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# The Association Between COMT Gene Genotypes and EEG Activity in Assessing the Emotional Valence of Visual Scenes

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## Abstract

**Introduction.** The recognition of emotional context in visual scenes plays a crucial role in an individual's successful socio-psychological adaptation to various conditions in both real and virtual life. However, the current understanding of genetic factors related to the neurobiological mechanisms of spatio-temporal patterns of brain electrical potentials during the differentiation of emotional valence in visual scenes is limited. The catechol-O-methyltransferase ferment, COMT, is linked to the duration of monoamine presence in the synaptic cleft and influences the duration and intensity of emotional reactions. Genotypes for the Val158Met polymorphic locus (rs4680) are associated with various characteristics in the emotional and cognitive domains of carriers, such as anxiety and cognitive control. Consequently, our study aimed to explore the spontaneous electrical activity of the brain in carriers with different genotypes of the COMT gene when tackling challenges related to determining the emotional valence of visual scenes. **Methods.** To achieve this objective, we employed several methods, including genotyping (on DNA extracted from buccal epithelial cells), electrophysiological techniques (EEG recording in 128 leads), behavioral assessments (evaluation of accuracy in recognizing the emotional valence of visual scenes), and statistical analyses (spectral and coherence EEG analyses, ANOVA, Kruskal-Wallis Test, Dunn's Post Hoc Comparisons for behavioral data). **Results.** The EEG data analysis, categorized by genotypes, revealed a correlation between COMT gene genotypes and spectral characteristics of the EEG. Additionally, we found

associations between different COMT gene genotypes and the accuracy in assessing the emotional valence of visual scenes. **Discussion.** These findings contribute to and broaden existing knowledge regarding the link between the catechol-O-methyltransferase gene, spontaneous electrical brain activity, and the proficiency in tasks involving the determination of emotional valence in visual scenes.

## Keywords

EEG, scenes, emotions, COMT, functional connectivity

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# Introduction

Scenes, defined as sets of visual patterns, hold particular scientific significance owing to their natural prevalence in everyday life. Additionally, scenes carry evolutionary importance, serving as stimuli that convey information not only about depicted objects but also about their relationships and contextual placements (Ermakov et al., 2022). The categorization of scenes is a fundamental challenge in computer vision. Following Xiao J. and his colleges, who view a scene as a spatial location where a person can potentially or actually position themselves and take action (Xiao et al., 2010).

Despite extensive research into the neurophysiological aspects of perceiving emotionally charged stimuli, interest remains robust. Spatio-temporal patterns of electrical potentials in the brain, specific to each emotional state, are currently harnessed to advance human-computer technology, particularly Brain-Computer Interfaces (BCI). Utilizing deep neural networks, including artificial neural networks like autoencoders, researchers have compiled databases of physiological signals indicative of emotion recognition based on electroencephalographic indicators (Liu et al., 2020). Studies are also exploring the influence of physical parameters of visual stimuli on the success of recognizing emotional context and the corresponding reflection of these processes in EEG parameters (Babenko et al., 2022; Rodionov, Yavna, Babenko, 2023).

Over the past years, EEG indicators related to the intensity (arousal/intensity) and valence of human emotional reactions in both health and disease, as well as electrophysiological correlates of the motivational significance of emotionally charged stimuli, have been extensively documented. According to Frantzidis C. A. et al.'s study (2010), the reliability of classifying emotional states from EEG signals is approximately 80%.

In contemporary studies special attention has been paid to the EEG microstates, which reflect the temporal dynamics (by millisecond) of the processing of complex emotionally charged stimuli. This states are viewed as neurophysiological correlates of socio-affective mind (Schiller, 2023). There are also some progress in improving the approaches to mathematical processing of the EEG data (for example, the InvBase method, including baseline power removal) (Ahmed, 2023).

Undoubtedly, the physiological response to the presentation of emotionally charged stimuli is a complex phenomenon involving various physiological changes across cardiovascular, respiratory, endocrine, and other bodily systems (Lapin & Alfimova, 2014). Contemporary research increasingly embraces an interdisciplinary approach, leading to the development of multimodal databases that incorporate a range of psychological and physiological parameters. These parameters encompass personality traits, physiological indicators, and success in recognizing emotionally charged stimuli. Notable examples of such databases include the ASCERTAIN database (Subramanian et al., 2018), K-EmoCon (Park et al., 2020), DREAMER (Katsigiannis & Ramzan 2018), DEAP (Koelstra et al., 2012), GAMEEMO (Alakus et al., 2020), and others (Liu et al., 2020; Seal et al., 2020).

