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ORIGINAL ARTICLE

The association of CD40 polymorphism (rs1883832C/T) and soluble CD40 with the risk of systemic lupus erythematosus among Egyptian patients

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Abstract

Background Systemic lupus erythematosus (SLE) is a complex autoimmune disorder of unknown etiology. Considerable evidence supports a genetic basis for susceptibility to SLE. Genetic and functional data suggested the CD40 receptor (CD40) and CD40 ligand (CD40L) as strong candidate genes for SLE.

Aim To investigate whether CD40 gene rs1883832 C/T single-nucleotide polymorphism (SNP) and/or soluble CD40 (sCD40) are associated with SLE in the Egyptian population.

Subjects and methods The study included a hundred SLE patients, and a fifty age- and gender-matched healthy control subjects. CD40 gene rs1883832 C/T genotyping was carried out using restriction fragment length polymorphism (RFLP), while sCD40 levels were measured by ELISA.

Results CD40 rs1883832C/T genotypes (CC, TT, and CT) as well as CD40 alleles (C and T) did not differ between SLE patients and normal control ($p = 0.63$, 0.37, and 0.31 respectively). Though did not reach statistical significance, carriers of genotype CT had 1.5 times more chance to develop SLE compared to wild homozygous CC genotype carriers (OR 1.44), while carriers of genotype TT had ~2 times more chance to have SLE than CC carries (OR 1.96). Accordingly, the carriers of the T allele had ¬ 1.5 times more chance to get SLE compared to the carriers of the C allele (OR 1.4). The serum sCD40 level was significantly higher in SLE patients compared to healthy control (3.4 vs. 0.8 ng/mL, $p < 0.001$). In SLE patients, using CC as the reference genotype, serum sCD40 level was significantly higher in the carriers of the homozygous genotype TT (3.8 ± 1.3 vs. 2.9 ± 1.9, $p = 0.0001$), and T allele (3.6 ± 1.4 vs. 3.0 ± 1.5, $p = 0.003$). Moreover, sCD40 could discriminate SLE patients from normal subjects at a cutoff value of 0.885 ng/mL with 98% sensitivity and 96% specificity (AUC = 0.999, $p < 0.001$).

Conclusions The study did not prove CD40 gene (rs1883832 C/T) polymorphism as a clear risk factor of SLE in this cohort of Egyptian patients, though it was highly likely associated with the carriers of T allele. In the same context, significant high sCD40 levels were observed in the T allele carriers.

Keywords CD40 genotypes · Egypt · RFLP

Introduction

Systemic lupus erythematosus (SLE) is a chronic multisystem autoimmune disease that primarily affects women of reproductive age. SLE is characterized by loss of tolerance and the generation of autoantibodies, which are classically directed against nucleic acids. The resulting accumulation of immune complexes (ICs) promotes inflammation and organ damage [1]. Tissue damage is mediated by recruitment of inflammatory cells, reactive oxygen intermediates, and

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production of inflammatory cytokines [2]. SLE prevalence rates range from 20 to 70 per 100,000 [3]. The prevalence is influenced by ethnicity, where African-Americans/African-Caribbeans and Hispanics are three times as likely to contract the disease compared to European-Caucasians [4].

There is no specific cause of SLE, instead, a number of genetic susceptibilities, immunological, and environmental triggers [5]. Among them, considerable evidence supports a genetic basis for susceptibility to SLE.

Genome-wide association studies (GWAS) on SLE patients have identified hundreds of gene loci involved in the susceptibility to SLE [6–8]. However, this explained only a small fraction of the heritability in those patients, suggesting that many more loci remain to be discovered [9, 10]. One of the genes that play a vital role in adaptive immunity of SLE is CD40 [11]. CD40 is a transmembrane glycoprotein that belongs to the tumor necrosis family. Within the thymus, CD40 has a key role in T cells selection and enhancing self-tolerance by promoting medullary thymic epithelial cells development after birth [12]. CD40 gene falls in the region 20q11–13, which has been linked with SLE in three early independent investigations in European-Caucasians, Mexican-Americans, and African-Americans [13–15].

