

## Original Research

# Association of COMT, BDNF and 5-HTT functional polymorphisms with personality characteristics

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## 1. Abstract

**Background:** The real impact of genetic factors on personality is still unknown, even if in literature about 50% of variance in personality traits are considered genetically determined. The determination of the genetic variance in personality traits could promote psychological well-being and the prevention of psychopathologies, because there are many experimental evidences showing that mental illness is associated to personality. Numerous studies have showed that Catechol-O-methyltransferase (*COMT*), brain derived neurotrophic factor (*BDNF*) and serotonin

transporter (*5-HTT*) are genes whose variants are associated with personality traits. This aim of this study is the investigation of the association between personality traits and *5-HTTLPR/rs255315-HTT* promoter variant, *COMT* Val158Met and *BDNF* Val66Met gene polymorphisms. **Methods:** The sample was composed by 132 healthy female students. Genomic DNA was extracted from buccal swab, while personality was assessed with Cloninger’s Temperament and Character Inventory-Revised (TCI-R). Linear discriminant analysis was used to analyze how personality characteristics can differentiate individuals in re-

lation to their genetic polymorphisms. **Results:** Data showed that the temperament trait Reward Dependence discriminated individuals with different *BDNF* variants; Novelty Seeking and Harm Avoidance discriminated individuals with different *5HTTLPR* variants; Persistence discriminated individuals with different *COMT* variants. **Conclusions:** Since these traits are connected to psychological diseases as depression, social anxiety, anorexia and obsessive-compulsive disorders of personality, the study of their genetic component can be used as intermediary issue to better define the connection between genes and predisposition toward maladaptive behavior and mental illness.

## 2. Introduction

The latest epidemiological world data show an increment of mental illness, together with a parallel increment of health care costs. For example, in Italy about 6% of adults (18–69 years) report depressive symptoms and reduction of perceived well-being. Moreover, in Iceland, Norway and Switzerland, 27% of adults (18–65 years) experienced at least one episode of mental disorder in the past year (including eating disorders or anxiety) [1]. In literature, genetic factors are considered capable to predict about 50% of the variance in personality traits, but the real impact of genetic factors on personality is still unknown [2]. Because there is an association between personality and probability of suffering from mental diseases, the relation between personality and genetic factors is an important topic to analyze the influence of genetic factors on mental diseases [3, 4]. The determination of the genetic variance in personality traits could promote psychological well-being and the prevention of psychopathologies through the definition of possible associations between specific gene variants and personality traits [5]. The most important and known models of personality based on biological factors are Eysenck's three-factors model [6, 7] and Cloninger's model of personality [8]. The three personality factors of Eysenck's model are: Neuroticism (anxious and depressed mood and low self-esteem), Extraversion (characterized by high assertiveness, sociability and dominance), Psychoticism (characterized by aggressive, antisocial and impulsive behavior). Eysenck assumed that Neuroticism was based on low activation thresholds in the sympathetic nervous system, or visceral brain; that Extraversion was associated to higher arousal thresholds in react to the varying stimulations; that Psychoticism was related to the increased testosterone levels. Cloninger's model, instead, defined four basic personality dimensions: Harm Avoidance, Novelty Seeking, Reward Dependence and Persistence. These dimensions are linked to tendency to feel emotions of fear, anger, love and tenacity, respectively. These factors are genetically determined and produce automatic behavioral reactions to emotive stimuli. In addition, Cloninger defined other three personality dimensions, Self-Directed be-

havior, Cooperativeness and Self-Transcendence, considered as specific character traits that are mostly affected by environment influence [9]. Behavior genetic research (e.g., Genomic-wide association and genetic linkage studies) is an ever increasingly growing area of analysis of the relation between genes and personality, but this relation is far from being clarified [10]. The most studied personality trait in association with genetic characteristics of individuals is Neuroticism, that is the trait with the strongest association with depression and anxiety [1]. Extraversion is the trait which showed to be strongly associated with agoraphobia, social phobia and dysthymia [11]. Cloninger's High Reward Dependence, Persistence and Cooperativeness are personality dimensions that seemed to be involved as causes of several of psychopathologies, but, nowadays, it is necessary to clarify their real impact on psychiatric disorders [12–15]. The major psychological diseases associated to Cloninger's personality dimensions are depression, social anxiety, anorexia and obsessive-compulsive disorders of personality. In particular, depression is associated to the stress during the performance, the higher attention for negative details during the performance and the constant presence of ruminative thoughts [16–24]. Social anxiety is characterized by a fear of social situations in which the person is exposed to unfamiliar people and the possibility to be judged or criticized [25–28]. Some personality theories showed a connection between the serotonergic, noradrenergic and dopaminergic neurotransmitter and personality traits [29–31]. Novelty Seeking and Extraversion are the personality factors prevalently studied in the association with the neurotransmitter circuit. Indeed, some studies showed a positive correlation between Extraversion and the density of the volume of the medial orbitofrontal brain's area. This area is innervated by dopamine fibers, that play an important role in elaborating emotive contents of stimuli [32]. Several neuroimaging studies [33–36] established that the orbital region of prefrontal cortex is implicated in motivational and emotive states (e.g., to give an emotive value to a stimulus) [37–41]. The Behavioral Activation System theory asserts that dopamine is associated to a motivational system, sensible to the reward signals and responsible for escape from punishments [42]. According to this neuropsychological theory, an increase of dopamine causes a growth of neural activity, that leads to seek positive and negative reinforcements. This mechanism is maintained, through Persistence and Cooperativeness, to successfully achieve a target. Persistence and Cooperativeness allow elevated levels of resilience and emotional intelligence which favors social approval [43–45].