At the same time, there is currently insufficient data on genetic factors influencing the determination of the emotional valence of stimuli. At the same time, within the framework of the stated topic, among others, the gene of the monoaminergic system, expressed in the limbic and striopallidal structures, as well as the prefrontal zones of the cerebral cortex (Arnsten et al., 2015), which is responsible for cognitive processes, emotional reactions, exploratory behavior, may be of interest: COMT (rs4680) affects the activity of enzymes that break down monoamines (Tunbridge et al., 2006; 2019) and is interrelated with the functioning of hormonal systems (Jacobs & D'Esposito, 2011; Louis et al., 2023). The Val allele is found in people with greater cognitive flexibility, allowing the integration of new relevant stimuli; the Met allele is associated with stable and focused attention, as well as with features of functional connectivity within the limbic system (hippocampus, amygdala) and the prefrontal cortex (Morris et al., 2020). At the physiological level, this influence extends to the processes of excitation and inhibition in the central nervous system.

Based on the above, the purpose of our study was to study the spatiotemporal EEG patterns recorded when solving problems to determine the emotional valence of visual scenes in carriers of different genotypes of the COMT gene.

## Methods

A visual stimulus bank comprising 360 images was established through expert assessments, categorizing images sourced from the internet into three emotional valence groups (120 stimuli each): neutral, positive, and negative. The visual stimuli were standardized for angular size, average brightness, and RMS contrast.

The study involved 87 participants (Europeans, 63% women, average age 20.44 $\pm$ 2.6 years), recruited from the Southern Federal and Don State Universities. Prior to the experiment written confirmation of voluntary participation and declarations of the absence of neurological or mental diseases were obtained. All participants were informed of the study objectives and were familiarized to the experimental task. The research adhered to the SFU Ethics Commission's requirements, approved by the local ethics committee, and conducted in accordance with The Code of Ethics of the World Medical Association (Declaration of Helsinki).

During the experiment, participants were exposed to 360 stimuli (visual scenes with varying emotional valence) that were presented in a random sequence. Each stimulus was displayed for 700 ms, during which participants had to determine the scene's valence and select one of three response options (positive, neutral, or negative scene). The images used in trails were not used in the main experiment. Throughout the experiment EEG was recorded from 128 leads, covering a frequency range of 0.5 to 35 Hz.

Artifact removal using independent component analysis (ICA) was performed in the preprocessing of each subject's EEG recording for subsequent analysis. After this procedure, recordings from 2 subjects had to be excluded due to substantial EEG noise, resulting in data from 85 individuals for further processing.

In the subsequent EEG preparation stage, epochs were segmented with durations ranging from -1000 ms to +1000 ms relative to the stimulus. Epochs containing artifacts, even after artifact removal, were eliminated through visual inspection. The remaining EEG segments were categorized into three sets based on the stimulus valence.

To facilitate further analysis, two continuous epochs were generated for each subject within each category, comprising pre-stimulus and post-stimulus segments. The entire preparatory phase utilized the EEGLAB function package version 2022.0 in MATLAB version R2021a (The MathWorks Inc.: Natick, MA, USA). Data export for EEG processing in other software was executed using MATLAB scripts developed in the SFU laboratory.

Overall study involved electrophysiological and behavioral data analyses for each genotype of the COMT gene. EEG processing encompassed spectral and coherence analyses conducted in four frequency ranges: 0.5-4 Hz (delta), 4-8 Hz (theta), 8-13 Hz (alpha), and 13-25 Hz (beta).

Statistical analyses comprised pairwise comparisons using one-way analysis of variance with repeated measures (one-way ANOVA) at a significance level of $p \leq 0.01$.

Data processing for statistical analysis was carried out using the Statistica 12 program (TIBCO).

Spectral analysis involved determining amplitude spectra in pre-stimulus and post-stimulus intervals on EEG for each valence, calculating difference spectra in four frequency ranges across 128 leads, and subsequently conducting statistical comparisons.

Coherence analysis aimed to determine the correlation of EEG spectral power in each frequency range across 19 leads, corresponding to the standard 10x20 design. The topographic distribution of coherent connections was calculated separately for pre-stimulus and post-stimulus EEG, followed by the determination of differences between the maps.