The interaction between CD40 gene and its ligand CD40L regulates both the humoral and cellular immune responses. CD40 is expressed constitutively by B-lymphocytes, dendritic cells, endothelial cells, and macrophages; whereas, CD40L is upregulated on CD4 + T cells, platelets, mast cells, and basophils upon activation [16, 17]. It has been suggested that engagement of CD40 with CD40L plays a pivotal role in the pathogenesis of SLE [18]. Several polymorphisms in the gene encoding CD40 gene have been identified and a relationship between the CD40 gene polymorphisms and risks of different autoimmune and inflammatory diseases, such as multiple autoimmune diseases, Graves' disease, and rheumatoid arthritis have been reported [19–21].

CD40 gene polymorphisms may result in abnormal expression and associated with the development of autoimmune diseases [22, 23]. Previously, the rs4810485 minor allele T was underrepresented in SLE and correlated with reduced *CD40* expression in peripheral blood monocytes and B cells, with potential implications for the regulation of aberrant immune responses in the disease [24].

However, very little data is present regarding the association between polymorphisms in the CD40 gene and SLE. Moreover, few studies have addressed the relationship between the CD40 gene polymorphisms and the plasma level of CD40 gene. In this study, we have investigated whether CD40 gene rs1883832 C/T polymorphism is associated with increased risk for SLE and its impact on serum CD40 levels in a cohort of Egyptian patients.

Subjects and methods

One hundred patients were recruited from the rheumatology and nephrology departments of the Suez Canal University Hospital, Ismailia. Fifty age- and gender-matched healthy individuals were randomly selected as a control group. SLE diagnosis was on the basis of the clinical and laboratory criteria proposed by the American College of Rheumatology (ACR) for the classification of SLE [25].

The study was approved by the IRB of the Faculty of Medicine, Suez Canal University and all patients were consented before being included in the study. All study populations were subjected to an interview questionnaire, clinical examination, and laboratory assessment. Lab investigations included complete blood count (CBC) (Sysmex XT 5 parts differential cell counter, Germany). Erythrocyte sedimentation rate (ESR) (Westergren method) [26], C-reactive protein (CRP), complement levels C3 and C4 (COBAS, Roche Diagnostics, Germany), anti-dsDNA (IFA, Crithidia luciliae, Bio-Rad), and antinuclear antibody (ANA), (IFA, HEp-2 cells, Bio-Rad).

CD40 SNP (rs1883832C/T) genotyping

DNA extraction: DNA was extracted from the whole blood using the spin column technique according to the manufacturer's instructions (Qiagen, Hilden, Germany). The extracted DNA amount was measured by Nanodrop spectrophotometer (Thermo Scientific™ Nanodrop™ 2000/2000c UV-Vis).

Amplification CD40 gene

A DNA fragment of 503 bp from the CD40 gene was amplified using the following:

I) Primers: F: 5′-CCC CGA TAG GTG GAC CGC GAT TG-3′ R: 5′-CCC GCC CTC TGA ACC CCC TAC CA-3′ [27].
II) A pre-mixed PCR Master Mix solution (× 2 One PCR™ Plus, Taf Quality Management, Taiwan) that contained: *Taq* DNA polymerase (50 units/mL), a reaction buffer (pH 8.5), dATP, dGTP, dCTP, dTTP (400 μM each), and $MgCl_2$ (3 mM) was used.

DNA Amplification: this was carried out using genomic DNA (2 μg/μl), HotStar *Taq* Master Mix (25 μl), sterile deionized water (19 μl), and primer (2 μl of each) with a final volume of 50 μl. Amplification was carried out using Thermal cycler (Mastercycle personal, Eppendorf, Germany) using the following PCR conditions: initial denaturation for 2 min at 94 °C. Followed by thirty-five cycles of denaturation for 1 min at 94 °C, annealing for 1 min at 60 °C, an extension for 1 min at 72 °C and a final extension for 7 min at 72 °C, followed by cooling to 4 °C.

Visualization: the PCR product was visualized by gel electrophoresis (MSCHOICE10, multiSUB®Choice horizontal gel system) using 1.5% ethidium bromide–stained agarose gel. Electrophoresis was performed for 30 min at volt 180 using TBE buffer (45 mM Tris-borate, 1 mM EDTA).