There is growing evidence that particular cognitive-affective phenomena could be influenced by key gene variants altering the activity within specific neuronal circuits. One example is the catechol-O-methyltransferase (*COMT*) gene that codes for the COMT enzyme, which breaks down dopamine in the brain's prefrontal cortex [46].

In the exon three of the gene is mapped the Val158Met (rs4680) common coding Single-Nucleotide Polymorphism (SNP) including the substitution of guanine (G) with adenosin (A) that results in a change in the amino acid located at position 158 of the codon [47]. This changes the structure of the resultant enzyme with an activity modulation. Specifically, the Val/Val version of the COMT enzyme breaks down dopamine with a degradation rate 40% faster than the Met/Met version [46]. An allele carriers (Met158) have more dopamine in their prefrontal cortex, which may be responsible for many of the neuropsychological associations as well as lower pain threshold, enhanced vulnerability to stress, anxiety yet also more efficient at processing information under most conditions [48–50].

Some studies suggest that Val158 alleles are associated with schizophrenia, higher pain threshold, better stress resiliency, albeit with a modest reduction in executive cognition performance under most conditions [51, 52]. In conclusion Val158 alleles may be associated with an advantage in the processing of aversive stimuli (warrior strategy), while Met158 alleles may be associated with an advantage in memory and attention tasks (worrier strategy) [53, 54].

Several lines of evidence suggest that another high priority candidate gene related to behaviour phenotype is represented by *BDNF* gene. Neurobiological studies showed the implication of *BDNF* gene in fear memory, sensitivity to stress, and stress-related disorders [55]. *BDNF* encodes the protein brain-derived neurotrophic factor a regulator of synaptic transmission and plasticity at adult synapses and in response to injury. Different genetic polymorphisms have been shown to affect the availability and activity of *BDNF* [56, 57]. The most investigated single-nucleotide polymorphism in the *BDNF* gene is Val66Met (rs6265 A>G). This substitution, in exon 11, from valine (Val) to methionine (Met) at codon 66 has functional consequences with impairments in intracellular trafficking and activity. However, the substitution is not transferred to the final form of BDNF and the BDNF protein precursor can significantly decrease the secretion of BDNF extracellularly and subsequently reduce its availability to the Central Nervous System (CNS) neurons [58]. Studies also report associations between SNP and brain volume alterations in people with schizophrenia. Met allele carriers showed lower total brain volume, greater reductions in frontal, temporal, and occipital regions and greater reductions in hippocampal volume respect to Val/Val homozygotes [59]. Val66Me variant has also been implicated in modulating the clinical features of Bipolar Disorder, including impulsive aggression [60]. and susceptibility to environmental stress [61]. Other studies showed the implication of *BDNF* gene in modulation of negative emotion processing [62, 63].

Numerous studies have showed that several psychological processes, including individual differences in personality traits could be affected by serotonin [5-hydroxytryptamine (5-HT)] which plays a central role in regulating activity of the central nervous system [64, 65].

The promoter region of the serotonin transporter gene (*5-HTT*) includes the variable number tandem repeats (VNTR) polymorphism (*5-HTTLPR*). It is characterized by short and long functional variants which are associated with different levels of transporter expression. The short variant draws less serotonin back to the presynaptic neuron. When it is set again to the long (L) version, there is an overload of serotonin in the synaptic cleft that keeps stimulating, in this way, the serotonin receptors [66]. Afterwards a single nucleotide polymorphism (SNP) A → G (rs25531) has been disclosed inside the sixth repeat of the S- and L-variants. LG allele has a lower expression level compared to the LA allele.

In this view, S/S homozygosity is associated with the lowest 5-HTT mRNA expression while LA/LA homozygotes have the highest expression with inside the rs25531 (A/G) SNP [67].

