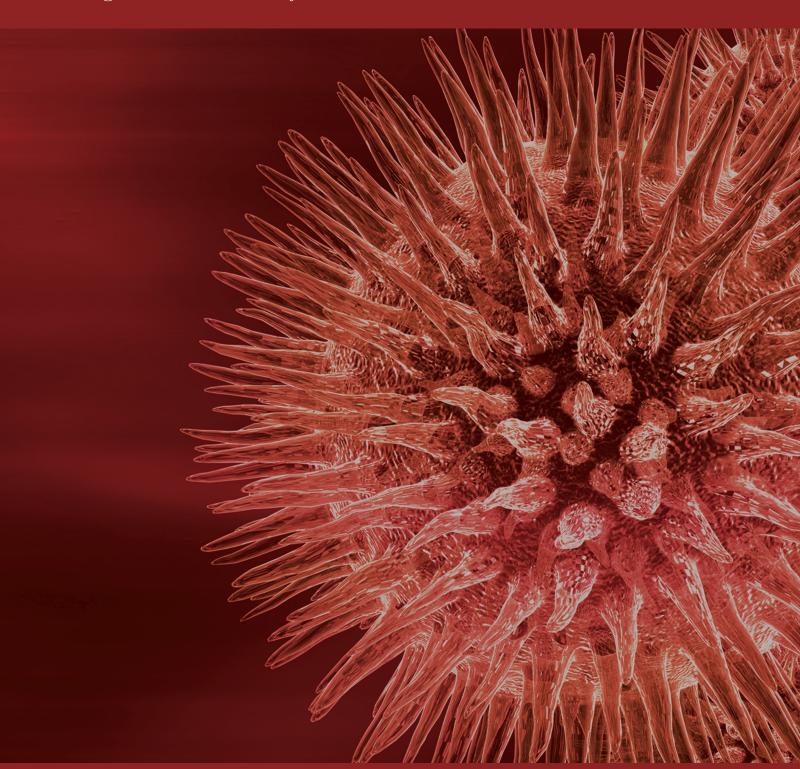
Autoimmune Rheumatic Diseases

Guest Editors: Juan-Manuel Anaya, Yehuda Shoenfeld, Frank Buttgereit, and Miguel A. González-Gay



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Editorial

Autoimmune Rheumatic Diseases

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The term autoimmune rheumatic diseases (ARDs) encompasses a heterogeneous group of conditions characterized by joint involvement along with a wide spectrum of systemic manifestations. The most common ARDs are rheumatoid arthritis (RA) and systemic lupus erythematosus (SLE). Nevertheless, all these conditions share similar pathophysiological mechanisms [1, 2] and a common risk of developing a process of accelerated atherosclerosis [3]. In this regard, in this special issue J. Amaya-Amaya and colleagues discussed the mechanisms associated with the increased risk of cardiovascular disease (CVD) in patients with autoimmune diseases. These authors emphasize the relevance of the CVD in rheumatic conditions and its connection with inflammation and autoimmunity. They also highlight the need of a more aggressive management of these conditions, both of disease activity and classic cardiovascular risk factors. A good example of accelerated atherosclerosis in the setting of an ARD is SLE, in which endothelial dysfunction, an early step in the atherogenesis process, is observed before cardiovascular events can occur. With respect to this, A. Mak and N. Y. Kow performed a comprehensive review of the mechanisms that are involved in endothelial damage. These authors focused on the factors involved in endothelial damage and repair and, therefore, in the development of CVD in patients with SLE. They discussed the relevant role of factors such as type 1 interferon, proinflammatory cytokines, inflammatory cells, immune complexes, costimulatory molecules, neutrophils

extracellular traps, lupus-related autoantibodies, oxidative stress, and dyslipidemia that along with the aberrant function of the endothelial progenitor cells lead to endothelial dysfunction and increased susceptibility to develop CVD in patients with SLE. Based on these lines of evidence, the authors' claim is in favor of early intervention at the preclinical stage of atherogenesis in these patients.

Interestingly, damage and activation of vascular endothelial cells are implicated in the pathogenesis of SLE [4]. Angiogenic factors play a significant role in vascular permeability, vascular growth, and inflammatory response observed in SLE. L. Zou and colleagues assessed the serum levels of 3 angiogenic factors in SLE and their clinical significance. These authors disclosed that the levels of PIGF, bFGF, and VEGF are higher in SLE patients with active disease than in those with inactive SLE. Their findings may have a potential interest in the management and development of future therapies for autoimmune diseases.

Besides cardiovascular complications, renal disease and the risk of infection overshadow the outcome of patients with SLE [5, 6]. In this regard, as reported in this special issue by E. Cairoli and colleagues, end-stage renal disease (ESRD) is an important cause of morbidity and mortality in patients with SLE. These authors analyzed the outcome and prognostic factors of renal transplantation in patients with ESRD due to SLE. They assessed 50 renal transplantations that were performed in 40 SLE patients. The most frequent

underlying lupus nephropathy that led to ESRD was type IV (72.2%). Graft failure occurred in 30% transplantations and the most common cause of graft failure was chronic allograft nephropathy. The patient survival rate was high. Recurrence of lupus nephritis in renal allograft was only observed in 1 patient. In this study the presence of anti-HCV antibodies and the type of donor source were related to the development of graft failure. According to these results, renal transplantation appears to be a good alternative for renal replacement therapy in patients with SLE.

Since some studies indicate an increased incidence of tuberculosis in patients with SLE [7], a diagnosis of latent tuberculosis infection is of major importance in these patients. M. D. M. Arenas Miras and colleagues report in this special issue a study to compare the tuberculin skin test and the newer T.SPOT.TB test to diagnose latent tuberculosis infection in SLE. Unlike T.SPOT.TB results, the tuberculin skin test results were negatively affected by corticosteroid and immunosuppressive therapy. Because of that, the authors support the use of the T.SPOT.TB test in SLE patients receiving corticosteroids or immunosuppressive drugs.

Patients with RA also have a higher risk for atherosclerosis [8, 9]. E. Gómez-Bañuelos and colleagues from Mexico evaluated the association between membrane expression of CD36 in peripheral blood mononuclear cells (PBMC) and carotid intima-media thickness (cIMT) in patients with RA in order to evaluate the association of membrane expression of CD36 with subclinical atherosclerosis. Other molecules related to cardiovascular risk such as ox-LDL, IL-6, and TNF α were also tested. A low membrane expression of CD36 in PBMC from patients with RA presenting with subclinical atherosclerosis and increased serum proinflammatory cytokines was observed.

Proteoglycan-induced arthritis (PGIA) is a widely used model based on the cross-reactivity of injected foreign (usually human) PG and mice self-PG. L. L. W. Ishikawa and colleagues evaluated the arthritogenicity of bovine proteoglycan (PG) and found that it can be used as an alternative antigenic source to PG-induced arthritis for the study of many RA aspects, including the immunopathogenesis of the disease and also the development of new therapies.

Anticitrullinated peptide antibodies (ACPA) are detected in the sera of patients with RA and have a profound role in the diagnosis of the disease [10]. M. L. Díaz-Toscano and colleagues evaluated the performance of using two assays for ACPA: second-generation anticitrullinated cyclic peptides antibodies (anti-CCP2) and antimutated citrullinated vimentin (anti-MCV) antibodies for the diagnosis of RA. Their study suggest that adding the assay of anti-MCV antibodies to the determination of anti-CCP2 increases the sensitivity for detecting seropositive RA, and authors propose the use of both assays in the initial screening of RA in longitudinal studies, including early onset of undifferentiated arthritis.

Since clinical response of biologic agents in RA can be influenced by their pharmacokinetics and immunogenicity, D. Mazilu and colleagues evaluated the concordance between serum drug and antidrug levels as well as the clinical response in RA patients treated with biological agents who experience

their first disease exacerbation while being on a stable biologic treatment. Detectable biologic drug levels correlated with a better clinical response in patients experiencing their first RA inadequate response while being on a stable biologic treatment with rituximab, infliximab, and etanercept (ETN).

Interleukin-6 (IL-6), a cytokine that can facilitate autoimmune phenomena, amplify acute inflammation, and promote the evolution into a chronic inflammatory state, has a pivotal role in synovitis, bone erosions, and the systemic features of RA [11]. A comprehensive review on IL-6 and the rationale for blocking this cytokine in RA are also presented in this special issue.

Pharmacogenomics, the study of how genes affect a person's response to drugs, will allow the development of tailored drugs to treat a wide range of health problems, including RA and many others. A. Lima and colleagues report in this special issue the role of methylenetetrahydrofolate reductase (MTHFR) C677T, aminoimidazole carboxamide adenosine ribonucleotide transformylase (ATIC) T675C polymorphisms, and clinicopathological variables in clinical response to methotrexate (MTX) in Portuguese patients with RA. MTHFR 677TT and ATIC 675T carriers were associated with over 4-fold increased risk for nonresponse to MTX. Authors suggest the use of these genotypes combined with clinicopathological data to assist clinicians in personalizing RA treatment.