CD40 rs1883832 genotyping: This was carried out by restriction fragment length polymorphism (RFLP). The PCR product (503 bp) was digested using *NcoI* restriction enzyme (Thermo Scientific restriction enzymes, USA) by adding PCR product (10 μl(, sterile deionized water (18 μl), × 10 restriction enzyme Buffer (1 μl), and restriction enzyme (*NcoI*) (1 μl). The tubes were incubated for 8 h at 37 °C. The presence of the T allele was diagnosed by the digestion of the PCR product into two fragments, 130 bp and 373 bp. While the C allele was diagnosed by the presence of one undigested band (503 bp) (Fig. 1). The digested PCR products were resolved by electrophoresis in 2% ethidium bromide–stained agarose gels and visualized using Vilber Lourmat Gel Quantification and Documentation System (QUANTUM-ST4, Vilber Lourmat BP 66, Torcy, France).

Assessment of soluble CD40

Soluble CD40 level was determined in serum samples by ELISA following the manufacturer's instructions (Abcam, UK) with a sensitivity of 4.9 pg/mL. A standard curve was created by plotting the mean OD value for each standard on the y-axis against the concentration on the x-axis and the best-fit curve through the points on the graph was drawn. Graphing software was used to draw the best smooth curve through these points to construct the standard curve.

Statistical analysis

Data were analyzed using SPSS program version16 software (SPSS Inc., Chicago, IL, USA). Data were presented as mean, standard deviation, or numbers and percentages as appropriate. Analytical statistics included Student's *t* test that was used to indicate the presence of any significant difference between two groups of quantitative variables, chi-square test and Fisher's exact test to compare between two groups or more regarding one qualitative variable. The odds ratio was used to assess the CD40 gene polymorphism (rs1883832C/T) as a risk factor for SLE. ANOVA test was used to compare means between the groups and Pearson's correlation analysis was used to show strength and direction of the association between two quantitative variables and Spearman correlation analysis was used to show strength and direction of association of non-parametric variables. Statistical significance was considered at P value < 0.05 and high statistical significance at P value < 0.01.

Results

Study population characteristics

The mean age of SLE patients was 32.9 ± 7.9 and 94% of them were females. The mean TLC was ($7.5 \pm 2.2 \times 10^3$/μL); hemoglobin (11.9 ± 1.2 g/dL); platelets (272 ± 7610^3/μL); C3 (97.5 ± 32.3 mg/dL); C4 (22.5 ± 14.9 mg/dL); and CRP (7.8 ± 6.5 mg/dL). High ESR was observed in 12 (24%) patients, positive ANA in 94 (94%), and positive dsDNA in 76 (76%). The mean SLEDAI was 4.2 ± 0.7.

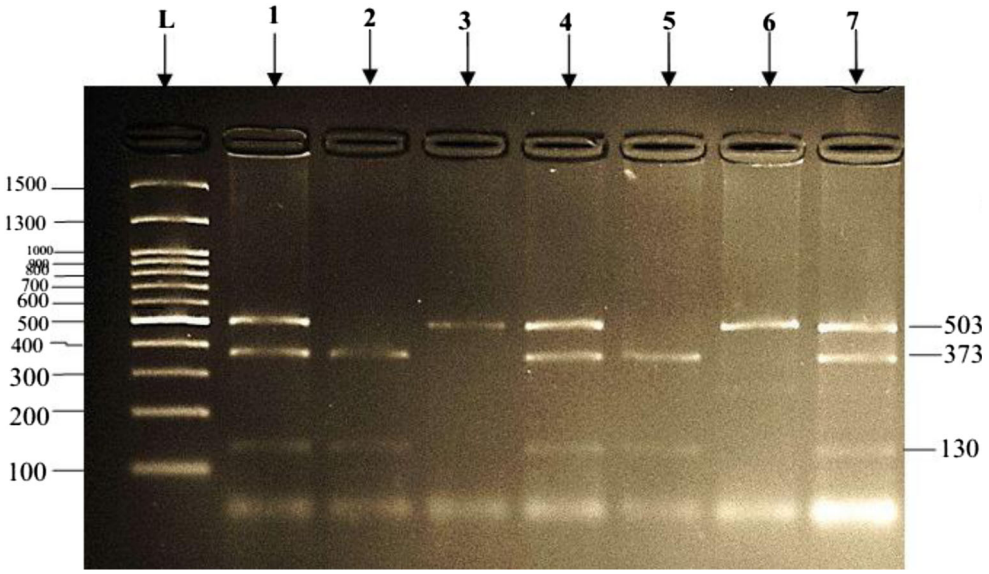


Fig. 1 Electrophoretic pattern of different CD40 gene polymorphism (rs1883832C/T) genotypes. A Photograph of a 2% (*w*/*v*) agarose gel showing the digested PCR products for CD40 gene polymorphism (rs1883832C/T) genotyping. Lane L, DNA ladder; lane 1, 4, and 7, heterozygous CT genotype (three bands 503,373,130 bp); lane 2 and 5, homozygous TT genotype (two bands 373,130 bp); lane 3 and 6, homozygous CC genotype (one band 503 bp)

