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Short communication

Association between catechol-*O*-methyltransferase Val^{158}Met polymorphism and configural mode of face processing

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HIGHLIGHTS

- We investigated the link between COMT gene and face recognition ability.
- Met/Met genotype was linked to superior ability of configual face processing.
- The effect of COMT gene was eliminated when faces were presented upside–down.

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ABSTRACT

Human visual system heavily relies on the spatial configuration among facial parts in discriminating faces. There are individual differences in the ability of configural face processing, which are supposed to be partly attributable to genetic predispositions. However, few studies have identified a specific gene linked to configural face processing ability. The present study investigated an association between configural mode of face processing and a single-nucleotide polymorphism in codon 158 of catechol-*O*-methyltransferase gene (COMT Val^{158}Met polymorphism) using part-spacing paradigm.

The results have revealed superior sensitivity to the changes in facial configuration in participants with Met/Met genotype of COMT Val^{158}Met polymorphism compared to the other genotypes. This effect was virtually eliminated when the faces were presented upside–down. There was no group-difference in the ability to detect the change in morphological features of individual facial parts. These results indicate that COMT Val^{158}Met polymorphism partly explains the individual differences in the ability of configural face processing.

1. Introduction

Face processing is the cornerstone of human social life; the visual system is so efficient in processing faces that it can discriminate thousands of individual faces at a glance [1]. The perceptual system relies mainly on two sources of information for face discrimination, namely, the morphological features of individual facial parts and the spatial configuration among them (the second-order configuration; [1,2]). As illustrated in behavioral effects such as the face inversion effect [3], face composite effect [4], and the part-whole effect [5], the sensitivity to facial configuration or holistic information confers great advantage in discriminating subtle differences among face exemplars.

There are well-documented individual differences in face processing ability [6]. Part of these individual differences is thought to be attributable to genetic causes. Reports on familial prosopagnosia support this claim [7,8]. Likewise, among populations with no known pathological conditions, monozygotic twins show higher concordance in their configural processing ability than dizygotic twins [9,10].

Recent studies have demonstrated that patients with schizophrenia showed marked impairments in the configural mode of face processing [11,12]. Furthermore, first-degree relatives of patients with schizophrenia also showed an atypical scan-path in face recognition [13]. On the basis of these findings, it seems plausible to postulate that possession of a genetic risk factor of schizophrenia may lead to lower sensitivity to configural face information.

Abbreviations: COMT, catechol-*O*-methyltransferase; Val, valine; Met, methionine; STS, superior temporal sulcus; SNP, single nucleotide polymorphism; RT, reaction time.

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Among the candidate genes linked to the etiology of schizophrenia, one of the most well-studied is the single-nucleotide polymorphism (SNP) in the catechol-*O*-methyltransferase gene (COMT; [14,15]). COMT is a methylation enzyme of dopamine and plays a primary role in dopamine metabolism. There is a genetic polymorphism in codon 158 of the COMT gene (COMT Val^{158}Met polymorphism), that substitutes valine (Val) to methionine (Met). The G (Val) allele stabilizes COMT, and consequently leads to a 3–4-fold increase in COMT catabolic activity [14,15]. A number of behavioral and neuroimaging studies have linked the COMT Val^{158}Met polymorphism to functions of broad neural regions including the prefrontal cortex (PFC) and amygdala in neurologically normal populations [16].

The G (Val) allele of the COMT Val^{158}Met polymorphism has been identified as one of the risk factors for schizophrenia. Furthermore, an association between the A (Met) allele and increased volume in the temporal cortex has been reported [17,18]. Based on these findings, we hypothesized that there would be an association between the COMT Val^{158}Met polymorphism and the configural mode of face processing ability. To examine this hypothesis, the present study measured performance in configural and featural modes of face processing in late adolescents (around 15–17 years old), and examined the association between their behavioral performance and the COMT Val^{158}Met polymorphism. We chose to recruit participants within this age range based on the following two reasons. First, developmental studies have shown that the ability for configural face processing does not mature fully until 9–13 years of age [19,20]. Second, the recruitment of an older population might mask the potential genetic influences due to the diversity of life-long experiences.

The configural and featural modes of face processing ability were measured using a part-spacing paradigm [6,21]. This paradigm required participants to detect the change in facial parts or configuration in the target face from the original face. In order to control for the influences of low-order perceptual parameters, the faces were presented in vertically-inverted and upright orientations.