We hope that readers will enjoy this issue and find accurate data and updated reviews on the most common ARDs.

Juan-Manuel Anaya Yehuda Shoenfeld Frank Buttgereit Miguel A. Gonzalez-Gay

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Review Article

Cardiovascular Involvement in Autoimmune Diseases

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Autoimmune diseases (AD) represent a broad spectrum of chronic conditions that may afflict specific target organs or multiple systems with a significant burden on quality of life. These conditions have common mechanisms including genetic and epigenetics factors, gender disparity, environmental triggers, pathophysiological abnormalities, and certain subphenotypes. Atherosclerosis (AT) was once considered to be a degenerative disease that was an inevitable consequence of aging. However, research in the last three decades has shown that AT is not degenerative or inevitable. It is an autoimmune-inflammatory disease associated with infectious and inflammatory factors characterized by lipoprotein metabolism alteration that leads to immune system activation with the consequent proliferation of smooth muscle cells, narrowing arteries, and atheroma formation. Both humoral and cellular immune mechanisms have been proposed to participate in the onset and progression of AT. Several risk factors, known as classic risk factors, have been described. Interestingly, the excessive cardiovascular events observed in patients with ADs are not fully explained by these factors. Several novel risk factors contribute to the development of premature vascular damage. In this review, we discuss our current understanding of how traditional and nontraditional risk factors contribute to pathogenesis of CVD in AD.

1. Introduction

Autoimmune diseases (ADs) represent a broad spectrum of chronic conditions that may afflict specific target organs or multiple systems with a significant burden on quality of life. These conditions have common mechanisms including genetic and epigenetic factors, gender disparity, environmental triggers, pathophysiological abnormalities, and certain subphenotypes which are represented by the autoimmune tautology [1-3]. Atherosclerosis (AT) was once considered to be a degenerative disease that was an inevitable consequence of aging. However, research in the last three decades has shown that AT is not degenerative or inevitable. It is an autoimmune-inflammatory disease associated with infectious and inflammatory factors characterized by lipoprotein metabolism alteration that leads to immune system activation with the consequent proliferation of smooth muscle cells, narrowing arteries, and atheroma formation [4]. Both humoral and cellular immune mechanisms have been

proposed to participate in the onset and progression of atheromatous lesions [5].

In recent years, many reports have focused on the immunological background of AT, and there is no longer any doubt that it shares several autoimmune pathways [6, 7]. Therefore, it is not surprising to find an accelerated AT in quite a lot of ADs. Several risk factors, known as classic risk factors, have been described since the Framingham heart study. Over time, these lead to endothelial dysfunction, subclinical AT, and cardiovascular (CV) events [8-12]. Interestingly, the excessive CV events observed in patients with ADs are not fully explained by these factors. Several novel risk factors contribute to the development of premature vascular damage. Sarmiento-Monroy et al. [13], based on a model of rheumatoid arthritis (RA), proposed a classification for nontraditional risk factors in ADs, which divided them into genetic determinants, AD-related, and miscellaneous [14, 15]. Therefore, a complex interaction between traditional and disease-specific traits leads to a premature AT process in

autoimmunity. All of these pathways may possibly converge into a shared proatherogenic phenotype [16]. While ADs are characterized by a high degree of cardiovascular disease (CVD), there are several subphenotypes such as arterial hypertension (HTN); coronary artery disease (CAD): angina, ischemic heart disease (IHD), and myocardial infarction (MI); congestive heart failure (CHF); peripheral vascular disease (PVD); left ventricular diastolic dysfunction (LVDD); cerebrovascular disease (cerebrovascular accidents (CVAs); transient ischemic attacks (TIAs)); thrombosis: deep vein thrombosis (DVT), pulmonary embolism (PE); and subclinical AT.

In this paper, we discuss our current understanding of how traditional and nontraditional risk factors contribute to pathogenesis of CVD in ADs. It has become evident over the last few years that some ADs are characterized by common pathogenic mechanisms and high rates of morbidity and mortality that are mainly CVD-related. The increased CV mortality in the 3 rheumatic disorders studied the most (i.e., RA, systemic lupus erythematosus (SLE), and antiphospholipid syndrome (APS)) appears to be caused by vascular damage secondary to accelerated AT. However, the burden of CV involvement in other ADs (Sjögren's syndrome (SS) and systemic sclerosis (SSc)) appears to be lower and it is characterized by specific risk factors in addition to those shared with the general population.

2. Methods

2

Studies were identified via a MEDLINE search using the following medical subject heading (MeSH) terms: "Arthritis, Rheumatoid" OR "Lupus Erythematosus, Systemic" OR "Antiphospholipid Syndrome" OR "Sjögren's Syndrome" OR "Scleroderma, Systemic" AND "Cardiovascular Diseases." Each group was cross-referenced with the following MeSH terms/keywords: "risk factors," "traditional risk factors," "classic risk factors," "nontraditional risk factors," and "novel risk factors." Each term was counted for the greatest number of results. Limits regarding language (i.e., English), age (i.e., adults), and humans were taken into account. Assessment for inclusion of studies was done independently by two blinded reviewers (JAA-LMS). Disagreements between them were resolved by consensus using predefined eligibility criteria, from inception up to February 2014.

2.1. Study Selection, Data Extraction, and Quality Assessment. Abstracts and full-text articles were reviewed in search of eligible studies. A study was included if (a) the abstract was available, (b) it contained original data, (c) it used accepted classification criteria for each AD, (d) it measured CV risk factors, and (e) it examined clinical endpoints. Articles were excluded from the analysis if they dealt with juvenile pathologies or were done on animal models. Studies were also excluded if they were reviews or case reports, if they discussed topics not related to CVD in AD, if they did not meet the inclusion criteria, if they had insufficient data, or if they had results that showed lack of statistical significance. Likewise, the two blinded reviewers (JAA, LMS) looked for duplicates,

excluded them, and organized selected articles. Only novel and classic risk factors [14, 15] with statistical significance were included.

3. Results

There were 6,324 articles identified in PubMed. Of these, 5,800 were identified as duplicates, lacking data or significant statistical associations. A total of 524 full-text articles were assessed for eligibility. Only 322 articles were included for methodological analysis. Finally, 168 articles that had interpretable data and fulfilled the eligibility criteria were included. Several traditional cardiovascular risk factors such as dyslipidemia, hyperhomocysteinemia, smoking, and T2DM had been reported. Many studies were associated with nontraditional risk factors such as genetic markers, autoantibodies, duration of the diseases, markers of chronic inflammation, polyautoimmunity, and familial autoimmunity. These factors and their associations are depicted in Tables 1, 2, 3, 4, and 5 and in Figures 1 and 2.

- 3.1. Rheumatoid Arthritis. A broad spectrum of subphenotypes and mortality due to CVD, including stroke, HTN, IHD, intima-media thickness (IMT), CAD, MI, PVD, thrombosis, and LVDD were described in RA, and the general prevalence range is 30%–50% [17–26]. Table 1 shows the main traditional and nontraditional risk factors associated with CVD in RA, and Figure 1 exemplifies these associations.
- 3.2. Systemic Lupus Erythematosus. CVD is at least doubled among SLE patients compared to other populations and mortality is also increased [27]. CVD burden in SLE includes carotid plaques, MI, angina, CHF, stroke, IMT, PVD, pericarditis, and others discussed below [16, 28–35]. Table 2 shows traditional and nontraditional risk factors associated with CVD in SLE.
- 3.3. Antiphospholipid Syndrome. The prevalence of CVD ranges from 1.7 to 6%, and it could increase up to 14% in patients with antiphospholipid antibodies (APLA). On the other hand, the prevalence of CVD in asymptomatic AT reaches 15% compared to 9% in SLE patients and 3% in normal controls [36, 37]. In the Euro-Phospholipid cohort, MI was the presenting manifestation in 2.8% of the patients, and it appeared during the evolution of the disease in 5.5% of the cohort [38]. Cardiac manifestations may be found in up to 40%, but significant morbidity appears in only 4–6% of these patients. Most of these manifestations are explicable on the basis of thrombotic lesions either in the coronary circulation or on the valves [39]. Table 3 shows the main traditional and nontraditional risk factors associated with CVD in APS.
- 3.4. Sjögren's Syndrome. CV events occurred in 5–7.7% with stroke, MI, CVA, DVT, and arrhythmias [40–44] being the most frequent. Furthermore, tricuspid regurgitation, injured mitral and aortic valves, pulmonary hypertension, and increased left ventricular mass have also been reported

TABLE 1: Traditional and nontraditional risk factors associated with CVD and RA.