Both spectral and coherence analyses utilized a Hann window function (4-second analysis epoch with 50% overlap) to minimize leakage at the boundaries of connected EEG segments.

For behavioral data processing, the number of correct recognitions and "false alarms" for stimuli of each valence were calculated. The sensitivity index (d') was calculated using the PAL_SDT_1AFC_PHFtoDP function from the Palamedes toolbox (Prins & Kingdom, 2018). Intergroup comparisons of sensitivity indicators in carriers of different COMT gene genotypes were carried out using the Kruskal-Wallace test with Dunn's test and Holm's correction for multiple comparisons as a post hoc procedure. Statistical analysis of results was performed using JASP Computer software package (Version 0.16, 2021).

Genetic analysis, conducted at the Laboratory of Medical Genetics of Rostov State Medical University, involved DNA extraction from buccal scraping cells and PCR. The Val158Met polymorphic locus of the COMT gene (472A>G, rs4680) was examined, and genotypes were determined as Val/Val, Val/Met, Met/Met. The frequency distribution of genotypes aligns with the Hardy-Weinberg equilibrium.

## *Results*

### *Characteristics of spontaneous electrical brain activity in task of determining the emotional valence of visual scenes were examined in individuals with different genotypes of the COMT gene*

In this section, we discuss the results of spectral analysis, with the genotype of the COMT gene serving as the grouping variable. The difference spectra, derived for the entire sample, were categorized into three groups based on the COMT gene genotype: Val/Val, Val/Met, and Met/ Met. Pairwise comparisons (ANOVA) were conducted between these groups for values obtained in recognition of scenes with specific valences. The outcomes of the comparison of difference spectra are presented in Tables 1-3.

**Table 1**

*Comparison of Difference Spectra in recognition of Neutral Scenes by Carriers of Val/Met and Met/Met Genotypes of the COMT Gene*

| Leads | Beta Range | | | Means | |
|---|---|---|---|---|---|
| | F-ratio | p-level | $\eta^2$ | $M_{VM}$ | $M_{MM}$ |
| FC1 | 7,446 | 0,008 | 0,093 | -0,062 | -0,242 |
| CP1 | 10,273 | 0,002 | 0,124 | -0,153 | -0,371 |
| P3 | 9,369 | 0,003 | 0,115 | -0,185 | -0,388 |
| Pz | 8,917 | 0,003 | 0,110 | -0,206 | -0,450 |
| CP3 | 9,001 | 0,003 | 0,111 | -0,141 | -0,331 |
| P1 | 9,208 | 0,003 | 0,113 | -0,188 | -0,420 |
| CPP3h | 7,616 | 0,007 | 0,095 | -0,159 | -0,360 |
| PPO1h | 7,379 | 0,008 | 0,093 | -0,216 | -0,419 |
| FCC1h | 6,959 | 0,010 | 0,088 | -0,070 | -0,257 |
| CCP3h | 9,836 | 0,002 | 0,120 | -0,125 | -0,337 |
| CPP1h | 10,326 | 0,002 | 0,125 | -0,171 | -0,413 |

***Note.*** *Here and in subsequent tables, only statistically significant differences are presented.*

Tables 1 and 2 reveal differences observed in the spectral analysis in recognition of neutral and positive scenes. These differences are characterized by a more pronounced decrease in the amplitude spectrum in the beta range, particularly in the parietal and central leads of the left hemisphere, within the group of carriers with the Met/Met genotype.

**Table 2**

*Comparison of Difference Spectra in recognition of Positive Scenes by Carriers of Val/Met and Met/Met Genotypes of the COMT Gene*

| Leads | Beta Range | | | Means | |
|---|---|---|---|---|---|
| | F-ratio | p-level | $\eta^2$ | $M_{VM}$ | $M_{MM}$ |
| FC1 | 7,068 | 0,009 | 0,090 | -0,022 | -0,211 |
| T8 | 7,324 | 0,008 | 0,093 | -0,004 | -0,121 |
| CP1 | 7,320 | 0,008 | 0,093 | -0,087 | -0,255 |
| CP6 | 8,143 | 0,005 | 0,102 | -0,053 | -0,19 |
| P3 | 6,939 | 0,010 | 0,089 | -0,118 | -0,275 |
| Pz | 9,348 | 0,003 | 0,116 | -0,118 | -0,328 |
| CP3 | 7,273 | 0,008 | 0,092 | -0,089 | -0,238 |
| P1 | 7,722 | 0,007 | 0,098 | -0,105 | -0,278 |
| PO3 | 7,776 | 0,006 | 0,098 | -0,081 | -0,262 |
| PPO1h | 8,134 | 0,005 | 0,102 | -0,109 | -0,293 |

As indicated in Table 3, the differences between Val/Met and Val/Val are less prominent, emerging solely in delta range for recognition of the positive scenes. The amplitude spectrum in Val/Val carriers is decreasing and an increasing (in the same leads) in Val/Met carriers.