CD40 genotypes and SLE

We compared CD40 (rs1883832C/T) genotypes and allele frequencies in SLE patients versus healthy control (Table 1). CC homozygous genotypes, as well as the C allele, were used as the reference genotype and allele respectively. CD40 rs1883832C/T genotypes (CC, TT, and CT) as well as CD40 alleles (C and T) did not differ between SLE patients and normal control ($p = 0.63$, 0.37, and 0.31 respectively). Comparing CC genotype with other genotypes (TT homozygous and CT heterozygous genotypes) revealed that the carriers of genotype CT has one and half times more chance to get SLE than CC homozygous (OR 1.44), the carriers of genotype TT has ~2 times more chance to get SLE than CC carries (OR 1.96). Accordingly, the carriers of the T allele have ¬ 1.5 time more chances to get SLE compared to the carriers of the C allele (OR: 1.4). However, all of them did not reach statistical significance.

CD40 genotypes and SLE characteristics

The CD40 (rs1883832C/T) genotype and alleles frequencies were tested in relation to clinical and laboratory features of SLE patients (Table 2). The three genotypes (CC, TT, and CT), as well as the two alleles (C and T), were not associated with any of the tested variables (i.e., age, SLEDAI, C3, C4, CRP, ANA, anti-dsDNA). Interestingly, all men included in the study ($n = 6$) had TT genotype ($p = 0.06$) and T allele (0.02).

Soluble CD40 and SLE

The serum sCD40 level was significantly higher in SLE patients compared to healthy control (3.4 vs. 0.8 ng/mL, $p < 0.001$) (Fig. 2).

Table 1 CD40 SNP (rs1883832C/T) genotypes and allele frequencies in SLE patients versus healthy control

CD40 SNP (rs1883832C/T)	SLE ($n = 100$)	Control ($n = 50$)	P#	OR (95%CI)
Genotypes				
CC (reference)	10 (10%)	8 (16%)		
CT	36 (36%)	20 (40%)	0.63[a]	1.440 (0.313–6.618)
TT	54 (54%)	22 (44%)	0.37[b]	1.964 (0.443–8.713)
CT + TT	90 (90%)	42 (84%)	0.45[c]	1.714 (0.417–7.044)
Alleles				
C (reference)	56 (28%)	36 (36%)	0.31	1.446 (0.701–2.983)
T	144 (72%)	64 (64%)		

Data are presented as numbers (%); SLE, systemic lupus erythematosus; OR, odds ratio; CI, confidence interval. Statistical significance at $p \leq 0.05$; # χ^2 test, [a] (CC vs. CT), [b] (CC vs. TT), [c] (CC vs. CT + TT)

Soluble CD40 and CD40 genotypes

Using CC as the reference genotype, serum sCD40 level was significantly higher in the carriers of the homozygous genotype TT (3.8 ± 1.3 vs. 2.9 ± 1.9, $p = 0.0001$) and T allele (3.6 ± 1.4 vs. 3.0 ± 1.5, $p = 0.003$) (Table 3).

Correlation of sCD40 and SLE characteristics

We tested the correlations between serum CD40 levels and some clinical and laboratory variables. No correlation was found between sCD40 and age ($r = 0.029$, $p = 0.7$), gender ($r = -0.043$, $p = 0.6$), duration of disease ($r = -0.046$, $p = 0.6$), SLEDAI ($r = -0.016$, $p = 0.8$), C3 ($r = -0.019$, $p = 0.8$), C4 ($r = 0.062$, $p = 0.5$), CRP ($r = 0.096$, $p = 0.3$), ESR ($r = 0.079$, $p = 0.4$), ANA ($r = -0.190$, $p = 0.1$), or anti-dsDNA($r = 0.130$, $p = 0.3$).