Risk factor	Comments	References
	Traditional risk fact	ors
 (i) Insulin resistance due to release of inflammatory cytokines such as TNF-α. Obesity (ii) Increased coronary calcification due to insulin resistance. (iii) ↑ Abdominal fat. 		
Dyslipidemi	(i) ↓ HDL and ↑ LDL and TAG.(ii) Induces higher risk of IHD.	[14, 19, 97, 233–238]
Advanced ag	(i) Old age prompts structural and functivessels structure.(ii) Senescent immune system is normally functional changes.	[233, 230]
Family history of	CVD Heritable factors: HTN and familial hype	rcholesterolemia. [97, 240, 241]
T2DM	(i) Coexistence of T2DM and RA increaseCVD.(ii) Abdominal obesity, antihypertensive	[14, 242, 243]
	GCs affect glucose metabolism in RA pat (i) It is considered as biomarker for AT at CVA.	ients. nd a risk factor related to CAD and
Hyperhomocystei	agent of cardiovascular damage of only as (iii) A high prevalence of this biomarker gender and higher radiological damage.	n epiphenomenon of inflammation. nad a statistical association with male
Metabolic syndi	(i) Alteration in the production of cytokin leads to an increasing activity of RA and a (ii) It was related to pain and functional s (iii) Increased prevalence of waist circum glucose (i.e., worse prognosis). (iv) Increased epicardial adipose tissue vo	an accelerating AT. tatus, suggesting disease activity ference, blood pressure, and fasting [103, 236, 242, 247, 249–252]
Sedentary lifes	(i) Patients are less physically active than deformity, and impaired mobility. (ii) Impairment of altered lipid pattern.	controls due to pain, stiffness, [97, 252, 253]
Hypertensio	Increases the risk of IHD and CVA with i	mportant impact on mortality. [249, 254, 255]
Male gende	Cardiovascular disease is more frequent i	n male gender. [14, 254, 256–260]
Smoking	(i) Smokers with RA have worse prognosterms of RF titers, disability, radiological (ii) Premature CVD mortality.	s than nonsmokers RA patients in
	Nontraditional risk fa	ctors
HLA-D:	(i) Its alleles are related to chronic inflamendothelial dysfunction, increasing CV emortality. Some of them are independent (ii) Being a carrier of a single copy of HL with an increased risk of atherosclerotic parts.	vents, AT plaque, and premature of autoantibody status. [97, 145, 262–268] A-DRB1 SE was significantly associated
Genetic Non-HI	(i) Polymorphisms in <i>endothelin-1</i> , <i>MTH-PAI-1</i> , <i>TNFR-II</i> , <i>LT-A</i> , <i>LGALS2</i> , <i>TGF-β</i> , contributed to CVD risk and adverse out (ii) Interaction between smoking and pol associated with IHD and MI in RA patier (iii) The <i>IL6-174</i> gene polymorphism may subclinical atherosclerosis in patients wit (iv) <i>TNFA</i> rs1800629 (G>A) gene polymorpredisposition to CV complications in RA be restricted to individuals carrying the S (v) Genetically determined high serum le agalactosyl IgG are associated with increadeath.	GSTT1, ACP1, and NF- $\kappa\beta1$ genes may be come. The symorphism in the VEGFA gene is set to the set of the symorphism in the development of the play a role in the development of the RA. The preprince of the symorphism is associated with the patients. This predisposition seems to E. The symorphism is associated with the patients. This predisposition seems to E. The symorphism is associated with the patients. This predisposition seems to E.

Table 1: Continued.

]	Risk factor	Comments	References
	RA per se	(i) Independent factor for developing MI and accelerated AT.(ii) It represents a broad spectrum of conditions related with the autoimmune nature of the disease.	[14, 19, 287]
	Familial autoimmunity	(i) It confers additional susceptibility to CVD in RA patients, as well as presence of atherosclerotic plaque, radiographic progression, high disease activity, and persistent inflammation.(ii) Increased frequency of HLA-DR4.	[14, 97]
	Glucocorticoids	 (i) It targets inflammation but its adverse effects include carotid plaques, arterial stiffness, decreased insulin sensitivity, elevated lipid levels, hypertension, and CVD. (ii) Patients that are treated with a daily dose >7.5 mg/day appeared to have twice as the risk of heart disease as patients that are in nonsteroidal treatment. (iii) The increased mortality in patients under low-dose oral GC for more than 10 years has been related mainly to CVD. 	[14, 19, 111, 124, 240, 288–294]
	Long duration of disease	(i) Disease duration over 10 years was significantly associated with increased risk of atherosclerotic plaque in Colombian population. (ii) Patients with prolonged RA have more atherosclerosis than patients of the same age with more recent disease onset. They have more extensive subclinical atherosclerosis or CAC, independent of other CHD risk factors. (iii) RA duration is independently associated with LVDD suggesting the impact of chronic autoimmune inflammation on myocardial function.	[97, 102, 240, 290, 295–298]
RA- associated	Polyautoimmunity Autoantibodies	It was associated with CVD in Colombian population. (i) Immune complexes from RF can be deposited in the endothelium generating endothelial dysfunction and AT through inflammatory reactions. (ii) RF-positive patients were at increased risk of CV events following exposure to GC. (iii) RF titers were independently predictive of endothelial dysfunction and increased mortality in RA. (iv) Anti-CCP and RF-IgM were related to impaired endothelial function independent of other CV risk factors, and they are independently associated with impaired left ventricular relaxation and development of IHD. (v) Anti-ox-LDL, ACLA, APLA, and anti-ApoA-1 are associated with early atherosclerotic changes and future thrombotic events. (vi) The presence of ACLA and an altered lipid profile may represent an important risk factor for thrombotic events in patients affected by RA. Anti-PC, anti-HSP 60/65, and anti-MDA-LDL may have independent roles in subclinical AT. (vii) Anti-ox-LDL was strongly related with the degree of inflammation and carotid plaque and may predispose to a higher risk for CVD, as they were independently associated with subclinical atherosclerosis. (viii) High levels of anti-MCV and LDL-immune complexes are risk factors for increased AT and are associated with inflammation.	[9, 97, 238, 299– 314]
	Chronic proinflammatory state	 (i) It may accelerate atherogenic processes and microvascular dysfunction: accentuation of known pathways of plaque formation. (ii) Inflammatory stimuli may be involved in the initiation of CHF among patients with RA. (iii) Markers of chronic inflammation (i.e., current and cumulative inflammation) such as CRP, ESR, TNF-α, IL-6, IL-17, and haptoglobin are present in endothelial activation and increased in carotid IMT, carotid plaque, CAD, CV complications, and mortality. (iv) Both established CV risk factors and manifestations of RA inflammation contribute significantly to carotid atherosclerosis in RA and may modify one another's effects. 	[8, 24, 73, 75, 99, 260, 300, 315–319]
	High disease activity	(i) Higher activity index is associated with CV events and mortality.(ii) DAS-28 was a significant predictor of major adverse CV events and mortality.(iii) The occurrence of new CV events in very early RA was explained by traditional CV risk factors and was potentiated by high disease activity.	[97, 268, 300, 316, 320, 321]

TABLE 1: Continued.

Risk factor		Comments	References
	EAMs	 (i) Increases three times the risk of having CVD and these patients, also present greater IMT. (ii) CVD is considered a severe EAM of the disease. (iii) Severe EAM manifestations are associated with an increased risk of CVD events. Systemic EAM disease is a major determinant of CVD morbidity. 	[145, 240, 266, 296, 322–324]
	Household duties	Employed women are somewhat less physically disabled than their unemployed counterpart (including housework).	[14, 325, 326]
Others	Hypothyroidism	Fourfold higher risk of CVD even after adjustment for other traditional CV risk factors.	[241, 327, 328]
	Thrombogenic and other factors	(i) State of hypofibrinolysis is associated with CVD progression and levels of von Willebrand factor, PAI-1, and tissue type plasminogen(ii) Other biomarkers have been related to CVD: OPG, OPN, sPTX-3, periodontal disease, hepcidin, seric uric acid, para-articular bone loss, and MBL.	[254, 289, 297, 311, 329–341]
	Rheumatoid cachexia	Associated with high levels of LDL, low levels of atheroprotective anti-PC, and high frequency of HTN in RA patients. Patients with RA experience a 4.3% increase in body fat mass for a given BMI compared to healthy individuals.	[24, 336, 342, 343]

ACPI: acid phosphatase locus; anti-ApoA-I: anti-apolipoprotein A-1 antibodies; ACLA: anticardiolipins antibodies; anti- β 2 glycoprotein I antibodies; anti-CCP: anti-cyclic citrullinated peptide antibodies; anti-HSP: anti-heat shock proteins antibodies; anti-MCV: anti-modified citrullinated vimentin antibodies; anti-MDA-LDL: anti-malondialdehyde modified LDL antibodies; anti-oxLDL: anti-oxidized low-density lipoprotein antibodies; APLA: antiphospholipid antibodies; AT: atherosclerosis; BMI: body mass index; CAC: coronary artery calcification; CAD: coronary artery disease; anti-PC: antiphosphorylcholine antibodies; CRP: c-reactive protein; CV: cardiovascular; CVA: cerebrovascular accident; CVD: cardiovascular disease; DAS: disease activity index; EAM: extra-articular manifestations; ESR: erythrocyte sedimentation rate; GCs: glucocorticoids; GSTT-1: glutathione S-transferase, HDL: high-density lipoprotein; HTN: hypertension; IHD: ischemic heart disease; IMT: intima-media thickness; LDL: low-density lipoprotein; LGALS2: galectin-2; MBL: mannose-binding lectin; MI: myocardial infarction; LT-A: lymphotoxin-A; MTH-FR: methylene tetrahydrofolate reductase; NFκBI: nuclear factor of kappa light polypeptide gene enhancer in B-cells 1; NO: nitric oxide; OPG: osteoprotegerin; OPN: osteopontin; PAI-1: plasminogen activator inhibitor type-1; RA: rheumatoid arthritis; RF: rheumatoid factor; SE: shared epitope; sPTX-3: serum pentraxin-3; STAT4: signal transducer and activator of transcription 4; T2DM: type 2 diabetes mellitus; TAG: triglycerides; TGF- β 1: transforming growth factor beta; TNF- α 1: tumor necrosis factor receptor II; TRAFI/C5: TNF receptor-associated factor 1; VEGF-A: vascular endothelial growth factor A.