Individuals with at least one short allele of the *5-HTTLPR*, have more depressive symptoms in response to early life or recent stress, and was associated with anxiety and schizophrenia [68].

The purpose of the present study is to examine the possible role of the combined *5-HTTLPR/rs25531-5-HTT* promoter variant and *COMT* Val158Met, *BDNF* Val66Met gene polymorphisms with specific personality factors that resulted associated to psychological well-being according to literature, to find a genetic mechanism of personality which can guarantee the prevention of mental illnesses associated to personality.

### 3. Materials and methods

#### 3.1 Subjects

Participants were 132 healthy female students attending courses at the University of Chieti-Pescara. Their ages ranged from 18 to 24 years, with an average value of 19.76 (SD = 0.99).

#### 3.2 Genotyping

Genomic DNA was extracted from buccal swab samples using NucleoSpin Tissue kit (Macherey-Nagel, Düren, Germany). The identification of the *BDNF* Val66Met (rs6265 G>A) and *COMT* VAL158Met (rs4680) was assayed by polymerase chain reaction (PCR) followed by PCR-based restriction fragment length polymorphism (RFLP)-PCR. Primers for detection of the SNPs were: for Val158Met: 5'-GGAGCTGGGGCCTACTGTG-3' (forward) and 5'-GGCCCTTTTCCAGGTCTGACA-3' (reverse) and for Val66Met were: 5'-CCCATGAAAGAAGCAAACA-

3' (forward) and 5'-TTTGTCTGCTGCCGTTACC-3' (reverse). The PCR was performed using 10 pmol of each constructed primer and 20ng gDNA as template in 25  $\mu$ L final volume, containing 1 $\times$  Kapa Taq buffer, 0.2 mM dNTPs, 1.5 mM MgCl<sub>2</sub>, 1U Kapa Taq (Kapa biosystems, Wilmington, MA, USA). PCR cycling conditions were: an initial denaturation at 94 °C for 10 min, 35 cycles of 94 °C for 1 min, 59 °C for 30 s and 63 °C, and 72 °C for 1 min with a final extension at 72 °C for 10 min. The resulting PCR products were subjected to restriction digestion for 2 h at 37 °C using 5 U Nla III (New England Biolabs, Ipswich, MA, USA) in a 12  $\mu$ L volume. Following digestion, the fragments were resolved by 3% agarose gel stained with ethidium bromide. The *COMT*-Val/Val genotype was represented by 114-bp, 36-bp, and 35-bp fragments, *COMT*-Met/Met by 96-bp, 35-bp, 36-bp, and 18-bp fragments, and *COMT*-Val/Met by 114-bp, 96-bp, 36-bp, 35-bp, and 18-bp fragments. *BDNF*-Val homozygote samples produced a visible band of 245 bp. *BDNF*-Met homozygote samples produced a visible band of 168 bp and heterozygosity resulted in two visible products of 245 and 168 bp.

The 5-*HTTLPR* was amplified by PCR using Kapa Taq (Kapa biosystems, Wilmington, MA, USA) and the primer pairs were 5'-GGCGTTGCCGCTCTGAAT-3' (forward) and 5'-GAGGGACTGAGCTGGACAACCCAC-3' (reverse). PCR conditions were as follows: initial denaturation at 94 °C for 10 min, followed by 35 cycles of 94 °C for 30 s, 61 °C for 30 s, 72 °C for 30 s, and a final extension at 72 °C for 10 min. The observed alleles yield either a 486 bp (short) or 529 bp (long) product. To distinguish among the SA, LA, and LG fragments, the PCR fragment was digested with MspI (New England Biolabs, Ipswich, MA, USA) and the digested products were separated by 3% agarose gel (LA: 340, 127, and 62 bp, LG: 174, 166, 127, and 62 bp, SA: 297, 127, 62 bp).

### 3.3 Personality assessment

Temperament and Character Inventory-Revised [69]. It is a 240-item self-administered questionnaire, rated on a 5-point Likert scale format (from 1 = "Definitively False" to 5 = "Definitively True"). The TCI-R is composed by 7 scales, which measure four temperament traits, mostly affected by genetic factors, and three personality factors, mostly affected by environmental factors according to Cloninger's theory. The temperament traits are: Novelty Seeking (NS), Harm Avoidance (HA), Reward Dependence (RD) and Persistence (P). These dimensions reflect the different response to novelty, to avoiding aversive stimuli, to reactions to reward and the time invested in staying on the task. These traits are stable throughout life and they are moderately heritable. Each temperament scale is composed by several facet scales: NS includes Exploratory excitability (NS1), Impulsiveness (NS2), Extravagance (NS3) and Disorderliness (NS4); HA consists