Diagnostic performance of serum sCD40 in SLE

The accuracy of serum sCD40 to discriminate SLE cases from the normal population was evaluated using Receiver Operating Characteristic (ROC) curve analysis. According to our data, sCD40 could discriminate SLE patients at a cutoff value of 0.885 ng/mL with 98% sensitivity and 96% specificity (AUC = 0.999, $p < 0.001$) (Fig. 3).

Discussion

The etiology and pathogenesis of SLE is still largely unknown, however, a complex interaction of genetic, environmental, hormonal, and immunological factors are accountable for the local or systemic tissue damage in SLE patients [28, 29]. Multiple genetic variants, together with environmental and hormonal factors, contribute to disease risk. In recent years, an increasing evidence showed that CD40 contributes to the pathogenesis of chronic inflammatory and autoimmune diseases due to its biological activity. In SLE, CD40 has either been indirectly or directly shown to be a contributing factor to the disease.

As previously reported, SNPs in non-coding regions may affect mRNA structure, alter the level of expression of a gene, and increase disease susceptibility [30]. The rs1883832 locus, previously demonstrated to be associated with CD40 expression, is located at the − 1 position within the Kozak sequence [31, 32]. CD40, rs1883832 polymorphism, can produce high expression of CD40 by upregulating the transcription or translation efficiency of the CD40 gene. This abnormal expression of CD40 would lead to an increase in the production of many pro-inflammatory cytokines and increase the risk of SLE [33, 34]. However, relatively few researchers had investigated the association between rs1883832C/T polymorphisms in the

Table 2 CD40 SNP (rs1883832C/T) genotypes/alleles frequencies and SLE characteristics

Variables	CD40 (rs1883832C/T) genotypes				CD40 (rs1883832C/T) alleles		
	CC $N=10$	CT $N=36$	TT $N=54$	p	C allele ($n=56$)	T allele ($n=144$)	p
Age (years)[@]	32.5 ± 5.9	34.8 ± 7.1	33.7 ± 8.8	0.52	33.2 ± 7.1	32.7 ± 8.2	0.68
Gender N (%)							0.02
Male	0	0	6 (11.1%)	0.06	0	12 (8.3%)	
Female	10 (100%)	36 (100%)	48 (88.9%)		56 (100%)	132 (91.7%)	
SLEDAI							
No	6 (60%)	22(61.1%)	32 (59.2%) 16	0.293	34 (60.7%)	86 (59.7%)	0.32
Mild/moderate	4 (40%)	(33.3%)	12 (29.7%)		20 (35.7%)	44 (30.6%)	
Severe	0	2 (5.6%)	6 (11.1%)		2 (3.6%)	14 (9.7%)	
C3 (mg/dL)[@]	103.2 ± 15.6	95.1 ± 30.9	98.1 ± 36.3	0.865	90.8 ± 26.3	97.2 ± 34.5	0.21
C4 (mg/dL)[@]	26.4 ± 12.4	20.2 ± 11.5	23.3 ± 17.5	0.667	22.4 ± 11.7	22.5 ± 16.1	0.96
CRP (mg/dL)	3.4 ± 2.8	8.5 ± 6.4	8.2 ± 7.1	0.289	6.6 ± 5.0	8.2 ± 6.8	0.11
ANA (IF)							0.67
Negative	0	4 (11.1%)	2 (3.7%)	0.495	4 (7.1%)	8 (5.6%)	
Positive	10 (100%)	32 (88.9%)	52 (96.3%)		52 (92.9%)	136 (94.4%)	
Anti-ds-DNA (IF)							
Negative	2 (20%)	10 (27.8%)	12 (22.2%)	0.891	14 (25%)	34 (23.6%)	0.83
Positive	8 (80%)	26 (72.2%)	42 (77.8%)		42 (75%)	110 (76.4%)	

SLE, systemic lupus erythematosus; CRP, C-reactive protein; C3, complement protein 3; C4, complement protein 4; ANA, antinuclear antibody; Anti dsDNA, anti-double-stranded DNA; IF, immunofluorescence assay; SLEDAI, SLE disease activity index. [@] Data are presented as mean ± SD

CD40 gene in conjunction with serum CD40 in SLE patients. Moreover, the results of these studies have been inconsistent. Little if any information is available about the association between CD40 polymorphisms and its soluble level in Egyptian SLE patients. In this study, we searched the rs1883832 C/T polymorphism of CD40 as well as soluble CD40 as potential genetic markers for SLE in a cohort of Egyptian patients.