[45]. Table 4 shows the main traditional and nontraditional risk factors associated with CVD in SS.

3.5. Systemic Sclerosis. A broad spectrum of subphenotypes and mortality due to CVD have been described. Mortality in patients with SSc caused by CVD is between 20 and 30% and, despite being similar to the general population, it occurs a decade earlier (11). CV symptoms are found in 10% of the SSc patients while asymptomatic patients with coronary artery calcification (CAC) accounted for approximately 33.3% in diffuse SSc and 40% in limited SSc [46–54]. However, Doppler results have shown that 64% of the patients have carotid stenosis, compared to 35% of the control patients [55]. Arrythmias, coronary spasm, MI, PVD, CVA, CAD, LVDD, and myocardial fibrosis [46, 52, 54, 56–60] are also defined. Table 5 shows the main traditional and nontraditional risk factors associated with CVD in SSc.

4. Discussion

This review adds further evidence about high frequency of CVD in patients with ADs and their traditional (i.e., dyslipidemia, abnormal BMI, and male) and nontraditional risk factors (i.e., steroids, household duties, and autoantibodies) [14, 15]. It also highlights the impact on public health and the need to develop new strategies in prediction, prevention, and

treatment. Through the review, several factors and outcomes related to CVD were also identified.

4.1. Physiopathology of Atherosclerosis in AD. AT is a multifactorial, chronic, and inflammatory disease that had been traditionally viewed as a lipid-based disorder affecting the vessel walls. Nowadays, this theory has been modified, and it is known that all arms of the immune system take part in atheroma formation. The increased understanding of the mechanisms promoting vascular damage has recently led to a sharper focus on proinflammatory pathways, which appear to play a key role in the development and propagation of the disease. Thus, some of the mechanisms that drive atherosclerotic plaque formation, and therefore CVD, are shared with several ADs although each disease may have particular immunological aberrations that provide specific proatherogenic pathways [5-7, 16, 24, 61-68]. This process is characterized by the accumulation of lipid particles, immune cells, autoantibodies, autoantigens, and the multiple production of inflammatory cytokines such as tumor necrosis factor- α (e.g., TNF- α). All these components lead to a gradual thickening of the intima layer, thus causing a decrease in elasticity, narrowing of the arterial lumen, reduction of blood flow, plaque rupture, and, finally, the CV event [69, 70]. The systemic inflammatory response that characterizes AT also involves acute-phase reactants such as erythrocyte

Table 2: Traditional and nontraditional risk factors associated with CVD and SLE.

Risk factor	Comments	References
	Traditional risk factors	
Hypertension	(i) It is more frequent among SLE patients than people with noninflammatory disorders (ii) It acts as CVD subphenotype as well as a risk factor and also influences the risk of death by CVD. It increases the risk of thrombosis and it is more prevalent among SLE patients with atherosclerotic plaque. (iii) Lupus patients with abnormal myocardial scintigraphic findings and hypertension, as risk factor for CAD, had a higher risk of abnormal findings on coronary angiography.	[32, 152, 344–360]
T2DM	 (i) T2DM has influence on abnormal myocardial perfusion in asymptomatic patients with SLE. (ii) Alterations in glycemic profile were associated with traditional risk factors for CHD and lupus characteristics, including CVD, damage index, and renal involvement. (iii) Patients with SLE and T2DM were at increased risk of thrombosis, atherosclerotic plaque, and CAC. This risk remains elevated throughout the course of the disease. 	[32, 252, 349– 352, 357, 358, 361, 362]
Dyslipidemia	 (i) The main risk factor for death in SLE was heart involvement, which was influenced by dyslipidemia. The inflammatory context of SLE leads to dysregulation of lipid metabolism pathways → increased risk of atherosclerotic disease and thrombotic events. (ii) Alterations in lipid profile were a risk factor for endothelial dysfunction, myocardial perfusion abnormalities, and premature CAC and CAD in young women. 	[252, 344, 345, 350– 352, 354, 356, 357, 363–369]
Male gender	(i) Male gender was a risk factor for developing severe organ damage (CVD) and mortality in SLE patients.(ii) Males with SLE were at increased risk of thrombosis and CAC. This risk remains elevated throughout the course of the disease.(iii) Patients had more peripheral vascular and gonadal involvement.	[32, 350, 351, 357, 361, 367, 370, 371]
Metabolic syndrome	 (i) SLE patients had a high prevalence of MetS that directly contributes to increasing inflammatory status and oxidative stress. (ii) MetS were associated with traditional risk factors for CAD and lupus characteristics, including CVD, damage Index, and renal involvement. (iii) HCQ use proved to be protective against MetS. (iv) Insulin sensitivity and intima-media thickness are altered in SLE patients, especially those with MetS comorbidity with an associated increase in disease activity and damage (v) Renal lupus, higher corticosteroid doses, Korean and Hispanic ethnicity are associated with MetS in SLE patients 	[252, 358, 359, 372– 377]
Obesity	 (i) Patients with SLE who had excess weight present distinct clinical-laboratory findings, sociodemographic characteristics, and treatment options when compared to normal weight patients. Excess weight is associated with SLE poor prognosis. (ii) Increased weight has influence on abnormal myocardial perfusion in asymptomatic SLE patients. (iii) SLE patients with high BMI have increased QT interval parameters, presence of CAD, and carotid plaque. This prolongation may lead to an increased CV risk. 	[32, 252, 345, 349, 352, 357, 358, 369, 378–380]
Smoking	 (i) Smoking is an important determinant in the occurrence of thrombotic (central and/or peripheral, arterial and/or venous) events in SLE patients, due to atherosclerotic plaque and thrombosis (ii) Smoking habits influence abnormal myocardial perfusion in asymptomatic SLE patients. (iii) Smoking was a risk factor for premature CAC and CAD in young women with SLE. 	[252, 345, 350– 352, 354, 357, 358, 370, 372, 381, 382]

Table 2: Continued.

Risk factor		Comments	References
Advanced age		Several traditional risk factors, including age, appear to be important contributors to atherosclerotic CV damage.	[349, 352, 361, 383, 384]
Menopausal status		 (i) High percentage of SLE patients with abnormal angiographic findings was in postmenopausal status. (ii) There is high prevalence of premature menopausal status as risk factor for CVD. (iii) Postmenopausal status was a risk factor for premature CAC in young women with SLE. (iv) Postmenopausal women had a higher prevalence of subclinical AT and abnormal myocardial perfusion in asymptomatic patients with SLE. 	[351, 352, 354, 356– 358, 367, 385, 386]
Family hi	istory of CVD	(i) Familial history of CVD was an independent risk factor for atherosclerotic process and premature CAC in women with SLE.(ii) Family history of CVD influences abnormal myocardial perfusion in asymptomatic SLE.	[32, 351, 352, 354, 357, 358]
HRT		HRT use was not associated with the occurrence of vascular arterial events in the LUMINA patients. HRT use in women with SLE should be individualized, but data suggest its use may be safe if APLA are not present or vascular arterial events have not previously occurred.	[32]
Hyperhon	nocysteinemia	(i) Hyperhomocysteinemia was a risk factor for CAC in SLE patients.(ii) The presence of polyautoimmunity and hyperhomocysteinemia was a risk factor for thrombotic events.	[351, 387]
		Nontraditional risk factors	
	Ancestry	There are several differences regarding clinical (including CVD), prognostic, socioeconomic, educational, and access to medical care features in GLADEL cohort according to ancestry (White, Mestizo, and African-LA).	[15, 360, 388]
Genetic determinants	Non-HLA	(i) A SNP in <i>FGG</i> rs2066865 demonstrated association with arterial thrombosis risk in Hispanic American patients with SLE. (ii) The <i>CRP GT20</i> variant is more likely to occur in African-American and Hispanic SLE patients than in Caucasian ones, and SLE patients carrying the GT20 allele are more likely to develop vascular arterial events (LUMINA multiethnic cohort). (iii) <i>TRAF3IP2</i> may affect disease phenotype and, particularly, the occurrence of pericarditis. (iv) There is a considerable genetic component for CAD with <i>IRF8</i> as a strong susceptibility locus.	[382, 389–391]
Polyautoimmu		(i) The presence of APS and its characteristic antibodies was the major independent contributor to the development of thrombotic events and severe organ damage.(ii) Polyautoimunity (e.g., APS) may suggest concerted pathogenic actions with other autoantibodies in the development of thrombotic events.	[3, 15, 353, 392–394]
	SLE per se	 (i) SLE diagnosis is associated with carotid plaque formation and development of CV event. (ii) High percentage of patients with abnormal angiographic findings had higher ACR criteria number for SLE. (iii) Endothelial dysfunction is associated with traditional and SLE-specific risk factors, and early data suggest reversibility of endothelial dysfunction with therapy. 	[34, 356, 369, 388]
	Autoantibodies	(i) One of the independent predictors of vascular events in a multiethnic US cohort (LUMINA) was the presence of any APLA. (ii) Anti- β 2GPI antibodies were strongly associated with thrombosis. The decrease of anti- β 2GPI levels at the time of thrombosis may indicate a pathogenic role.	[32, 365, 371, 392, 395, 398]

