



TNF-alpha promoter -308 and PTPN22 C1858T genes polymorphisms in Systemic lupus erythematosus

Thesis

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Ву

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بسم الله الرحمن الرحيم

(قالوا سبحانك لا علم لنا إلا ما علمتنا إنك أنت العليم الحكيم)

صدق الله العظيم

Abstract

Objective: To assess the role of TNFα-308 G/A and PTPN22 C1858T SNP with

respect to SLE susceptibility in Egyptian patients and whether these genetic

polymorphisms are associated with the clinical and immunological features of the

disease. Also determination of TNF alpha concenteration in relation to different

genotypes and in relation to disease activity.

Methods: 40 SLE patients & 40 healthy subjects were tested for TNF alpha -308

and PTPN22 (C1858T) genotypes by PCR-RFLP and TNFα concenteration was

measured in their serum using ELISA.

Results: No significant differences in TNF α -308 and PTPN22 (C1858T)

genotypes or alleles frequencies could be identified between SLE cases and controls

(P=0.108, 0.152 respectively). The level of serum TNF α was significantly higher in SLE

patients when compared with the healthy control volunteers (P < 0.001). Furthermore,

TNFα serum level was also statistically significantly higher in SLE patients with cardiac

affection, with vasculitis and with low complement level (P=0.045, 0.016, 0.015

respectively). The serum level of TNF was statistically significantly higher in SLE group

with high disease activity when compared with those low disease activity (P = 0.001).

Also, there was a significant positive correlation between serum TNF α and SLEDAI

(r = 0.723, P < 0.001).

Conclusion: The results of this study suggest that, TNF α -308 and PTPN22

(C1858T) polymorphisms, do not exhibit a significant influence on the susceptibility,

disease course or laboratory characteristics in SLE in Egyptian patients. Nevertheless,

serum TNF α level could be a sensitive marker of SLE disease activity.