**Table 3**

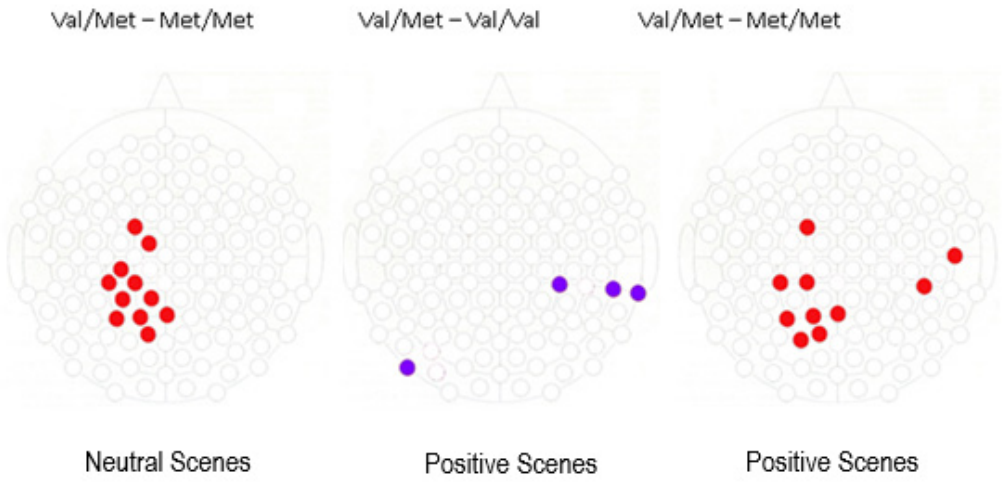
*Comparison of Difference Spectra in recognition of Positive Scenes by Carriers of Val/Val and Val/Met Genotypes of the COMT Gene*

| Leads | Delta Range | | | Means | |
|---|---|---|---|---|---|
| | F-ratio | p-level | $\eta^2$ | $M_{VV}$ | $M_{VM}$ |
| TP10 | 8,865 | 0,004 | 0,132 | -0,531 | 0,114 |
| CP4 | 7,883 | 0,006 | 0,119 | -0,444 | 0,191 |
| TP8 | 9,175 | 0,003 | 0,136 | -0,583 | 0,072 |
| PO9 | 7,616 | 0,007 | 0,116 | -0,55 | 0,102 |

The differences in EEG activity, recorded during tasks to determine the emotional valence of visual scenes, are observed between the Val/Met group and the other groups in recognition neutral and positive scenes. Figure 1 illustrates that more substantial differences are noticeable between carriers of the Val/Met and Met/Met genotypes.

**Figure 1**

*Comparison of the Difference in Amplitude Spectra between Pre-stimulus and Post-stimulus EEG during the Perception of Scenes with Different Emotional Valence in Carriers of Different Genotypes of the COMT Gene**




***Note.*** * This figure displays leads where statistically significant differences were identified. On the left, leads show a more pronounced decrease in the spectrum in the beta range in carriers of the Met/Met genotype during the perception of neutral scenes. In the center, leads depict multidirectional changes in the delta range for the Val/Met (increasing spectrum) and Val/Val (decreasing spectrum) groups during the perception of positive scenes. On the right, leads show a more pronounced decrease in the spectrum in the beta range in carriers of the Met/Met genotype during the perception of positive scenes.