Table 2: Continued.

Risk factor		Comments	References
		 (iii) The higher frequency of aPT found in thrombosis may suggest concerted pathogenic actions with other autoantibodies in the development of thrombotic events. (iv) Patients with ACLA seem to be at an increased risk for arterial and venous thrombotic events and showed an association with echocardiographic abnormalities. (v) There was correlation between lupus anticoagulant and thrombotic events in Brazilian lupus patients. 	
	Immune cells aberrations	 (i) Complement fixing activity of ACLA seems to be relevant in thrombotic venous events. (ii) Activation of endothelial MMP-2 by MMP-9 contained in NETs as an important player in endothelial dysfunction and MMP-9 as a novel self-antigen in SLE. These results further support that aberrant NET formation plays pathogenic roles in SLE. 	[393, 399]
	Inflammatory markers	(i) Increased ESR and CRP were independently associated with MetS and vascular events in lupus patients.	[32, 361, 373]
	Endogenous dyslipidemia	 (i) HDL distribution and composition (-HDL2b, +HDL3b, and +HDL3c) were abnormal in SLE patients. (ii) Low HDL levels and increased TAG levels were associated with AT by cIMT measurement. (iii) SLE pattern of dyslipoproteinemia may increase the risk of developing CAD. 	[400-402]
SLE-associated	Disease activity	 (i) Disease activity (SLAM) is an important determinant in the occurrence of thrombotic (central and/or peripheral, arterial and/or venous) events in the LUMINA cohort. (ii) SLEDAI scores were positively correlated with abnormal BMI and WC. (iii) Higher disease activity (i.e., SLEDAI and SLICC) is a predictor of CAC and it was independently associated with MetS, myocardial perfusion abnormalities, and thrombosis. Higher score of SDI was associated with atherosclerotic plaque in Brazilian SLE patients. (iv) SLE patients have a lipid profile abnormality which is aggravated by disease activity and may reside in a defect of VLDL metabolism. (v) There is a close link between MeTS and SLICC/ACR score with increased aortic stiffness. 	[350, 351, 356, 369, 372, 373, 381, 402–404]
	Organ damage	 (i) Baseline and accrued damage increase mortality risk (including due to CVD). (ii) Measured by SDI, patients had more peripheral vascular involvement. (iii) MetS was associated both with traditional risk factors for CHD and with lupus characteristics including damage index. (iv) There was a correlation between IMT and revised damage index (SLICC). (v) Atherosclerotic CV damage in SLE is multifactorial, and disease-related factors (including CRP levels and SDI at baseline) appear to be important contributors to such an occurrence. 	[358, 361, 369, 371, 405, 406]
	Long duration	 (i) Longer duration of SLE was associated with atherosclerotic plaque and CV events. (ii) A correlation between IMT and duration of the disease was found in SLE patients. (iii) Disease duration was an independent predictor for premature CAC in young women with SLE. 	[352, 354, 369, 383]
	Medications	(i) PDN >10 mg/day was independently associated with MetS and IMT in SLE patients.(ii) IHD was observed in SLE patients: those with long term steroid therapy and those with frank episodes of vasculitis.	[352, 355, 373]

TABLE 2: Continued.

Risk factor		Comments	References
	Vasculopathy	(i) Current vasculitis was associated with abnormal myocardial scintigraphy.(ii) Patients with SLE and RP seem to be at increased risk for arterial and venous thrombotic events. IHD was observed in SLE patients: those with long term steroid therapy and those with frank episodes of vasculitis.	[355, 357, 396]
	Renal involvement	MetS were associated with traditional risk factors for CHD and lupus characteristics, including damage index and renal involvement (nephritic syndrome).	[358]
	BMD	Decreased BMD was an independent predictor for premature CAC.	[354]
Miscellaneous	Sociodemographic factors	A low education and monthly income were associated with MetS.	[252]
	25(OH) levels	Lower baseline 25(OH) vitamin D levels are associated with higher risk for CVD and more active SLE at baseline.	[403, 407, 408]

25(OH) vit D: 25-hydroxy vitamin D; ACLA: anticardiolipins antibodies; ACR: American College of Rheumatology; anti-β2GPI: anti-beta 2 glycoprotein 1 antibodies; aPT: antiprothrombin antibodies; APLA: antiphospholipid antibodies; APS: antiphospholipid syndrome; AT: atherosclerosis; BMD: bone mineral density; BMI: body mass index; CAC: coronary artery calcification; CAD: coronary artery disease; cIMT: carotid intima-media thickness; CRP: C-reactive protein; CV: cardiovascular; CVD: cardiovascular disease; ESR: erythrocyte sedimentation rate; GLADEL: Grupo Latino Americano De Estudio de Lupus; HDL: high-density lipoprotein cholesterol; HRT: hormone replacement therapy; IHD: ischemic heart disease; IMT: intima-media thickness; IRF8: interferon regulatory factor 8; LA: Latin America; LDL: low-density lipoprotein cholesterol; LUMINA: Lupus in Minorities: Nature versus Nurture cohort; MetS: metabolic syndrome; MMP: matrix metalloproteinases; NETs: netosis bodies; PDN: prednisolone; RP: Raynaud's phenomenon; TAG: triglycerides; TRAF: tumor necrosis factor receptor-associated factors; T2DM: type 2 diabetes mellitus; SDI: SLE damage index; SLAM: systemic lupus activity measure; SLE: systemic lupus erythematosus; SLEDAI: Systemic Lupus Erythematosus Disease Activity Index; SLICC: Systemic Lupus International Collaborating Clinics score; SDI: SLICC damage index; SNP: single-nucleotide polymorphism; VLDL: very low-density lipoprotein cholesterol; WC: waist circumference.

sedimentation rate (ESR) and c-reactive protein (CRP) [71–75].

Endothelial dysfunction is the first step leading to AT and has been associated with both traditional and nontraditional risk factors related to several ADs. Other factors involved are high concentrations of angiotensin II, increased smooth muscle hypertrophy, peripheral resistance, and oxidation of low-density lipoprotein cholesterol (LDL) as well as elevated plasma homocysteine concentrations and genetic alterations [76-78]. Thus, the different forms of injury increase endothelium adhesiveness for leukocytes or platelets as well as endothelium permeability with the expression of multiple vascular cell adhesion molecules (VCAM), intercellular adhesion molecules-1 (ICAM-1), selectins, and chemokines [4, 79, 80]. In addition to their differentiation, macrophages $(M\phi)$ are associated with upregulation of toll-like receptors, which enhances a cascade of M ϕ activation and release of vasoactive molecules such as nitric oxide (NO), reactive oxygen, endothelins, and proteolytic enzymes. All of them lead to the plaque destabilization and the increased risk for rupture [4, 79, 81–83].