We found that the rs1883832 C/T polymorphism of CD40 was not associated with the presence of SLE in our patients. Meaning that CD40 rs1883832C/T genotypes (CC, TT, and CT), as well as CD40 alleles (C and T), did not differ between SLE patients and normal control. Interestingly, the risk of SLE increased in the carriers of CT and TT genotypes in comparison to the carriers of the homozygous wild-type genotype (CC). Though did not reach a statistical level, this finding would support that T allele may contribute to SLE development. In accordance, previous studies showed that the rs1883832 T allele was associated with a significantly increased risk of SLE compared with the rs1883832 C allele [35, 36]. Moreover, Zhang et al. (2013) reported that TT genotype carriers showed higher CD40 expression and serum soluble CD40 concentration in male patients with cerebral infarction [37].

Several studies have investigated associations between genetic variation in the CD40 gene and SLE but results of these studies have been inconsistent. In accordance with our findings, Joo et al (2013) had examined the association of CD40

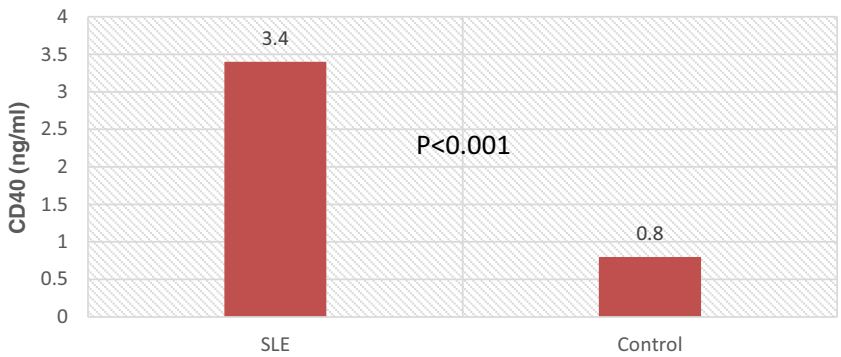


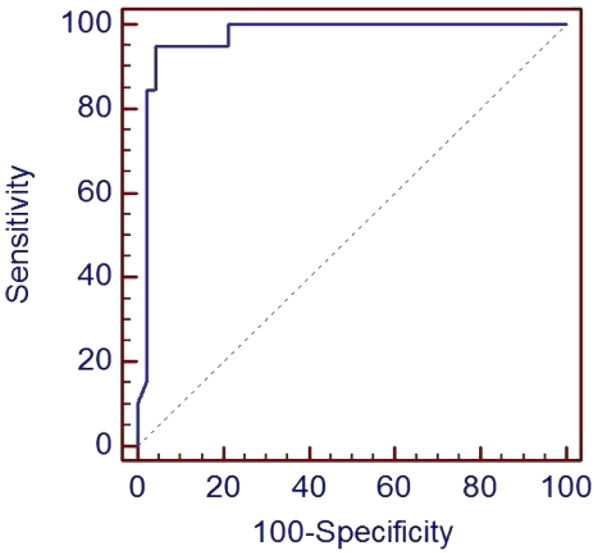
Fig. 2 Soluble CD40 in SLE patients versus control

Table 3 Soluble CD40 level in relation to CD40 SNP (rs1883832C/T) genotypes

CD40 rs1883832C/T	Soluble CD40 (ng/mL)			
	SLE ($n = 100$)		Control ($n = 50$)	
	Mean ± SD	*P*	Mean ± SD	*P*
Genotypes				
CC	2.9 ± 1.9	–	0.8 ± 0.2	–
CT	3.0 ± 1.4	0.672*	0.8 ± 0.4	1.0*
TT	3.8 ± 1.3	0.0001**	0.8 ± 0.2	1.0**
Alleles				
C	3.0 ± 1.5	–	0.8 ± 0.3	–
T	3.6 ± 1.4	0.003	0.8 ± 0.3	1.0

SLE, systemic lupus erythematosus. *CC vs. CT, **CC vs. TT
Statistical significance at $p \leq 0.05$

polymorphisms with the risk of SLE in Korean SLE patients and reported that SNP rs1883832 was associated with the risk of SLE in the dominant model, but its statistical significance disappeared after correction for multiple testing. They concluded that rs1883832 was not a risk factor for SLE development in their Korean population [38]. However, other studies had reported the presence of significant differences in the genotype and allele frequencies of the CD40 gene rs1883832 C/T polymorphism between the SLE and control groups among the Chinese population [35–37].



