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A passenger strand variant in miR-196a2 contributes to asthma severity in children and adolescents

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Emerging evidences supported the role of microRNAs in allergic airway diseases and inflammation. Genetic variants in microRNA genes might affect microRNA-mediated cell regulation. This preliminary study was designed to investigate the association of the microRNA-196a2 rs11614913 (C/T) polymorphism with asthma susceptibility and clinical outcome in children and adolescents. Genotyping of rs11614913 polymorphism were determined in 96 patients with bronchial asthma (6-18 year-old) and 96 unrelated controls using real-time polymerase chain reaction technology. In silico target prediction and network core analysis were performed. Asthma patients did not show significant differences in the genotype distribution ($p=0.609$) and allele frequencies ($p=0.428$) compared to controls. There were also no associations with disease duration, age at onset, asthma phenotype, asthma control, therapeutic level, airway hyper-responsiveness, or any laboratory investigations. However, CC genotype was associated with a more severe degree of asthma ($p=0.023$) and higher frequency of nocturnal asthma ($p=0.002$). Carriers for CC were 17 times more likely to develop nocturnal asthma and more than 2.5 fold to be at risk for poor outcome disease compared to CT and TT individuals. microRNA-196a2 rs11614913 polymorphism might be associated with asthma severity in our sample of the Egyptian population. Further investigations in studies with larger sample size and functional tests are needed to validate our findings and to explore the detailed biological mechanisms.

Biography

Mohammad H Hussein is a Pulmonologist and had his Master's degree in Chest diseases from Faculty of Medicine, Cairo University, Cairo, Egypt. He has publications on microRNA analysis, transcriptomics and pharmacogenomics.

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