of Anticipatory worry (HA1), Fear of uncertainty (HA2), Shyness (HA3) and Fatigability (HA4); RD comprises Sentimentality (RD1), Openness to warm communication (RD2), Attachment (RD3) and Dependence (RD4); P contains Eagerness of effort (P1), Work hardened (P2), Ambitious (P3) and Perfectionist (P4). Self-Directedness (SD), Cooperativeness (C), and Self-Transcendence (ST) are the three personality factors, that reflect the self-determination, the ability to establish positive relationships and the experiencing spiritual ideas. These factors are composed by different subscales: SD includes Responsibility (SD1), Purposeful (SD2), Resourcefulness (SD3), Self-acceptance (SD4) and Enlightened second nature (SD5); Comprises Social acceptance (C1), Empathy (C2), Helpfulness (C3), Compassion (C4) and Pure-hearted conscience (C5); ST is composed by Self-forgetful (ST1), Transpersonal identification (ST2) and Spiritual acceptance (ST3).

### 3.4 Statistical analysis

Genotype distributions was analyzed through Hardy-Weinberg equilibrium. We performed a linear discriminant analysis to investigate the differences between groups in relation to personality characteristics of individuals. The groups were composed by individuals with different gene polymorphism (*COMT*, *BDNF* and *5HTTLPR*). On the basis of genetic variants, we created two groups for *COMT* and *BDNF*. The *COMT* groups were targeted with 0 (VAL/VAL) and 1 (VAL/MET and MET/MET) genomic variants. The *BDNF* groups were targeted with 0 (VAL/VAL) and 1 (VAL/MET and MET/MET) genomic variants. The *5HTTLPR* groups were targeted with 1 (LA/LA), 2 (LA/LG = LA/S) and 3 (S/S = LG/LG = LG/S) genetic variants. The aim of the statistical analysis in discriminant analysis is to combine (weight) the variable scores in some way so that a single new composite variable, the discriminant score, is produced. The discriminant score is defined by a discriminate function which maximizes the differences between groups. In our case, the independent variables of the discriminate functions are the personality characteristics measured by the 29 TCI-R facet scales. We compared the results between the three genetic groupings to find which grouping has the highest difference. The level of difference indicates that the psychological characteristics have an important contribution in determining grouping separation and, therefore, that there is, probably, a connection between genetic variants and personality characteristics. We reported the eigenvalues, the explained variance, the Wilks' test, the standardized discriminant function coefficients, the classification tables and the histograms or groups plots for each genetic grouping [70]. All analyses were carried on using IBM-SPSS 26.0 (IBM Corp., Chicago, IL, USA).