T cells, predominantly lymphocyte T helper 1 (Th1), are also recruited to the subendothelial space. Th1 cells dominate over lymphocyte T helper 2 (Th2) as well as their anti-inflammatory mediators (i.e., IL-4, -5, and -10). This kind of reaction is greater in several ADs with a high production of TNF- α , IL-2, IL-6, IL-17, and so forth, which, in combination, activates T cells even more and favors smooth muscle cell migration, proliferation, and foam cell formation [16, 61, 84, 85]. Furthermore, activated M ϕ express human leukocyte antigen (HLA) II that allows them to present antigens to Tlymphocytes. Smooth muscle cells from

the lesions also have class II HLA molecules on their surfaces and can also present antigens to T cells such as ox-LDL and heat shock proteins (HSP) 60/65 [4, 61]. The immune regulatory molecule CD40 ligand and its receptor CD40 are expressed by M ϕ , T cells, endothelium, and smooth muscle. Both are upregulated in lesions of AT and thus provide further evidence of immune activation [5, 86]. As ox-LDL is a macromolecule with many potential autoantigens, it is possible that antioxidized low-density lipoprotein antibodies (anti-oxLDL) represent a family of autoantibodies against different autoantigens involved in CVD. Thus, the clinical impact of these autoantibodies might vary. However, there are reports showing that elevated anti-oxLDL titers have been detected in patients with early-onset PVD, severe carotid AT, CHF, CAD, MI, and death [87, 88]. This suggests a proatherogenic role for these autoantibodies and supports a key role for them in the progression of AT [87, 89, 90].

Beta-2 glycoprotein-1 (β 2GPI) is considered to be an autoantigen in APS. Moreover, it is abundantly expressed within the subendothelial regions and in the intima-media layers at the border of atherosclerotic plaque. Both IgM and IgG anti- β 2GPI levels are elevated in patients with AT and other inflammatory conditions [91]. β 2GPI is the actual autoantigen for most anticardiolipin antibodies (ACLA), a group of antibodies with procoagulant activity. The association between APLA, AT, and thrombosis can also be seen outside the setting of autoimmunity. Thus, ACLA promote AT by attracting monocytes into the vessel wall and inducing monocyte adherence to endothelial cells. All of this is mediated by adhesion molecules such as ICAM-1, VCAM-1, and E-selectin [7, 92]. The APLA should be considered more than an AT marker since they can enhance AT and are proatherogenic

TABLE 3: Traditional and nontraditional risk factors associated with CVD and APS.

Risk factor	Comment	Reference		
Traditional risk factors				
Metabolic syndrome	The most common risk factors are hypertriglyceridemia, low HDL levels, and visceral obesity.	[409, 410]		
Hyperlipidemia	High levels of APLA may be a marker for earlier endothelial damage caused by hyperlipidaemia.	[410, 411]		
T2DM	It is associated with cardiovascular disease among APS patients. It did not show any difference between APS patients and the general population.	[410, 412]		
Smoking	CVD risk factor increases risk of AT.	[410, 412]		
Obesity	Increases the risk of insulin resistance and MetS.	[410, 412]		
HTN	Increases risk of ischemic events and CVD.	[410, 412]		
Sedentary lifestyle	Increases risk of obesity and comorbidities, propending CVD.	[410, 412]		
	Nontraditional risk factors			
APS per se	Patients with primary APS have a high prevalence of carotid IMT and a decreased lumen diameter. IMT in primary APS may be associated with stroke. Patients with primary APS with IMT must be considered as carriers of atherosclerosis.	[204]		
Autoantibodies	 (i) ACLA are associated with a higher risk of venous thrombosis and arterial thrombosis. (ii) Lupus anticoagulant is a major risk factor for arterial thrombotic events. (iii) Immunoinflammatory mechanisms, primarily APLA, have an outstanding role in APS-related vasculopathies. (iv) Patients having APLA and AT may have greater risk for ischemic events than patients with the same degree of AT but without APLA. (v) β2GPI is abundantly present in the atherosclerotic plaque. (vi) Anti-β2GPI and ACLA may be involved in CAD and stroke. (vii) CAD and PVD occurred more often in patients with elevated serum levels of IgG or IgM APLA, including ACLA or anti-β2GPI. 	[145, 186, 204, 413–419]		

ACLA: anticardiolipins antibodies; anti- β 2 glycoprotein I antibodies; APLA: antiphospholipid antibodies; APS: antiphospholipid syndrome; AT: atherosclerosis; β 2 glycoprotein I; CAD: coronary artery disease; CVD: cardiovascular disease; HDL: high-density lipoprotein; HTN: hypertension; IMT: intima-media thickness; MetS: metabolic syndrome; PVD: peripheral vascular disease; T2DM: type 2 diabetes mellitus.

[93, 94]. Likewise, serum from patients with CVD shows a high prevalence of antibodies against HSP60, which mediate lysis of stressed endothelial cells [91, 95, 96].

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4.2. Rheumatoid Arthritis. In addition to diarthrodial joints, RA can damage virtually any organ thus leading to potential extra-articular manifestations (EAMs). CVD is considered an EAM and represents the major predictor of poor prognosis and the main cause of death in this population [13, 17, 97, 98]. There is evidence that vascular damage accrual begins prior to the diagnosis of RA and accelerates as the disease progresses. RA patients present with endothelial dysfunction and increased subclinical AT compared to age-matched controls [99–101]. Endothelial function, assessed by brachial artery flow-mediated vasodilation, also worsens with disease

duration [102]. The CV mortality is higher in RA and life expectancy of patients with RA is three to ten years less than that of the general population [103, 104]. CVD is known to appear earlier and 3.6 times more frequently than in the general population [70, 98, 105]. Thus, CVD is the leading cause of death for RA patients around the world [106, 107]. Currently, IHD secondary to AT is the most prevalent cause of death associated with CVD in RA patients [108]. Almost all mortality studies have been done on populations of European origin, and there is limited information on other ethnic groups. A meta-analysis of 24 RA mortality studies, published between 1970 and 2005, reported a weighted combined all-cause standardized mortality ratio (meta-SMR) of 1.50 with similar increases in mortality risk apparent from the ratios for IHD (meta-SMR 1.59) and for CVA (meta-SMR 1.52)

TABLE 4: Traditional and nontraditional risk factors associated with CVD and SS.

Risk factor		Comment	Reference
		Traditional risk factors	
Dyslipidemia		(i) High prevalence of hyperlipidemia and low HDL are associated with CVD and first-degree heart block.(ii) SS patients showed 1.5-fold higher prevalence of hypertriglyceridemia.	[12, 42–44, 210, 420]
	T2DM	It is associated with CV compromise in SS patients.	[210]
Adv	vanced age	Age is a predictor for valve compromise	[45]
		Nontraditional risk factors	
	Systemic compromise	Articular, renal, liver, peripheral neuropathy, CNS, joint and gastrointestinal involvement, and parotid enlargement are associated with stroke, IHD and lower flow-mediated vasodilation	[12, 42, 210]
	Polyautoimmunity	SS patients with APS were significantly associated with APLA in thrombotic events.	[41]
SS-associated	Autoantibodies	 (i) SS-A is associated with stroke, IHD, and carotid thickening. (ii) SS-B is related to first-degree heart block, valve compromise, and lower nitrate mediated vasodilation. (iii) APLA and lupus anticoagulant are associated with thrombotic events. (iv) ACLA IgG is associated with arrhythmias (v) RF is related to lower nitrate mediated vasodilation. (vi) Anti-HDL. 	[12, 41–43, 210, 211, 420]
	Long duration of disease	Longer duration of the disease is associated with stroke and IHD.	[210, 420]
	Chronic proinflammatory state	Elevated CRP is associated with stroke and IHD	[43, 210]
	Glucocorticoids	(i) Steroid use is associated with stroke and IHD(ii) Patients with GCs showed a higher frequency of HTN, T2DM, and elevated TAG.	[42, 210]
Others	Hematological alterations	 (i) Hypogammaglobulinemia, leukopenia, thrombocytopenia, and s-VCAM-1 are associated with thrombotic events and lower nitrate mediated vasodilation. (ii) Low C4 and cryoglobulinemia are predictors for valve injury 	[12, 42, 45, 210, 211, 420]

ACLA: anticardiolipins antibodies; anti-HDL: anti-high-density lipoprotein antibodies; APLA: antiphospholipid antibodies; APS: antiphospholipid syndrome; CNS: central nervous system; CRP: c-reactive protein; CV: cardiovascular; CVD: cardiovascular disease; GCs: glucocorticoids; HDL: high-density lipoprotein cholesterol; HTN: hypertension; IHD: ischemic heart disease; RF: rheumatoid factor; SS-A: anti-Ro/SSA antibodies; SS-B: anti-La/SSB antibodies; SS: Sjögren's syndrome; s-VCAM: soluble vascular cellular adhesion molecules; TAG: triglycerides; T2DM: type 2 diabetes mellitus.

[109]. RA patients with CVD frequently experience "silent" IHD with no symptoms before a sudden cardiac death. Indeed, sudden cardiac deaths are almost twice as common in patients with RA as in the general population [110]. According to the above, the Rochester Epidemiology Project [100] showed that patients with RA had a greater risk of MI than controls of equivalent age and sex. Recently, Sarmiento-Monroy et al. [13] did a systematic literature review of CVD in the Latin American (LA) population. A wide range of prevalence for CVD has been reported (13.8–80.6%) for this population. The highest prevalence was indicated in Puerto Rican patients (55.9%) by Santiago-Casas et al. [111], while for Brazil [112, 113], Colombia [14, 97, 114, 115], and

Argentina [116, 117], a similar prevalence was reported (47.4, 35.1, and 30.5%, resp.). However, the mortality in RA patients has been poorly evaluated in this population. Acosta et al. [118] demonstrated a mortality rate of 5.2% in a six-year follow-up. For both, the most frequent cause of death was CVD in 44.7% and 22.2% of the cases, respectively. Table 1 and Figure 1 give a summary of the main findings related to traditional and nontraditional CVD risk factors in RA patients. In the Colombian population, Amaya-Amaya et al. [14] found that the traditional risk factors including male gender, hypercholesterolemia, and an abnormal body mass index (BMI) were associated with CVD. Nevertheless, the increased prevalence of CV events in RA is not fully explained

TABLE 5: Traditional and nontraditional risk factors associated with CVD and SSc.

