Association of P2X7 1513A/C polymorphism with susceptibility to tuberculosis among Sudanese patients

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Background: Tuberculosis is a chronic, systemic infectious disease caused by M. tuberculosis mostly infecting the lung to cause pulmonary tuberculosis or localize in alternate body sites leading to extra-pulmonary tuberculosis (EPTB). The P2X7 receptor expressed in a wide variety of normal and disease-associated cell types, activated by extracellular adenosine 5’-triphosphate results in numerous events including the release of pro-inflammatory mediators, cell proliferation or death, and killing of intracellular pathogens. A deficiency of P2X7-mediated control of mycobacterial infection within macrophages in the lung may permit spread to extrapulmonary sites where the infection either progresses to post–primary TB disease.

Methods: One hundred and twenty tuberculosis patients with 46 apparently healthy controls were included for genotyping of the P2X7 polymorphism using Polymerase chain reaction and restriction fragment length polymorphism (PCR –RFLP) and confirmed by sequencing a subset of samples.

Results: This study found that the P2X7 1513A/C polymorphism is significantly associated with tuberculosis infection (CC, AC OR=4.615, 2.058). The pulmonary tuberculosis was the most predominant in the study population but the CC, AC allele had statistical significant association with the Extra-pulmonary tuberculosis infections (OR=2.65). Another polymorphisms rs2230912 was detected from sequencing results may be associated with TB infections.

Conclusion: The CC genotype is associated with susceptibility to TB infections among Sudanese patients and associated with the extrapulmonary TB. Keywords: TB, P2X7, susceptibility, pulmonary TB, Extra-pulmonary, PCR, RFLP.

Biography

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