
CATECHOL O-METHYLTRANSFERASE VAL158MET GENOTYPE AND NEURAL MECHANISMS RELATED TO RESPONSE INHIBITION IN CHRONIC CANNABIS USERS

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Introduction

Neuropsychological and neuroimaging studies of response inhibition in cannabis users have reported inconsistent results. The age of onset of cannabis use and individual genetic differences may play a critical role in the regulation of inhibition in cannabis users.

Aims

We examine the influence of COMT Val158Met functional polymorphism on the response inhibition brain network in a group of early-onset chronic cannabis users compared with healthy controls.

Methods

fMRI data was acquired from 27 chronic cannabis users who began use cannabis before 16 years of age, and 29 non-using control subjects matched in terms of age, educational level and intelligence quotient while undergoing the Multi-Source Interference Task (MSIT). Participants were male, Caucasians aged between 18 and 30 years. All were assessed by a structured psychiatric interview (PRISM) to exclude any lifetime Axis-I disorder (DSM-IV). COMT genotyping was performed and resonance imaging data was analysed by voxel-based morphometry (VBM).

Results

Both groups did not differ on their behavioural performance and brain responses during the MSIT task. A significant group-by-genotype interaction was observed on task-related brain activation (and on MSIT reaction times), in which *met* carrier load was associated with increased activation in cannabis users and *val* carrier load with increased activation in controls. The interaction pattern included the medial frontal cortex, ACC, inferior frontal gyrus, ventral striatum, anterior mesencephalon, inferior parietal and superior temporal cortices and the PCC.

Conclusion

Chronic cannabis exposure interacts with the genetically driven dopamine function in the modulation of the neural mechanisms related to response inhibition.

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