Association of the 5HTR2C gene Ser23 variation with childhood allergic asthma

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Abstract

Allergic asthma is the most frequently observed asthma phenotype in the majority of individuals with asthma. Whereas, non-atopic asthma is a phenotype with no allergic sensitization. Serotonin (5-hydroxytryptamine, 5-HT) controls several physiological functions through different serotoninergic receptors (5-HTR). However, the exact role of the serotonin in pathophysiology of asthma has not been understood clearly. Importantly, genetic, epigenetic and environmental risk factors play a crucial role in the etiology of asthma. Evidence suggests that psychosocial stress has been identified as one of the environmental risk factors for the asthma development. Previously, the 5HTR2C gene rs6318 G>C variation has been associated with HPA-mediated response to stress, blood cortisol levels, cardiovascular diseases and psychological disorders. In addition, it has been recognized that 5HTR2C receptor acts like an immunomodulator by controlling the release of different inflammatory cytokines from bronchial epithelial cells. However, there was no study found in the literature to show the association between the 5HTR2C gene rs6318 G>C and asthma. Thus, this particular study aimed to investigate the association between the 5HTR2C gene rs6318 G>C and allergic asthma in pediatric patients. This study included 181 individuals, (120 control and 61 patients). Skin prick test was performed for each patient to confirm asthma diagnosis and to evaluate atopic status. Genotyping for the 5HTR2C was completed by Quantitative-PCR analysis. The genotype distribution frequencies were not in compliance with Hardy-Weinberg equilibrium for patients group ($p<0.00001$, $X2=28.0$). Additionally, the frequency of risk allele (allele C) was no significantly difference between two groups ($p=0.476$, OR=0.785, 95%CI= 0.404-1.526). The genotypic distribution of between atopic asthma and non-atopic asthma within patients groups were in agreement with HWE ($p<0.00001$, $X2= 14.130$; $p= 0.007$, $X2=14.130$, respectively). The allele frequency of the disrupting allele C showed a statistically significance between atopic and non-atopic asthma patients groups ($p= 0.0318$, OR= 3.555, 95%CI= 1.117-11.317). Overall, this results indicated that there is an association between 5HTR2C rs6318 C variant and childhood non-atopic asthma.

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