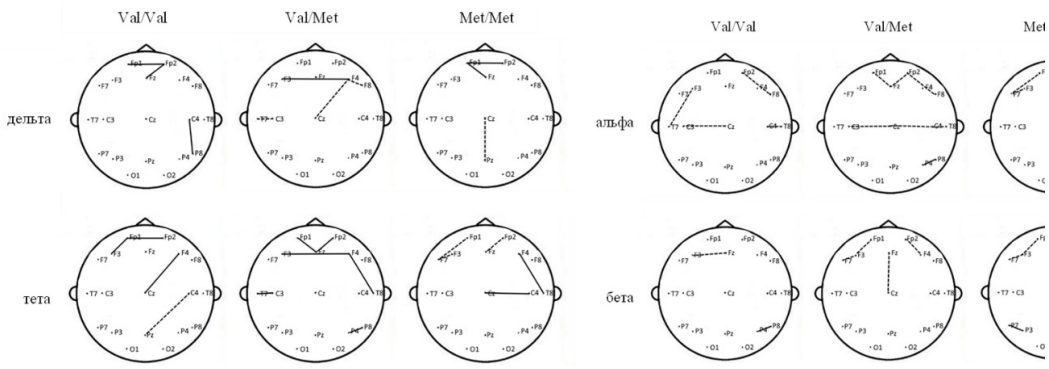
In summary, groups with homozygous genotypes of the COMT gene (Val/Val and Met/Met) exhibit greater similarity in the nature of EEG changes during the transition from stimulus anticipation to the recognition of visual scenes with different emotional valences. Conversely, the Val/Met group demonstrates distinct EEG characteristics compared to both the Val/Val and Met/Met groups.

## *Results of Coherence Analysis with the Genotype of the COMT Gene as the Grouping Variable*

In the coherence analysis, difference coherence maps were constructed and compared for three genotypes of the COMT gene. Notably, for negative scenes (Fig. 2) an increase in synchronization between some leads in the delta and theta ranges was observed in the Val/Val and Val/Met groups. In all other instances, a decrease in the correlation of EEG spectral power was noted during the transition from the stimulus anticipation phase to its analysis.

**Figure 2**

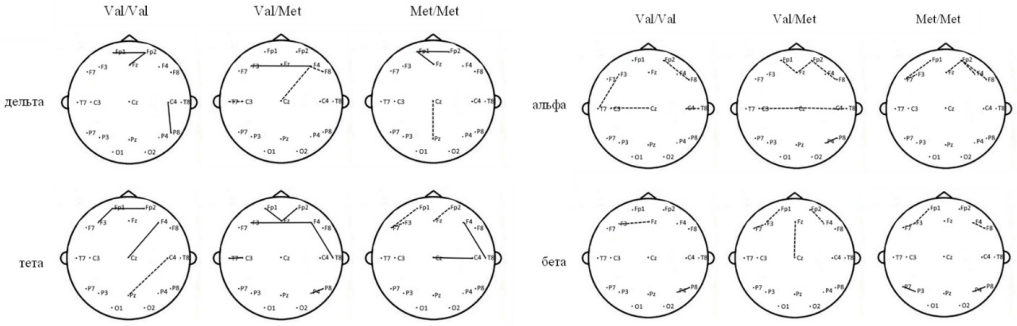
*Difference Coherence Maps (showing difference between Pre-stimulus and Post-stimulus EEG Coherence Maps) for Carriers of Different COMT Genotypes in recognition of Negative Scenes*




During the perception of neutral scenes (Fig. 3), the most significant differences between genotypes were observed in the beta range. These differences were characterized by the formation of new functional connections in the Val/Val and Met/Met groups, while the Val/Met group exhibited a decrease in EEG correlation between frontal leads.

**Figure 3**

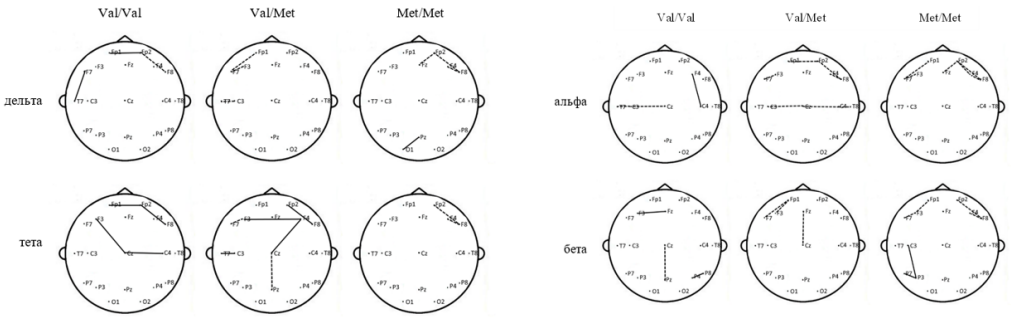
*Difference Coherence Maps (showing difference between Pre-stimulus and Post-stimulus EEG Coherence Maps) for Carriers of Different COMT Genotypes in recognition of Neutral Scenes.*



In the perception of positive scenes (Fig. 4), differences between the groups were evident in both the beta and delta ranges. Similar to the analysis of neutral scenes, the Val/Met group displayed a decrease in functional connectivity among frontal leads without the formation of new connections.