Risk factor	Comments	References
	Traditional risk factors	
Dyslipidemia	 (i) The alteration of lipid profile has been described, given by the increased levels of LDL and lipoprotein A, which are related to the reduction in the fibrinolysis and thrombotic and coronary events. (ii) Decreased levels of HDL are related to anticentromere antibodies positivity. (iii) There is elevation of TAG, total cholesterol, and LDL and decrease in HDL levels. 	[214, 218, 421–424]
T2DM	It is associated with CV events in SSc patients.	[54, 424]
Hypertension	Its prevalence increased with the age, and it is correlated with MI.	[54]
Hyperhomocysteinemia	Increased levels are related to AT and endothelial dysfunction.	[218]
	Nontraditional risk factors	
SSc per se	It is an independent risk factor for MI	[54]
Autoantibodies	 (i) oxLDL/β2GPI and anti-oxLDL/β2GPI complex: these are considered proatherogenic. (ii) anti-ox-LDL: higher levels are correlated with AT and thrombosis. (iii) anti-LPL: its presence is related to TAC elevated. 	[0] 220 422 425 420]
Autoantibodies	 (iii) anti-LPL: its presence is related to TAG elevated and AT and CV events. (iv) AECA may also contribute to an increased risk of early AT in SSc (v) Others: anticentromere, anti-HSP65/60, and APLA. Increase of CRP levels and intercellular adhesion 	[91, 220, 423, 425–429]
Chronic inflammation	molecule-1 may also contribute to an increased risk of early AT in SSc.	[218, 429]

AECA: anti-endothelial cell antibodies; anti-HSP: anti-heat shock proteins antibodies; anti-LPL: anti-lipoprotein lipase antibodies; an anti-oxLDL/ β 2GPI complex: anti-oxidized low-density lipoprotein/ β 2 glycoprotein I antibodies; APLA: antiphospholipid antibodies; AT: atherosclerosis; CRP: c-reactive protein; CV: cardiovascular; CVD: cardiovascular disease; HDL: high-density lipoprotein cholesterol; LDL: low-density lipoprotein; oxLDL/ β 2GPI complex: oxidized low-density lipoprotein/ β 2 glycoprotein I; SSc: systemic sclerosis; TAG: triglycerides; T2DM: type 2 diabetes mellitus.

by these classic risk factors. Both nontraditional RA risk factors and traditional risk factors act together to develop CVD (Figure 1).

Regarding CV risk screening and management, strategies have been developed for the general population and are based on CV risk score calculators such as the Framingham score and the Systematic Coronary Risk Evaluation (SCORE) model, but the accuracy of these models has not been adequately evaluated in inflammatory arthritis [119]. Recent studies have shown that the SCORE underestimates the actual cardiovascular risk of patients with RA. In this regard, a study showed a high frequency of carotid plaques in the group of individuals included in the category of moderate risk according to SCORE risk charts [120]. The major strategy is to develop healthy life styles as a way to maintain control of classical risk factors. Statins can effectively lower total cholesterol in RA patients and significantly improve the rates of CV-related and all-cause mortality when used for primary prevention of vascular events [121, 122]. Similarly, ACE inhibitors and angiotensin II blockers may also have a favorable effect on inflammatory markers and endothelial function in RA [123, 124]. Regarding novel risk factors, it is necessary to establish an adequate management of the disease [19]. The main goal of the treatment should be to reduce the disease activity, and, therefore, decrease the CV burden [124]. Both conventional [125] and biological disease modifying antirheumatic drugs (DMARDs) are used for this purpose. Some studies have shown greater disease control with nonconventional DMARDs such as anti-TNF agents, which lower CRP and IL-6 levels, increase HDL levels, and improve endothelial function [126-129]. Effective treatment may also result in improved physical activity which subsequently leads to a decreased risk of hypertension, obesity, and diabetes, all important determinants of CV disease [127]. The antimalarial (AMs) drugs have been associated with a better CV outcome, enhanced glycemic control, improved lipid profiles, a decreased thrombosis risk, and a reduced probability of developing T2DM in patients with RA [127, 130, 131]. The glucocorticoids (GC) should be used prudently to minimize CV risk secondary to their effects on metabolic parameters and blood pressure. Altogether, there is no clear evidence that low doses of GC contribute significantly to an enhanced CV risk in inflammatory arthritis in contrast to high doses. GCs rapidly and effectively suppress inflammation in RA and their use might be justified for short-term treatment, for example, for "bridging therapy" in the period between initiation

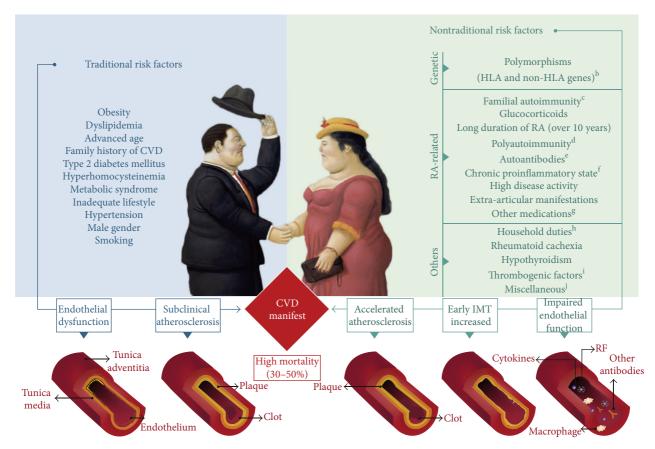
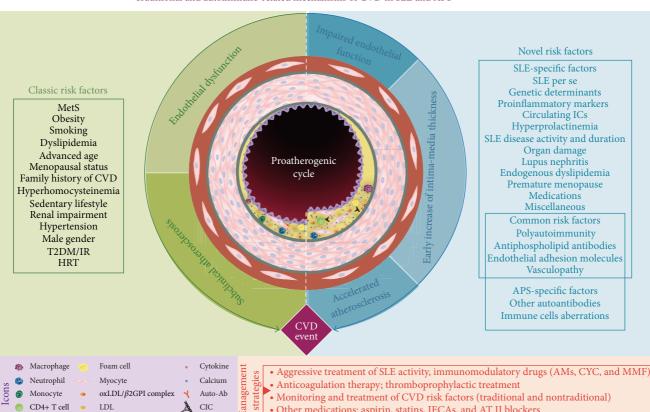


FIGURE 1: Traditional and nontraditional risk factors for cardiovascular disease in rheumatoid arthritis. AD: autoimmune disease; CVD: cardiovascular disease; IMT: intima-media thickness; RA: rheumatoid arthritis; RF: rheumatoid factor. ^aCVD includes a broad spectrum of subphenotypes: stroke/transient ischemic attack, coronary artery disease, myocardial infarction, angina, congestive heart failure, arrhythmias, ventricular diastolic dysfunction, hypertension, pulmonary embolism, deep vein thrombosis, and peripheral arterial/venous disease. ^bMainly HLA-DRB1*0404 shared epitope alleles. ^cThe presence of any diagnosed AD in first-degree relatives of proband. ^dThe presence of two concomitant AD in a single patient on the basis of international criteria. ^eRheumatoid factor, anti-cyclic citrullinated peptides antibodies, anti-oxidized low-density lipoprotein, anticardiolipins, anti-phosphorylcholine, anti-modified citrullinated vimentin, anti-apolipoprotein A-1, and anti-cytokeratin 18 antibodies. ^fHigh levels of c-reactive protein and erythrocyte sedimentation rate. ^gMethotrexate, leflunomide, and nonsteroidal anti-inflammatory drugs. ^hPatients (females and males) with RA working on household duties. ⁱvon Willebrand factor, plasminogen activator inhibitor-1, and tissue plasminogen activator. ^jHypothyroidism, periodontal disease, and other markers such as mannose-binding lectin, serum pentraxin 3, osteopontin, osteoprotegerin, and seric uric acid.

and response to DMARD treatment, although the debate does not appear to be settled yet. Therefore, a conservative approach was chosen in which the use of the lowest dose for the shortest period possible was recommended [19, 124, 125, 132]. Reports indicate that anti-TNF is independently associated with a lower CV risk due to the fact that it reduces CV events in young patients by improving the lipid profile, insulin resistance, endothelial function, and aortic compliance and decreasing progression rates of subclinical AT [124, 133-138]. Other biological therapy also produces the same effect. A good example of that was the improvement of endothelial function following rituximab therapy in patients with RA that had been refractory to anti-TNF-alpha drugs [139, 140]. Finally, data about other biologics are conflicting and preliminary; as such, randomized, controlled studies are needed to identify their CV risk reduction role [69, 70].