Key words: Genetics - polymorphism - TNF - PTPN22 - SLE

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LIST OF ABBREVIATIONS

A Adenine

aCL anticardiolipines antibodies

ACR American college of Rheumatology

ALT Alanine aminotransferase

ANA Antinuclear antibody

Anti-RNP Anti ribonucleoprotein

Anti-Sm Anti Smith

AP-4 activator protein-4

APCs Antigen presenting cells
APLA Antiphospholipid antibodies

APL Antiphospholipid

APS Antiphospholipid syndrome

ARMS Amplification refractory mutation system

ASO Allele specific oligonucleotide

AST Aspartate aminotransferase

ATP Adenosine triphosphate

B2GP1 Beta-2 glycoprotein 1

BCR B-cell antigen receptor

BILAG British Isles lupus assessment group

Bp Base pair

BUN Blood urea nitrogen

C Cytosine

C3 Complement component 3C4 Complement component 4

CBC Complete blood picture

CL Cardiolipin

CNS Central nervous system

CPK Creatine phosphokinase

CRP C-reactive protein

Csk C-terminal Src tyrosine kinase

CTH C-terminal homology

Cu Copper

CVA cerebrovascular accident

DNA Deoxyribonucleic acid

dNTPs Deoxynucleotides Triphosphate

dsDNA Double stranded DNA

EBV Epstein Barr virus

ECLAM European Community Lupus Activity Measure

EDTA Ethylenediamine tetra-acetic acid

ELISA Enzyme linked immunosorbant assay

ESR Erythrocyte sedimentation rate

F Forward

FAM 6-carboxyfluorescein

Fe Iron

G Guanine

GM-CSF Granulocyte-monocyte colony stimulating factor

Grb2 growth factor receptor-bound protein 2

HLA Human leukocytic antigen

HRP Horseradish peroxidase

HRT Hormonal replacement therapy

ICAM-1 Intercellular Adhesion Molecule 1

IF Immunofluorescence

IFN Interferon

Ig Immunoglobulin

IL Interleukin

ISN/RPS International Society of Nephrology/Renal Pathology Society

ISN/RPS International Society of Nephrology/Renal Pathology Society

Kb Kilo base

kD Kilo Dalton

LAC Lupus Anticoagulant

LDL Low-density lipoprotein

Lt Left

LYP Lymphoid tyrosine phosphatase

M.W. Molecular Weight

MgCl₂.6H₂O Magnesium Chloride Hexahydrate

MHC Major histocompatibility comlex

ml Milliliter

mM Millimole

n Number

NaCl Sodium Chloride

NaOH Sodium hydroxide

ng Nanogram

NK Natural killer

nm Nanometer

NSAIDs Nonsteroidal anti-inflammatory drugs

oxLDL Oxidized LDL

P Value Probability Value

PCR Polymerase chain reaction

PEP Proline-enriched protein tyrosine phosphatase

pg Picogram

PPi Pyrophosphate

PTPN22 Protein tyrosine phosphatase non-receptor 22

PTT Partial thromboplastin time

R Reverse

R Arginine

r Correlation coefficient

RA Rheumatoid arthritis

RBCs Red Blood Cells

RFLP Restriction fragment length polymorphism

RHD Rheumatic heart disease

RIA Radioimmunoassay

RNA Ribonucleic acid

Rt Right

S35 serine 35

SD Standard deviation

SH3 Src homology 3

SLAM Systemic lupus activity measure

SLE Systemic lupus erythematosus

SLEDAI Systemic lupus erythematosus disease activity index

SNP Single nucleotide polymorphism

sTNFRs soluble TNF receptors

T Thymine

TAMRA Tetramethylrhodamine

TBE Tris Borate EDTA

TCR T-cell receptor

TET Tetrachlorofluorescin

TGFB Transforming growth factor beta

Th Thelper

TMB Tetramethylbenzidine

TNF Tumor necrosis factor

TNFR Tumor necrosis factor receptor

TNFα Tumor necrosis factor alpha

TNFβ Tumor necrosis factor beta

Tris-HCl Tris – Hydrochloric Acid

ul Microlitre

UV Ultraviolet light

W Tryptophan

W.H.O. World health organization

Zn Zink

INTRODUCTION

Systemic lupus erythematosus (SLE) is a chronic systemic autoimmune disease, characterized by the production of multiple autoantibodies, complement activation, and immune-complex deposition, resulting in tissue and organ damage (*Pan et al.*, 2011).

Investigators have studied several cytokines involved in SLE pathogenesis. The association between SLE and inflammation emphasize the importance of cytokine network genes (*Lin et al.*, 2009).

Tumour necrosis factor alpha (TNF α), an important proinflammatory cytokine, exerts a variety of physiological and pathogenic effects, including the activation of a cascade of inflammatory events, which lead to tissue destruction in autoimmune diseases (*Serrano et al.*, 2006).

The presumptive pathophysiological role of TNF α in SLE suggests that genetic polymorphisms affecting the TNF α production capacity may influence the susceptibility to SLE. The single-nucleotide polymorphism TNF α –308 G/A is located in the promoter region of TNF α gene. The TNF α –308A allele has been reported to be a stronger transcriptional activator in vitro than the common TNF α –308G allele (**Zou et al., 2010**).

Multiple abnormalities of T and B lymphocytes are frequently found in patients with SLE and are central to pathogenesis of the disease (*Mustelin et al.*, 2004).

The gene protein tyrosine phosphatase nonreceptor type 22 (*PTPN22*) encodes the lymphoid protein tyrosine phosphatase (Lyp) that is known to be involved in the control of T-cell activation. Under normal conditions, this enzyme (Lyp) works as a 'negative regulator' and keeps immune cells from becoming overactive (*Reddy et al.*, 2005).

The functional PTPN22 C1858T (R620W) polymorphism resides in a motif involved in C-terminal Src tyrosine kinase (Csk) binding. When a tryptophan (W) residue replaces an arginine (R) at this site, it disrupts the interaction of Lyp with Csk, thereby disturbing the regulation of the T cell receptor (TCR) signaling kinases (*Akosy et al.*, *2011*).

It seems that the R620W polymorphism, by suppressing TCR and BCR (B cell receptor) signaling, globally alters maturation, selection, and function of both T- and B-lymphocytes that predisposes to inducing autoimmunity (*Stanford et al.*, 2010).

AIM OF THE WORK

The aim of the present study was to assess the role of TNF α -308 G/A and PTPN22 C1858T SNPs with respect to SLE susceptibility in Egyptian patients and whether these genetic polymorphisms are associated with the clinical and laboratory features of the disease. Also determination of serum TNF alpha concenteration in relation to different genotypes and in relation to disease activity.