AN ASSOCIATION STUDY ON CHILDREN WITH GILLES DE LA TOURETTE'S SYNDROME AND COMT GENE POLYMORPHISM

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Objective: To investigate the association between catechol-O-methyl transferase (COMT) gene polymorphism and Gilles de la Tourette´s syndrome (GTS).
Methods: Using Amplification Refractory Mutation System(ARMS) PCR genotyping assay method, a polymorphism (val158met) of COMT gene was genotyped in 112 of all GTS patients including 54 GTS-alone patients, 48 GTS+ADHD patients among of them and 71 healthy controls. The correlation between positive association of polymorphism (val158met) of COMT gene in GTS and the age of onset in patients with GTS was also analyzed.
Results: When compared with healthy controls, genotype of val158met did not differ in total GTS patients or alone- GTS patients (x^2=0.56, P = 0.756; x^2= 1.05, P = 0.600 respectively). There is also no significant difference (P>0.05) in allele distribution of val158met in total GTS patients or alone- GTS patients when respectively compared with controls (x^2= 0.18, P = 0.669; x^2= 0.29, P = 0.593 respectively). However, Genotype distribution of val158met was significantly different between GTS+ADHD patients and controls (x^2=6.35, P = 0.041). The frequency of the val allele of this locus was significantly higher in GTS+ADHD patients than those in controls (x^2= 5.49, P = 0.019).The age of onset in children with GTS having the val/val genotype of COMT gene val158met polymorphism were significantly earlier than no val/val genotype (P = 0.016).
Conclusion: Polymorphism (val158met) of COMT gene may be associated with GTS children with comorbid ADHD, which may play an important role to make the age of onset in children with GTS become earlier.