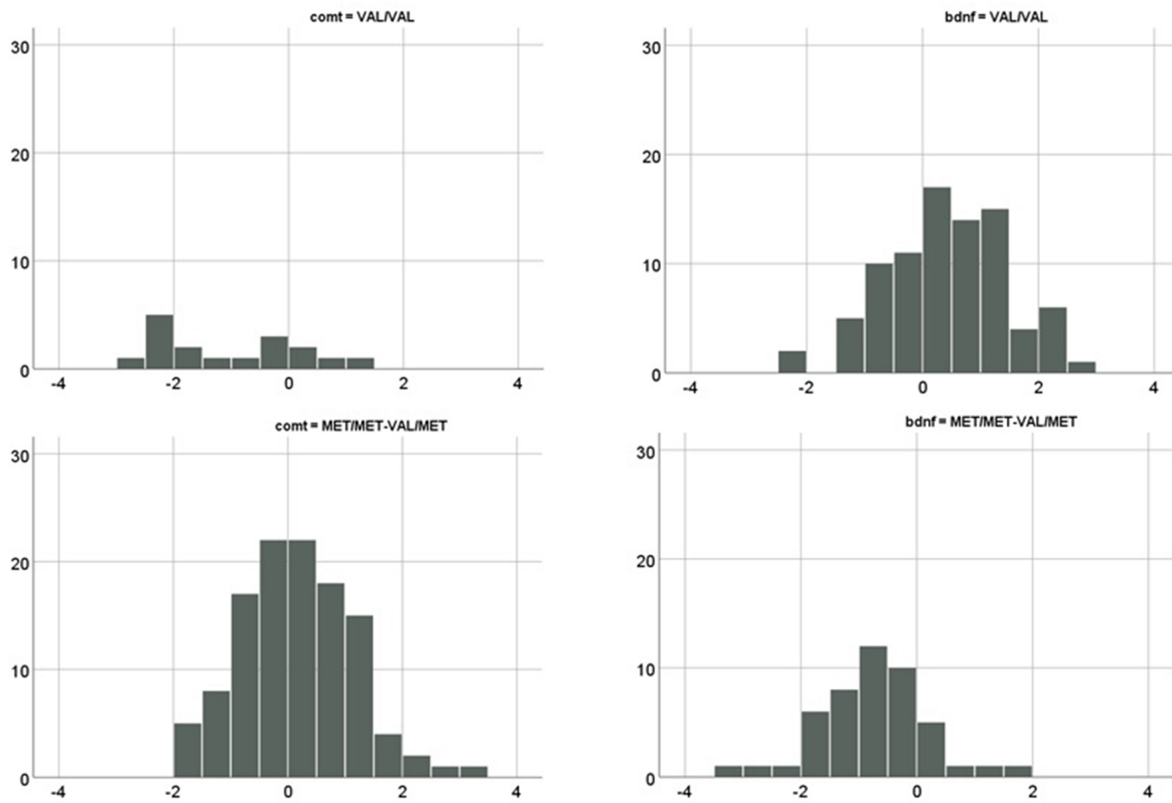


Fig. 1. Histograms of discrimination function for *COMT* (left plots) and *BDNF* (right plots) grouping.

### 3.5 Procedure

All respondents were asked to participate on a voluntary basis, and were provided written informed consent before administering the questionnaire and extracting buccal swab. Anonymity was guaranteed to all participants. Anonymity and privacy of the participants were guaranteed according the Italian and the European laws about privacy (Italian law n. 196/2003 and EU GDPR 679/2016, respectively). The study was approved by the Department of Psychological Science, Health and Territory. The Genetics Laboratory of University of Chieti-Pescara/CAST is in accordance with the DL 81/08 for Biological Safety and has issued an IQNet recognized certificate number 51897 (Registration number: IT-134045).

## 4. Results

**Supplementary Table 1** was provided with descriptive statistics (mean, standard deviation and standard error) for each variant of *COMT*, *BDNF* and *5HTTLPR*.

### 4.1 Hardy-Weinberg equilibrium

Genotype distributions is reported in Table 1. They were consistent with what is typically observed in the general population and did not deviate from Hardy-Weinberg equilibrium.

Table 1. Genotype frequency distribution.

Gene/SNP	Genotype	Frequency	N%
<i>BDNF</i>	VAL/VAL	85	64.4
	Val66Met (rs6265 A>G)	40	30.3
	MET/MET	7	5.3
<i>COMT</i>	VAL/VAL	72	54.6
	Val158Met (rs4680)	43	32.6
	MET/MET	17	12.8
5-HTT	La/La	58	44
	<i>5HTTLPR</i> /rs255315- <i>HTT</i>	39	29.5
	La/Lg	19	14.4
	Lg/S	3	2.3
	Lg/Lg	8	6
	S/S	5	3.8

Note. Genotype frequencies were in Hardy-Weinberg equilibrium ( $\chi^2$  test  $p$  value > 0.05).

### 4.2 Eigenvalues, Wilks' lambda and Chi-squared test

Table 2 shows the eigenvalue, percentage of explained variance, Wilks' lambda and Chi-squared test for each genetic grouping (*COMT*, *BDNF* and *5HTTLPR*). *BDNF* and *5HTTLPR* grouping had the lowest lambda values. Lambda values indicate the proportion of total unexplained variance. *BDNF* and *5HTTLPR* had 75.6% and 62.6% of unexplained variance, respectively, while *COMT* had 84.9%, conversely.

**Table 2. Eigenvalues Wilks' lambda ( $\Delta$ ) test and percentage of variance for *COMT*, *BDNF* and *5HTTLPR* gene polymorphisms.**

Genetic grouping	Discriminant function	Eigenvalue	Variance (%)	Wilks' D	chi squared	df	<i>p</i> ( $\Delta$ )
<i>COMT</i>	function 1	0.177	100	0.849	18.870	29	0.925
<i>BDNF</i>	function 1	0.323	100	0.756	32.299	29	0.307
<i>5HTTLPR</i>	function 1	0.302	57.0	0.626	53.949	58	0.627
	function 2	0.228	43.0	0.814	23.616	28	0.702