**Figure 4**

*Difference Coherence Maps (showing difference between Pre-stimulus and Post-stimulus EEG Coherence Maps) for Carriers of Different COMT Genotypes in recognition of Positive Scenes.*




Consequently, the most substantial differences in coherence maps were identified between the Val/Met group and the other groups when perceiving neutral and positive scenes, particularly in the delta and beta bands.

## *Analysis of Behavioral Data: Recognition of Emotional Valence in Carriers of Various COMT Gene Genotypes*

To assess the recognition of emotionally charged and neutral visual scenes in carriers of different genotypes of the COMT gene, a thorough behavioral data analysis was conducted. The results highlight an association between the Val158Met polymorphic locus of the COMT gene and the evaluation of the emotional valence of visual scenes (Table 2).

**Table 2**

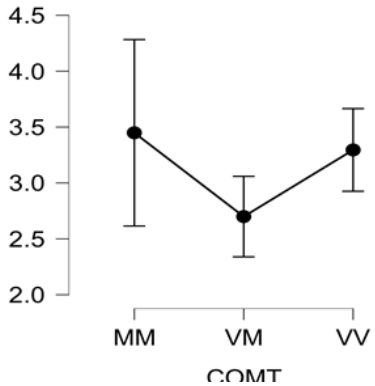
*Results of Assessing the Reliability of Differences in Sensitivity to the Emotional Valence of Presented Visual Scenes in Carriers of Different Genotypes of COMT Genes (Kruskal-Wallis Test, * – p <0.05)*

| Genotypes of the COMT gene | | Total Sensitivity | Scenes | | |
|---|---|---|---|---|---|
| | | | Negative | Neutral | Positive |
| Mean ranks for COMT (Val158Met, rs4680) | Val/ Met | 38,52 | 40,29 | 37,37 | 39,75 |
| | Met/ Met | 45,80 | 43,98 | 48,22 | 44,72 |
| | Val/Val | 60,91 | 57,00 | 60,64 | 57,77 |
| Kruskal-Wallis test | H | 7,548 | 4,051 | 9,088 | 4,782 |
| | p | 0,023□ | 0,132 | 0,011□ | 0,092 |

The Kruskal-Wallis Test revealed significant differences in the success of recognizing neutral scenes among carriers of different COMT gene genotypes (H=9.1, df=2, p=0.01). Dunn's Post Hoc Comparisons indicated that carriers of the heterozygous Val/Met genotype exhibited the poorest performance in recognizing neutral images. Moreover, the accuracy of recognition of neutral scenes in Val/Met carriers was statistically significantly lower than in Val/Val carriers (VM – VV, z = -2.798, pholm = 0,008) (Fig.5).

Figure **5**

*Accuracy of Recognition of Neutral Scenes by Carriers of Different Genotypes of the COMT Gene*

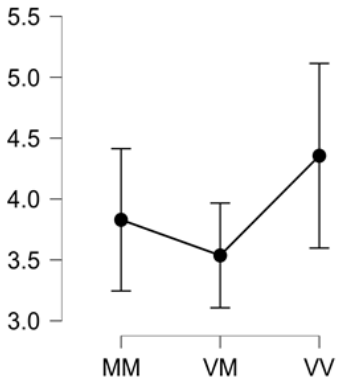



***Note:*** *Y-axis represents sensitivity (d'), and X-axis denotes genotypes for the COMT gene: MM – Met/Met, VM – Val/Met, VV – Val/Val.*

Significant differences among carriers of different COMT gene genotypes were also observed concerning sensitivity to the emotional content of scenes (H = 7.458, df = 2, p = 0.02). Dunn's post-hoc analysis revealed that carriers of the Val/Val genotype generally outperformed others in recognizing the emotional valence of stimuli. Specifically, the accuracy of recognizing the emotional valence of scenes in Val/Val carriers was statistically significantly higher than in Val/Met carriers (VM – VV, z=-2.692, pholm=0,011) (Fig. 6).