Curve characteristics	Values
The area under the curve	0.999
Standard error	0.001
95% confidence interval	0.997-1.002
p-value	<0.001
Predictive characteristics	
Best cut off value	885.05 pg/ml
Sensitivity	98%
Specificity	96%

Fig. 3 Serum CD 40 as a potential predictor of SLE (ROC curve analysis)

Previous studies have tested other polymorphisms of the CD40 gene and their results were erratic. Vazgiourakis and co-workers (2011) have identified CD40 as a new susceptibility locus in Greek and Turkish patients with SLE where rs4810485 minor allele T was underrepresented in SLE and correlated with reduced CD40 expression in peripheral blood monocytes and B cells, with potential implications for the regulation of aberrant immune responses in the disease [24]. Meanwhile, Piotrowski et al., (2013) reported the absence of a between CD40 gene rs4810485 G/T polymorphisms with the risk of SLE in Polish patients [39].The reason for the discrepancies between the different studies in the relation between CD40 and SLE remains unclear, but several possibilities should be considered. First, it may be due to the genetic differences; CD40 gene polymorphisms were distinct in a specific population, various ethnicities, and geographic region. Additionally, the nature of SLE as a multifactorial disease and individual exposure to various environmental factors and genetic susceptibility cannot be excluded. In addition, the inadequate study design such as non-random sampling and a limited sample size should also be considered. Finally, the presence of genes in linkage disequilibrium with the CD40 gene or the effect of CD40 on another peptide cannot be excluded [35]. Unlike CD40 polymorphism, sCD40 was significantly higher in SLE patients compared to normal controls. Accordingly, Chen et al. (2015) and Wu et al. (2016) showed that the plasma sCD40 levels were significantly higher in SLE patients compared to controls. The absence of an association between sCD40 levels and the polymorphisms of the CD40 gene in healthy controls could be related to the fact that sCD40 expression is inducible and that its expression is upregulated after inflammatory stimulation that should be absent in healthy control [35, 36].

According to our data, serum sCD40 level was significantly higher in the carriers of the homozygous genotype TT and T allele. However, there were no significant differences in the serum sCD40 levels between CC and CT genotypes. This finding directly suggests an association between CD40 genotypes and its soluble form and indirectly suggests CD40 as an interesting candidate gene for the etiology and pathogenesis of SLE. However, it should be noted that some factors other than this SNP could be involved in the observed higher sCD40 level in SLE patients, because 6 ng/mL of difference in the mean sCD40 level between C and T allele carriers in SLE patients was smaller than 2.2 ng/mL of difference between C allele carriers in SLE patients and C allele carriers in control subjects.

According to our data, sCD40 could discriminate SLE at a cutoff value of 0.885 ng/mL. Consequently, other clinical studies demonstrated that rs1883832 C/T polymorphism of CD40 and the levels of sCD40 may predict the risk of SLE [35, 36]. However, no correlations were found between sCD40 and the tested clinical and laboratory parameters in our SLE patients which could be related the inadequate study design the limited sample size of our study as well as the probable selection bias that might have been present in the hospital-based studies. Future studies on a larger population would give more conclusive results.

Due to the critical role of CD40–CD40L in B-cell activation, CD40 was previously suggested as a therapeutic target in SLE. Furthermore, an anti-CD40L antibody in clinical trials in patients with SLE have shown promising results and that the drug has immunomodulatory actions [40, 41]. Finally, the study needs to be expanded over a larger population to confirm the specificity and sensitivity of using rs1883832 C/T polymorphism of CD40 as a risk factor of SLE

Conclusion

The study did not prove CD40 gene (rs1883832 C/T) polymorphism as a clear risk factor of SLE in this cohort of Egyptian patients, though it was highly likely associated with the carriers of T allele. In the same context, significant high sCD40 levels were observed in the T allele carriers.

Compliance with ethical standards

The study was approved by the IRB of the Faculty of Medicine, Suez Canal University and all patients were consented before being included in the study

Disclosures None.

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