**Table 3. Standardized coefficients of discriminant functions for *COMT*, *BDNF* and *5HTTLPR* grouping.**

Predictors	<i>COMT</i>	<i>BDNF</i>	<i>5HTTLPR</i>	
			function 1	function 2
NS1	-0.01	-0.08	-0.58	0.04
NS2	-0.22	-0.18	0.18	0.29
NS3	0.13	0.16	0.75	0.07
NS4	0.23	0.33	0.53	-0.04
HA1	-0.23	-0.62	-0.28	-0.72
HA2	0.06	0.04	0.31	0.08
HA3	-0.45	0.25	-0.51	0.63
HA4	0.17	0.34	-0.13	0.67
RD1	0.25	0.20	0.46	0.24
RD2	0.05	0.45	-0.90	0.16
RD3	-0.13	-0.56	0.34	0.18
RD4	0.17	0.78	0.38	-0.38
PS1	-0.06	0.30	-0.32	-0.30
PS2	0.18	0.51	0.54	0.12
PS3	0.24	-0.31	0.02	0.56
PS4	0.16	-0.29	0.07	-0.36
SD1	0.33	0.31	0.14	0.17
SD2	0.44	-0.22	0.23	-1.07
SD3	-0.56	-0.14	-0.34	0.48
SD4	-0.37	0.21	0.29	0.36
SD5	0.04	0.44	0.35	-0.33
C1	-0.10	-0.19	0.14	0.65
C2	-0.84	-0.52	-0.22	-0.22
C3	-0.69	-0.14	-0.25	0.29
C4	0.27	-0.21	-0.15	-0.24
C5	0.49	0.22	0.09	0.61
ST1	0.47	0.36	0.08	0.01
ST2	0.33	-0.44	0.32	-0.66
ST3	-0.10	0.15	0.22	0.11

### 4.3 Discriminant function coefficients

Table 3 reports the standardized discriminant function coefficients for *COMT*, *BDNF* and *5HTTLPR* grouping. The standardized coefficients indicate the importance of each variable in differencing groups.

Discriminant loadings were estimated for each variable to determine the correlation of each variable with the determinant function. The variables with the largest discriminant loadings are those that best characterize the discriminant function. The logic applied to discriminant loadings is similar to that applied to factor analysis, in which variables with loadings  $<0.30$  are excluded [71]. Therefore, the predictors with loadings  $>0.30$  were PS3 and PS4

for *COMT*, RD4 for *BDNF* grouping and NS3 and HA4 for *5HTTLPR* grouping. Therefore, different combinations of personality characteristics characterize the discriminant functions for each genomic variant. In particular, Persistence is related to *COMT* grouping, Reward Dependence is related to *BDNF* grouping and Novelty Seeking and Harm Avoidance to *5HTTLPR* grouping.

### 4.4 Classification tables

Table 4 reports the classification table for each genomic grouping. The rows are the observed categories of the dependent and the columns are the predicted categories. When prediction is perfect all cases will lie on the diagonal. The percentage of cases on the diagonal is the percentage of correct classifications. The classification results reveal that 91.7%, 77.3% and 65.9% of individuals were correctly classified into the different genomic variants for *COMT*, *BDNF* and *5HTTLPR*, respectively. In particular, individuals of group 1 were identified with higher accuracy (100%) than those of group 0 (35.3%) for *COMT*; individuals of group 0 were identified with higher accuracy (88.2%) than those of group 1 (57.4%) for *BDNF*; individuals of group 1 were identified with higher accuracy (67.2%) than those of group 2 and 3 (69% and 50%, respectively) for *5HTTLPR*.

Fig. 1 shows the histograms illustrating the distribution of the discriminant function scores for each group for *COMT* and *BDNF*, respectively. It is possible to see that for *BDNF* the overlap of group distributions is lower than that for *COMT*.

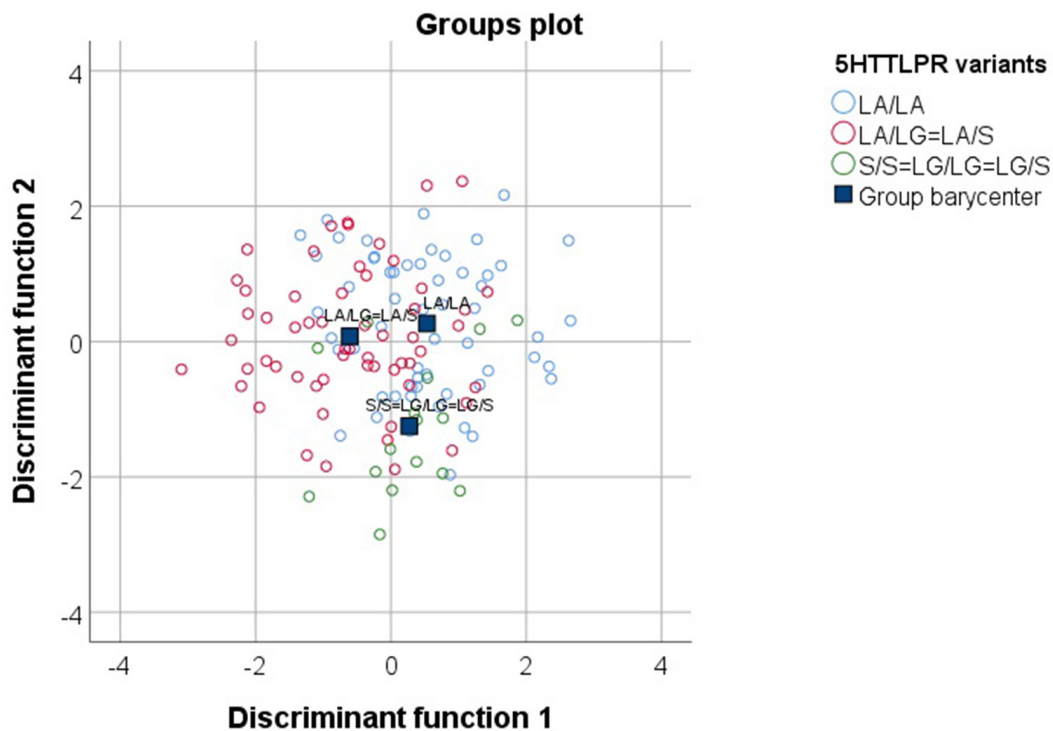
Fig. 2 shows the group distributions for *5HTTLPR*. All the three groups had different barycenters. Therefore, the personality factors can discriminate the *5HTTLPR* groups.

