Abstracts Accepted for Publication

Genomics, genetic basis of disease and HLA / T cell recognition

AB0001 FIRST DESCRIPTION AND FUNCTIONAL PROTEOMIC ANALYSIS OF A PROTECTIVE FOR RHEUMATOID ARTHRITIS GENE POLYMORPHISM

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Background: Rheumatoid Arthritis (RA) is the most common systemic autoimmune disease, with a respective expanded genetic research[1]. Immunogenetic studies have documented the positive correlation of various gene loci with incidence and/or disease profile. However, the description of gene loci negatively related to the incidence of RA is rarely documented. Apart from an early study involving HLA class II, there has been no reference to any genetic locus associated with a protective role against RA incidence.
Objectives: To identify the sequence of the functional areas of the TRAF1 (TNF receptor associated factor 1 - a protein involved in the intracellular signaling pathway of TNF) gene.
Methods: 172 patients and 95 controls were genetically assessed for the sequence of the seven exons of the gene TRAF1.
Results: On the position 9:120905076 of exon 7, the registered polymorphism G/A (rs143265058) was described in the controls group. The same polymorphism was not confirmed in any of the patients. Further functional proteomic study of the polymorphism with computing programs (software), revealed that the presence of this polymorphism leads to a differentiation of the quaternary structure of TRAF1 protein, possibly affecting the cohesion of intracellular TNF signaling pathway[2].
Conclusions: The present reference is one of the extremely rare genetic studies describing a protective gene locus against rheumatoid arthritis, and a pioneer of its kind in the use of Applied Informatics in the depiction of the quaternary structure of the encoded protein. At the same time, it is one of the few immunogenetic studies describing the functional proteomics of the encoded protein, plotting on a molecular level specific interaction modifications affecting the intracellular signaling pathway of TNF.
References:
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AB0002 GENETIC STUDY OF THREE-PRIME REPAIR EXONUCLEASE (TREX1) IN THE SUSCEPTIBILITY TO SYSTEMIC LUPUS ERYTHEMATOSUS (SLE) AMONG EGYPTIAN PATIENTS

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Background: Interferon-alpha (IFNα) pathway has a crucial role in the pathogenesis of SLE. Many genes have been encoding with this pathway and their impaired expression have been reported in patients with SLE. *TREX1* is a DNA exonuclease involved in the metabolism and clearance of single stranded DNA from apoptotic cells, which is impaired in SLE[1]. *TREX1* mutations have been reported in SLE[2].
Objectives: Our study was aiming to assess the role of *TREX1* in the genetic susceptibility to systemic lupus erythematosus (SLE) among Egyptian patients.
Methods: Fifty SLE Egyptian patients and 50 age & sex matched healthy controls were included in this study. Based on the clinical history and immunological investigations, the 50 SLE patients were divided into two groups according to the presence of positive family history of autoimmune disease: Group I: 28 patients with positive family history & Group II: 22 patients with no family history. Further, the single exon of *TREX1* and its flanking sequences were amplified by PCR and sequenced in both directions.
Results: Our work showed a recurrent *TREX1* polymorphism rs11797 (c.531C>T) among Egyptian patients (56%) in comparison to control group (36%) (p value of 0.070) especially in cases with NPSLE, seizures and chilblains; with minor allele frequency of 0.28 in cases and 0.18 in controls (p value=0.342). *TREX1* polymorphism was present in 57.1% patients (16/28) of SLE patients in group I versus 54.5% patients (12/22) of SLE cases in, group II. The polymorphism was positively associated with neuropsychiatric manifestations (OR=7.000, 95% CI=0.791–61.975) and chilblains (OR=10.532, 95% CI=0.550–201.679). Furthermore, there was a statistically significant difference in cases with oral ulcers (p value=0.004), photosensitivity (p value=0.047) and seizures (p value=0.029).
Conclusions: We confirm that rs11797 (c.531C>T) could be associated with the susceptibility to neurological manifestations among the studied SLE patients.
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AB0003 A MIF PROMOTER POLYMORPHISM IS ASSOCIATED WITH THE SUSCEPTIBILITY TO PULMONARY ARTERIAL HYPERTENSION IN DIFFUSE CUTANEOUS SYSTEMIC SCLEROSIS PATIENTS

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Background: Systemic sclerosis (SSc) is a fibrotic immune-mediated disease of unknown etiology. Among its clinical manifestations, pulmonary involvement is the leading cause of mortality in SSc patients. However, the genetic factors involved in lung complication are not well-defined.
Objectives: We aimed to revisit the association of the MIF gene, which encodes a cytokine implicated in idiopathic pulmonary hypertension among other diseases, with the susceptibility and clinical expression of SSc, besides testing the association of this polymorphism with SScrelated pulmonary involvement.
Methods: A total of 4,393SSc patients and 16,591 unaffected controls from six cohorts of European origin were genotyped for the MIF promoter variant rs755622. An inverse variance method was used to meta-analyze the data.
Results: A statistically significant increase of the MIF rs755622*C allele frequency compared to controls was observed in the subgroups of patients with diffuse cutaneous SSc (dcSSc) and with pulmonary arterial hypertension (PAH) indepen-