**Figure 6**

*Accuracy of Recognition of the Emotional Valence of Scenes by Carriers of Different Genotypes of the COMT Gene*




***Note:*** *Y-axis represents sensitivity (d'), and X-axis denotes genotypes for the COMT gene: MM – Met/Met, VM – Val/Met, VV – Val/Val.*

## *Discussion*

The study reveals an association between the Val158Met polymorphism of the COMT gene and differences in amplitude spectra of EEG rhythms during the visual recognition of emotionally charged scenes.

The Met/Met genotype is associated with a changes of the amplitude spectrum in the beta range primarily in the left hemisphere's parietal and central areas. In recognition of neutral and positive scenes we found a stronger spectrum decrease in the beta range, comparing to the Val/Met carriers. This, aligning with prior research, could be associated with alterations in the functional state of the cerebral cortex that are specific to Met/Met genotype and do not occur in carriers of one or two Val allele, and potentially indicate reduced focus of attention and subjective insignificance of stimuli (Nikishena et al., 2004).

The Val/Met and Val/Val genotypes are associated with characteristics in the delta range amplitude spectrum in the central and temporal-parietal part of the right hemisphere, as well as in the parietal-occipital part of the left hemisphere. In recognition of positive scenes Val/Val carriers exhibit stronger amplitude spectrum decrease, while Val/Met carriers show an increase. These findings align with existing data suggesting that Met allele carriers show higher performance rates in cognitive tasks, while Val allele carriers may demonstrate higher brain structure activation during cognitive load (Alfimova & Golimbet, 2011; Barnett et al., 2008). The absence of a decrease in activation (beta band power) during the recognition of negative scenes in Met/Met genotype carriers aligns with previous research linking this genotype to a pronounced neural response to unpleasant stimuli, increased limbic system and prefrontal cortex activation, and lower resistance to negative mood (Drabant et al., 2006). Wherein Val allele is associated with an increase in delta/theta Pz–Fz at rest (the posterior–anterior distribution of resting EEG), suggesting its role in the dopaminergic basis of extraversion (Wacker et al., 2010).

Coherence analysis reveals the formation of new functional connections in carriers of Val/Val and Met/Met genotypes in recognition of neutral scenes in the beta range and for positive scenes in both beta and delta ranges. In contrast, carriers of the Val/Met genotype exhibit a decrease in EEG correlation between frontal leads. This suggests greater functional connectivity of the cerebral cortex in carriers of homozygous genotypes in tasks for differentiating stimuli varying in emotional valence. In comparison, carriers of the heterozygous genotype show reduced connectivity of different cortex areas and independent frontal region activity during the categorization of emotionally charged and neutral scenes. These findings present variations compared to those reported in previous research, particularly the study by Liu et al. (2010), where a stronger connectivity was observed in carriers of the heterozygous genotype between specific nuclei of the prefrontal cortex, posterior cingulate cortex, retrosplenial and right inferior temporal cortex, and cingulate cortex. In contrast, carriers of the homozygous Val/Val genotype exhibited weaker connectivity between these regions. Wang et al. (2015) also found no

connectivity differences in the striatum and primary visual cortex between carriers of the Val/Val and heterozygous genotypes. Dang et al. (2013) confirmed a greater functional connectivity between the medial prefrontal cortex and the default mode network (DMN) in carriers of the heterozygous genotype. Additional studies, including Wang et al. (2018), have corroborated increased connectivity between the prefrontal cortex and limbic and striopallidal systems in carriers of the heterozygous genotype. However, there are conflicting data regarding the association of homo- and heterozygous genotypes of the COMT gene with functional connectivity. Lee et al. (2011) found that carriers of the Val/Val genotype exhibited the greatest functional connectivity of left-lateralized network of neurons in the delta/theta frequency ranges, with reduced connectivity for each Met allele. Damoiseaux et al. (2016) showed significantly greater connectivity between the posterior hippocampus and posterior cingulate cortex, as well as the retrosplenial cortex, in carriers of one or two Met alleles compared to Val/Val genotype carriers. A systematic review by Kim A. Morris et al. (2020) highlighted a general tendency associating the Val allele with greater functional connectivity at rest, and the Met allele with increased connectivity during tasks related to emotionally charged stimuli processing, various memory types (including working memory), executive functions and reward-based learning. Thus our findings contribute to our understanding of how genetic factors, specifically the Val158Met polymorphism of the COMT gene, influence neural responses during the perception of emotional scenes. The specificity of the current study's results may stem from the characteristics of the stimuli (emotionally charged and neutral scenes). It contributes to an enhanced understanding of the nuanced functional connectivity patterns between different brain structures in carriers of distinct COMT gene genotypes during diverse cognitive tasks.