## 5. Discussions

The aim of the present study was to analyze the undefined association among the *COMT*, *BDNF* and *5HTTLPR* gene polymorphisms with personality traits. Results showed that temperaments measured with TCI-R can discriminate individuals with different genomic polymorphisms. In particular, the temperament trait Persistence discriminates individuals with different *COMT* variants, Reward Dependence discriminates individuals with different *BDNF* variants, while Novelty Seeking and Harm Avoidance discriminate individuals with different *5HTTLPR* variants. Our results confirm the association among *COMT*,

**Table 4. Classification tables (frequencies and percentages %) for *COMT*, *BDNF* and *5HTTLPR* grouping.**

Observed membership	<i>COMT</i>	Predicted group membership			Total
		VAL/VAL	MET/MET-VAL/MET	Total	
Frequencies %	VAL/VAL	6	11		17
	MET/MET-VAL/MET	0	115		115
	VAL/VAL	35.3	64.7		100
	MET/MET-VAL/MET	0	100		100
Frequencies %	<i>BDNF</i>	VAL/VAL	MET/MET-VAL/MET	total	
	VAL/VAL	75	10		85
	MET/MET-VAL/MET	20	27		47
	VAL/VAL	88.2	11.8		100
Frequencies %	<i>5HTTLPR</i>	LA/LA	LA/LG = LA/S	S/S = LG/LG = LG/S	Total
	LA/LA	39	17	2	58
	LA/LG = LA/S	16	40	2	58
	S/S = LG/LG = LG/S	6	2	8	16
	LA/LA	67.2	29.3	3.4	100
	LA/LG = LA/S	27.6	69	3.4	100
	S/S = LG/LG = LG/S	37.5	12.5	50	100

**Fig. 2. Groups plot for *5HTTLPR*.**

*BDNF*, *5HTTLPR* and specific personality traits (Reward Dependence, Novelty Seeking, Harm Avoidance and Persistence) due to neurotransmitter circuit [29, 30]. The neuropsychological theory proposes a probable path that associates genes, environment and behaviour. In particular, genes and environment affect brain physiology, through the specific neurotransmitter function of dopamine, serotonin and noradrenalin. The brain activity affects directly behaviour (such as arousal in specific tasks) and indirectly

through behavioral tendencies (e.g., avoidance). These behavior tendencies have complex social consequences and modulate the vulnerability to mental illnesses [29]. For example, Cloninger *et al.* [9] associated HA to variation of *5HTTLPR*, NS to low activity of dopamine, P to low activity of noradrenaline. This neurochemical activity is genetically determined, but the link between polymorphisms and behavioral traits was not clearly defined [31].

Our study demonstrates that *COMT*, *BDNF* and *5HTTLPR* are associated to specific personality factors, by using personality characteristics to show how much individuals with different gene variants can be discriminated. Personality characteristics can discriminate groups with different genetic variants, and this result could be purposeful to use the personality profile of each individual to assess mental diseases and personality disorders [3–5]. For example, High scores in Persistence are associated to Obsessive-Compulsive Disorder [72, 73] and anorexia nervosa [74, 75]. Both disorders are associated to tendency toward perfectionism, that allows individuals to be prone to sacrifice to obtain a particular target. Specifically, Obsessive-Compulsive Disorder is characterized by meticulousness, abnormal preoccupation for orderliness and by an excessively commitment to work [76, 77]. Anorexia nervosa is determined by body dismorphism and a strong fear to increase in weight [78–80]. High levels of Conscientiousness (one of the five-factors of personality) are related to positive emotionality and social well-being [8, 9, 13]. This personality trait allows individuals to persist and to successfully achieve a target. Reward Dependence and Persistence are associated to persistence, resilience to stress and perfectionism and, thus, they are characteristic strongly related to Conscientiousness [17, 73]. If personality factors are connected to mental and psychological diseases, it is possible to define the genetic aspects of psychological diseases through the study of the association between genetic factors and personality traits or tendencies. The personality traits could allow researchers to select and define more precisely the genetic variants that have the greatest weight in determining psychological disorders. In other words, personality traits associated to mental illness can be used as intermediary elements to define the connection between genes and mental illness.

