Association of rapid scene categorization with a nicotinic acetylcholine receptor gene polymorphism

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In humans, a number of studies have found that the single nucleotide polymorphism (SNP) rs1044396 on the CHRNA4 gene influences individual differences in attention. However, its association with other cognitive functions remains to be clarified. In the present study, we explored the effects of genetic variations in CHRNA4 on rapid scene categorization by 100 healthy human participants. The rapid scene categorization task required participants to judge whether the category of a scene image (Natural or Man-Made) was compatible with a cue word presented at the response phase. The target-mask stimulus onset asynchrony (SOA) ranged from 13 ms to 93 ms. Heterozygotes and homozygotes for the CHRNA4 T allele responded more accurately at long SOAs (67 ms and 93 ms) compared with non-T allele carriers, but only with the Natural scene category. Our discoveries provide evidence that genetic variations in CHRNA4 can moderately contribute to natural scene categorization performance.

Key words: scene categorization, nicotinic acetylcholine receptor, CHRNA4

Introduction

The CHRNA4 gene is known to code for the alpha4 subunit of nicotinic acetylcholine receptors. A prior study in humans revealed that nicotine-related cognitive functions such as attention are associated with CHRNA4 (e.g., Greenwood et al., 2005).

It was recently proposed that the nicotine signal is also related to enhanced detection of visual stimuli (Disney, Aoki, & Hawken, 2007) and scene perception in rats (Goard & Dan, 2009). These discoveries imply that nicotine signaling is essential to the visual processing of scene perception and that nicotine signals of CHRNA4 may influence scene perception in humans. To our knowledge, however, the effect of nicotine on scene perception in healthy humans has not yet been investigated. In the present study, we examined the role of the nicotinic acetylcholine receptor in natural scene perception by investigating the potential association between CHRNA4 gene polymorphism and rapid scene categorization performance in healthy humans.

Method

Participants. One hundred healthy participants (37 women, 63 men, mean age 21.0 years, SD = 2.47) were sampled from undergraduate and graduate students at Kyoto University. The experimental protocol was approved by the local Institutional Review Board.

Materials. A total of 648 grayscale photographs from the Oliva and Torralba (2001) database were drawn from 6 basic level categories—3 natural (beach, mountain, and forest) and 3 man-made (city center, highway, and street)—with 324 images in each superordinate level category (Natural/Man-Made). Mask images were generated using full phase randomization, keeping the spatial frequency amplitude spectra and mean luminance identical to those of the original images (Figure 1).

Procedure. An experimental trial is schematically depicted in Figure 1. Each trial began with a fixation cross presented for 1000 ms. Either the Natural or Man-Made stimulus (i.e., the target) was displayed for 13 ms. This was followed by an inter-stimulus interval (ISI)—a blank screen display—of variable intervals (0 ms, 27 ms, 54 ms, or 80 ms), after which a mask stimulus was displayed for 53 ms. The stimulus onset asynchrony (SOA) from the target to mask stimulus was 13 ms, 40 ms, 67 ms, or 93 ms. Following the mask image, a blank screen was presented for 750 ms, after which the response screen was displayed. During the response phase, one of two terms, either "Natural" or "Man-Made", was displayed at the center of the screen. Participants were instructed to judge whether or not the displayed category was consistent with the target category. Accuracy and reaction times were recorded.

Summary of Awarded Presentation

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The number of practice trials was 36 and the number of experimental trials was 648 (12 blocks and 54 trials per block).

**Genotyping.** All participants were genotyped using the PCR-RFLP method. The 100 participants were genotyped as TT (n = 6), CT (n = 43), or CC (n = 51). The T allele frequency was 27.5%. These groups resulted in the Hardy-Weinberg equilibrium (p > 0.05 in χ² tests). Participants were classified as CHRNA4 T allele carriers (CT and TT genotypes) or non-T allele carriers (CC genotypes), because of the low number of TT carriers.

**Results and Discussion**

The mean proportion correct was analyzed for each experimental condition. Only the Natural category showed a significant interaction between CHRNA4 genotype and SOA [F(3, 588) = 2.86, η² = .0332, p < .05]. To interpret this interaction, we analyzed the genotype effect for the Natural category. We revealed a significant main effect of genotype for the 67 ms [F(1, 784) = 4.77, η² = .0568, p < .05] and 93 ms [F(1, 784) = 3.86, η² = .0442, p < .05] SOAs. Planned comparisons showed that T carriers (CT/TT) performed the natural scene categorization with greater accuracy than did non-T carriers (CC) for the 67 ms and 93 ms SOAs (Figure 2).

Although there is no known biochemical background to link this polymorphism to regulation of mRNA or protein structure, rodent studies yielded supporting evidence for our findings. Goard and Dan (2009) demonstrated that the visual receptive field response of rats to natural images was enhanced by nicotine injection into the nucleus basalis of the basal forebrain. Furthermore, Disney et al. (2007) proposed that nicotinic input to area V1 in macaque monkeys mediated the detection of visual stimuli. Thus, nicotine is thought to enhance encoding and visual information processing of the natural scene. If we extrapolate these results of rodent studies to humans, the nicotine receptor subunit CHRNA4 may be expected to play a critical role in the encoding of natural scene perception.

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**References**