The study identified a reduced accuracy in categorizing visual scenes by emotional valence in carriers of the Val/Met genotype of the COMT gene. This reduction in accuracy was found to be accompanied by less pronounced changes in the amplitude spectrum in the delta and beta EEG ranges during the transition from stimulus anticipation to analysis. Differences in the nature of coherent connections in the same frequency ranges were also observed.

These variations might be linked to the duration of monoamines in the synaptic cleft, regulated by the COMT gene. Carriers of Met alleles are characterized by a longer stay of monoamines in the synaptic cleft (Chen et al., 2004; Lotta et al., 1995) and increased dopamine content in the cortex (Zareyan et al., 2021). At the same time, the greater sensitivity of carriers of the Val/Val genotype of the COMT gene to the emotional content of visual scenes may be associated with a more rapid breakdown of monoamines (including dopamine) in the synaptic space, with a lower concentration of dopamine in the prefrontal cortex. A number of studies have found that the Met allele of the COMT gene in a group of healthy people is associated with greater efficiency of executive functions (Barnett et al., 2007), including greater performance of working memory (Weinberger D. R., & Scarabino T., 2006), while

the Val allele is associated primarily with the processing of emotionally charged information (Mier et al., 2010).

The study contributes novelty by describing spectral and coherent characteristics of spontaneous electrical brain activity in carriers of various COMT gene genotypes during the assessment of emotional valence in visual scenes. Behavioral data analysis, specifically the accuracy of recognizing emotionally charged and neutral visual scenes, was also a novel aspect of the study. Overall, the findings expand our understanding of the role of the COMT gene in evaluating the emotional valence of visual scenes by providing insights into both electrophysiological and behavioral correlates.

### *Conclusions*

Obtained results underscore the intricate interplay between genetic factors and cognitive-emotional processing, specifically tied to the COMT gene polymorphism. In terms of amplitude spectra differences, the Val/Met COMT group exhibits distinct EEG patterns during the transition from stimulus anticipation to scene analysis, setting it apart from the Val/Val and Met/Met COMT groups. Specifically, the Met/Met COMT group displays a more pronounced decrease in the amplitude spectrum in the beta range in certain brain regions when perceiving neutral and positive scenes compared to the Val/Met COMT group.

The Val158Met polymorphism of the COMT gene plays a pivotal role in the accurate assessment of the emotional valence of visual scenes. Notably, carriers of the Val/Val genotype demonstrate superior success in recognizing the emotional connotation of stimuli compared to individuals with other genotypes, emphasizing the influence of this genetic variation on emotional processing.

### *Implications and Future Directions*

The observed differences in EEG patterns and emotional valence assessment suggest potential ways for targeted interventions or personalized approaches based on an individual's genetic profile. Future research probably should delve deeper into COMT gene variations, advancing our understanding of their impact on cognitive and emotional functions and contributing to the evolving fields of neuroscience and personalized medicine.

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**Vitali V. Babenko** – development of research methodology; planning of research stages, critical revision of the article. Ekaterina M. Kovsh – analysis and generalization of the literature data; accumulation of research data (EEG registration, biomaterial collection for genetic samples, behavioral research), research results generalization; formulation of conclusions; research results interpretation; preparing the text of the article.

**Aleksander S. Stoletniy** – analysis and systematization of experimental data; application of statistical and mathematical methods for data analysis; processing of graphic material.

**Pavel N. Ermakov** – justification of the research concept (formulation of the idea, research goals and objectives); creation of a research model.

**Denis V. Yavna** – development of experimental research design; analysis and systematization of experimental data; application of statistical and mathematical methods for data analysis.

**Ekaterina G. Denisova** – accumulation of research data (EEG registration, biomaterial collection for genetic samples, behavioral research), research results generalization; editing the text of the article.

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## Conflict of Interest Information

The authors have no conflicts of interest to declare.