## 6. Conclusions

In conclusion, this study is part of the research area that analyzes the association between genes and personality. In particular, reactions to reward are associated to *BDNF* variants; response to novelty and avoidance of aversive stimuli are associated to *5HTTLPR*; finally, tenancy to achieve targets is associated to *COMT* gene polymorphisms.

The major limitations of this work concern the small sample size and the absence of comparison with a sample consisting of male subjects. In addition, future perspectives, are addressed to replicate the study for other ages, making the sample more heterogeneous. Further researches are necessary to study the association between genetic factors of individuals and their personality to reduce the still present undefined association between genes, behavior and psychological well-being [81].

## 7. Author contributions

MT, AS, VG designed the study; MRS, LP, ILF performed testing and data collection; MF, MP, FK performed the genetic data analysis and interpretation; MT, VG, AS, MRS, interpreted data and prepared the manuscript for publication; AS, VG, AG, LS reviewed the draft of the manuscript and provided critical revisions; All authors have read and approved the manuscript.

## 8. Ethics approval and consent to participate

All respondents were asked to participate on a voluntary basis, and were provided written informed consent before administering the questionnaire and extracting buccal swab. Anonymity was guaranteed to all participants. Anonymity and privacy of the participants were guaranteed according the Italian and the European laws about privacy (Italian law n. 196/2003 and EU GDPR 679/2016, respectively). The study was approved by the Department of Psychological Science, Health and Territory, University of Studies “G. d’Annunzio” Chieti-Pescara, code 21012.

## 9. Acknowledgment

Not applicable.

## 10. Funding

This research received no external funding.

## 11. Conflict of interest

The authors declare no conflict of interest. VG is serving as one of the Editorial Board members of this journal. We declare that VG had no involvement in the peer review of this article and has no access to information regarding its peer review. Full responsibility for the editorial process for this article was delegated to AGG.

## 12. Informed consent statement

Informed consent was obtained from all individual participants included in the study.

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**Supplementary material:** Supplementary material associated with this article can be found, in the online version, at <https://www.fbscience.com/Landmark/articles/10.52586/5009>.

**Abbreviations:** *COMT*, Catechol-O-Methyltransferase; *BDNF*, Brain derived Neurotrophic Factor; *5-HTT*, Serotonin transporter gene; RD, High Reward Dependence; P, Persistence; C, Cooperativeness; CNS, Central Nervous System; OCD, Obsessive-compulsive disorders of personality; PFC, Region of prefrontal cortex; BAS, Behavioral Activation System's theory; SNP, single-nucleotide polymorphism; G, Guanine; A, Adenosine; Val, Valine; Met, Methionine; 5-HT, serotonin 5-hydroxytryptamine; VNTR, Variable Number Tandem Repeats; L, Long; PCR, Poly-

merase Chain Reaction; RFLP-PCR, PCR-based restriction fragment length polymorphism; TCI-R, Temperament and Character Inventory-Revised; NS, Novelty Seeking; NS1, Exploratory excitability; NS2, Impulsiveness; NS3, Extravagance; NS4, Disorderliness; HA, Harm Avoidance; HA1, Anticipatory worry; HA2, Fear of uncertainty; HA3, Shyness; HA4, Fatigability; RD, Reward Dependence; RD1, Sentimentality; RD2, Openness to warm communication; RD3, Attachment; RD4, Dependence; P, Persistence; P1, Eagerness of effort; P2, Work hardened; P3, Ambitious; P4, Perfectionist; SD, Self-Directedness; SD1, Responsibility; SD2, Purposeful; SD3, Resourcefulness; SD4, Self-acceptance; SD5, Enlightened second nature; C, Cooperativeness; C1, Social acceptance; C2, Empathy; C3, Helpfulness; C4, Compassion; C5, Pure-hearted conscience; ST, Self-Transcendence; ST1, Self-forgetful; ST2, Transpersonal identification; ST3, Spiritual acceptance; AN, anorexia nervosa.

**Keywords:** Personality; Gene; Temperament and Character Inventory-Revised; Linear discriminant analysis

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