	0,195	0,846
	22,275	22,034	21	CC - TT			CC - TT	0,362	0,717
				CT - TT			CT - TT	0,296	0,767

Internet as a channel for expressing radical ideas

## Appendix 2

### ***Results of the analysis of the frequency of different genotypes of BDNF (rs6265), COMT (rs4680), and DRD2 (rs1800497) in the identified clusters***

Gene and allele variant		Total sample (N=193)	Cluster 1 (N=88)	Cluster 2 (N=55)	Cluster 3 (N=50)
BDNF (rs6265)	VV	148	63	42	43
		76,68%	71,59%	76,36%	86%
	VM	40	22	12	6
		20,72%	25%	21,82%	12%
	MM	5	3	1	1
		2,60%	3,41%	1,82%	2%
COMT (rs4680)	VV	44	21	12	11
		22,80%	24%	22%	22%
	VM	102	49	25	28
		52,85%	56%	45%	56%
	MM	47	18	18	11
		24,35%	20%	33%	22%
DRD2 (rs1800497)	CC	131	59	42	30
		67,88%	67%	76%	60%
	CT	58	27	13	18
		30,05%	31%	24%	36%
	TT	4	2	0	2
		2,07%	2%	0%	4%

Received: March 10, 2025

Revised: September 10, 2025

Accepted: November 1, 2025

### **Author Contributions**

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**Ekaterina Gennadyevna Denisova** — planning, data collection and analysis, manuscript drafting.

**Anastasia Vasilievna Grishina** — conceptualization and planning of the empirical study, overall project supervision, manuscript drafting.

**Nadezhda Valeryevna Sylka** — data collection and manuscript preparation.

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## Conflict of Interest Information

The authors have no conflicts of interest to declare.