2. Material and methods

2.1. Participants

Fifty six males and fifty seven females ($M = 16.0 \pm 0.96$ years old) with normal or corrected-to-normal visual acuity participated in the present study. All the participants were junior-high or high-school students in Nagasaki prefecture in Japan and were recruited mainly by flayers and telephone appointment. It was stated explicitly during the recruitment process that only students with no known medical conditions were eligible for participation. Except for this, no other exclusion criteria were applied. Their participation was rewarded by 1000 yen or a gift certificate with the same value. We ascertained that the participants had no known record of pathological conditions and were not on medication at the time of participation, by administering a brief open-ended questionnaire which asked the participants to fill in any record of pathological conditions or medications they were taking, if any. Further three students agreed to participate in the study, but their data were not included in the final analysis. This was because we failed to collect their data properly due to experimenter's mistakes in operating the stimulus program. The research protocol was approved by the ethical committee in Nagasaki University in accordance with the principles of the Declaration of Helsinki.

2.2. Stimulus

The original faces included one male and one female facial picture with black backgrounds. The target faces were created by changing either the facial parts (part-change condition) or the spatial configuration among the facial parts (configuration-change condition) using face morphing software (FUTON software, ATR Promotions Inc., Kyoto, Japan) and custom-made programs running on MATLAB R2007b (Mathworks Inc., Massachusetts, USA). Examples of the faces of each condition are shown in Fig. 1(a).

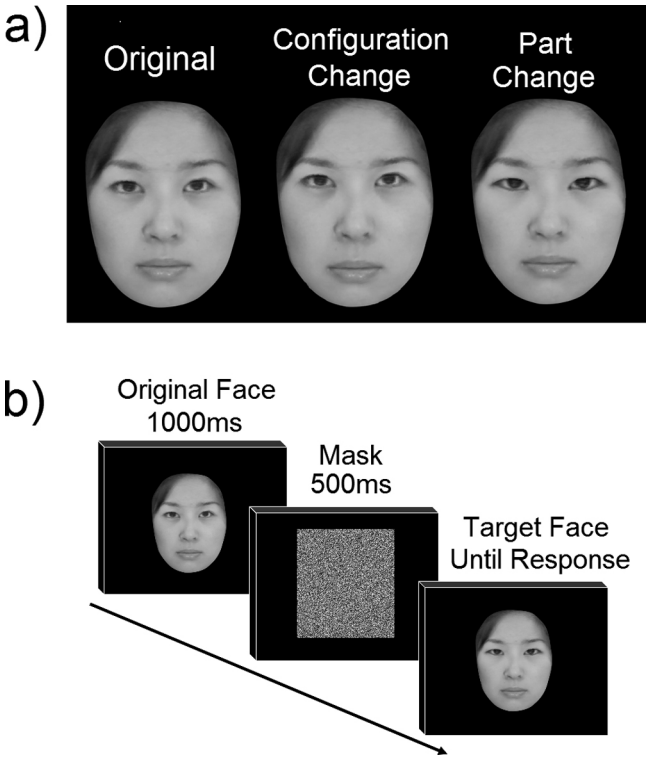

Fig. 1. (a) Examples of the original and target faces and (b) schematic representation of the temporal sequence of stimulus presentation.

In creating the target faces in the part-change condition, either the eye or mouth regions of the original faces were replaced with the corresponding facial parts of the other person selected from a pool of six same-sex models. Special care was taken to ensure that the original face and the models had roughly the same skin color. The color of the replaced region's edge was blended seamlessly with that of the original face, so that the participants could not use the sharp change in skin coloration as a cue.

The target faces of the configuration-change condition were created by changing either the inter-ocular distance or the vertical distance between the eye and the mouth. In total, four types of configural changes were created by orthogonally combing the location of the distance change (eye–eye or eye–mouth) and the distance manipulation (enlarged–shortened). The color in each pixel was interposed so that the skin coloration changed smoothly in the target faces.

2.3. DNA sampling and genotyping

DNA was extracted from swabs of buccal cells lining participants' cheeks. Genotyping of the COMT Val^{158}Met polymorphism (rs4680) was conducted with the Taqman genotyping platform using the real-time polymerase chain reaction by light cycler system (Roche diagnostics). The target sequence was CCAGCGGATGGTGGATTTCGCTGGC[A/G]TGAAGGACAAGGTGTGCATGCCTGA.