4.3. Systemic Lupus Erythematosus. SLE occurs most often in young women of child-bearing age, the same population that is at the highest relative risk of subclinical AT [141, 142]. Classically, there is a bimodal mortality pattern among SLE patients with an early peak in the first 3 years after diagnosis due to active disease, infections, and nephritis and a second peak with deaths occurring 4-20 years after SLE diagnosis due to CVD as described by Urowitz et al. [143]. Although the overall mortality rate for SLE patients has improved over the past 30 years, mortality due to CVD (i.e., 3-25%) has remained the same [144-146]. There is strong epidemiologic evidence that CVD risk among SLE patients compared to the general population is at least doubled [27]. Carotid plaque is prevalent in 21% of SLE patients under age 35 and in up to 100% of those over age 65 [147]. The increased risk of MI and angina among SLE patients



Traditional and autoimmune-related mechanisms of CVD in SLE and APS

FIGURE 2: Traditional and autoimmune-related mechanisms of cardiovascular disease in systemic lupus erythematosus and antiphospholipid syndrome. A complex interaction between traditional and disease-specific traits leads to premature atherosclerosis process. Several risk factors (left) have been described since the Framingham heart study, known as classic risk factors, which over time conduce to endothelial dysfunction, subclinical atherosclerosis, and CV event manifest. In the autoimmune setting (right), several novel risk factors contribute to development of premature vascular damage. This damage is represented by impaired endothelial function and early increase of intimamedia thickness, which are surrogates of the accelerated atherosclerosis process. These associations are even more pronounced in this case of polyautoimmunity (SLE and APS in the same individual), where risk factors have additive effects and atherosclerosis develops earlier. The cornerstone of management of CV risk includes an aggressive treatment of disease activity, the continuous monitoring and treatment of modifiable CV risk factors, and the use of other medications in order to diminish the CV burden. ACE-I: angiotensinconverting enzyme inhibitors; AMs: antimalarials; APS: antiphospholipid syndrome; AT-II blockers: angiotensin II receptor blockers; Auto-Ab: autoantibodies; AZA: azathioprine; CIC: circulating immune complex; CYC: cyclophosphamide; CVD: cardiovascular disease; HDL: high-density lipoprotein; HRT: hormone replacement therapy; IR: insulin resistance; MetS: metabolic syndrome; MMF: mycophenolate $mofetil; oxLDL/\beta 2 GPI \ complex: oxidized \ low-density \ lipoprotein/2 \ glycoprotein\ I; SLE: systemic \ lupus \ erythematosus; T2DM: type 2 \ diabetes$ mellitus.

HSP 60/65

VCAM/ICAM-1

• Other medications: aspirin, statins, IECAs, and AT II blockers

has been well characterized in a number of populationbased studies [146, 148-152]. Bengtsson et al. [152] further corroborated these results in their population-based Swedish study where they demonstrated that the risk of CVA and/or MI in the total SLE population was 1.27-fold higher than that in the general population, but among women with SLE aged 40-49, it was 8-fold higher over the 7-year follow-up period. Several research groups have reported prevalence rates in SLE cohorts. In the Systemic Lupus International Collaborating Clinics-Registry for Atherosclerosis (SLICC-RAS) cohort, there were 8 cases of PVD among 1,249 patients during a 2-year period [153]. In the Lupus in Minorities: Nature versus Nurture study (LUMINA), 5.3% of 637 patients developed PVD over a mean follow-up of 4.4 years [154].

In a recent meta-analysis, Schoenfeld et al. [27] showed that epidemiological data strongly support the hypothesis that SLE patients are at an elevated relative risk of CVD. The variability regarding the relative importance of risk factors for CVD among SLE patients in past epidemiological studies is likely due, in part, to different design methods and different patient and comparison groups. Independent predictive risk factors (from multivariate analysis) for CV events have been assessed in five large prospective cohorts of patients with SLE, including the Baltimore [155], Pittsburg [149], LUMINA [32], Toronto [156], and SLICC-RAS [153] cohorts. The main results are discussed in Table 2 and Figure 2. Diverse SLE cohorts have shown the influence of advanced age, dyslipidemia, obesity, HTN, and hyperhomocysteinemia as classical

risk factors for CVD in the lupus population [27, 157-159]. There is strong epidemiological evidence that traditional CVD risk factors also elevate CVD risk among SLE patients (Figure 2). Amaya-Amaya et al. [160] recently added further evidence of the high frequency of CVD in 310 consecutive patients with SLE (36.5%). Their findings on traditional risk factors (i.e., dyslipidemia, smoking), plus the confirmation that coffee consumption is another risk factor, showed that, in combination, they contribute to this complication in the LA population. It is well known that while traditional CVD risk factors are undoubtedly important in increasing the CVD risk among SLE patients, these do not fully account for the elevated risk of CVD in this population. Esdaile et al. [161] evaluated risk factors for CAD in two Canadian lupus cohorts by means of the Framingham multiple logistic regression model and found a high risk of developing CAD after removing the influence of these risk factors. Therefore, SLEassociated factors play an important role in the premature AT process characteristic of those patients [70, 162–166]. Hence, there is an increasing interest in identifying novel risk factors that might explain the development of accelerated AT in these populations. The proposal has been made that SLE be managed the same way that T2DM is—as a "CVD equivalent"—with lower lipid goals, more aggressive aspirin use, and potentially more aggressive monitoring [167, 168].

Recent studies have started to address the question of whether traditional treatment regimens may prevent or slow AT in SLE patients [142]. There are several new mechanisms of action described for AMs, many of which have beneficial effects in the management of CV risk in patients with SLE [131, 169]. There is evidence that AM drugs reduce LDL levels, elevate HDL, and, when taken concomitantly with steroids, can reduce TC [170]. In addition, beneficial effects of HCQ on thrombosis formation have also been described [171-174]. Ruiz-Irastorza et al. [175, 176] found that HCQ use conferred a 50-60% decrease in the risk of CVD. Otherwise, the recent randomized controlled Lupus Atherosclerosis Prevention Study by Petri et al. [28] suggests that atorvastatin did not in fact slow progression of subclinical AT in 200 SLE patients over 2 years. However, in other studies, it has been demonstrated that statins do reduce CD40 levels in vivo and in vitro and, therefore, interfere with CD40-CD40 ligand interactions in both SLE and AT [177]. As inflammation is one of the targets of therapy in SLE, several other immunosuppressant drugs and biological therapies currently employed in SLE could also be considered such as potential new antiatherogenic agents [178, 179].

4.4. Antiphospholipid Syndrome. The APS is a prothrombotic state that can affect both the venous and arterial circulations. The deep veins of the lower limbs and cerebral arterial circulation are the most common sites of venous and arterial thrombosis, respectively [180]. The heterogeneity of APS clinical manifestations is likely linked to the varied effects that APLA can induce on endothelial cells [181]. Thrombotic events are the clinical hallmark of APS, occurring in venous and arterial circulations with a high recurrence rate of arterial involvement. They can be expressed as carotid

disease, CVA, CAD, and PVD due to thrombus formation or AT [182–188]. Further, other cardiac manifestations may include irregular thickening of the valve leaflets due to deposition of immune complexes that may lead to vegetation and valve dysfunction, which are frequent and may be a significant risk factor for stroke [189-192]. Table 3 and Figure 2 show the main traditional and nontraditional risk factors associated with APS and CVD. Early diagnosis of APS through examination of the heart and aggressive control of all traditional risk factors through lifestyle modifications and pharmacotherapy, probably anti-inflammatory treatment, and close follow-up of APS patients may help to minimize CV risk in these individuals [189, 193]. The APS coagulopathy in these patients requires careful and judicious use of appropriate antiaggregant and anticoagulant therapy [39]. Specifically targeted therapies that exert anti-inflammatory or immunomodulatory effects become important therapeutic tools in APS. In order to achieve beneficial effects, these drugs should primarily antagonize the pathogenic effects of APLA. Moreover, these treatments should also control atheroma, which is one of the major causes of CV mortality in this pathology [177]. For instance, AM drugs may exert evident antiatherogenic properties [168, 194]. Statins also have pleiotropic characteristics, which include antiatherosclerotic (i.e., preventing endothelial dysfunction), anti-inflammatory (i.e., reducing CRP levels), antioxidant, immunomodulatory, and antithrombotic effects [195-200]. Likewise, aspirin has been used in primary and secondary prevention in APS patients particularly for its inhibitory effects on platelet aggregation [201, 202]. In addition to their anticoagulant effects, unfractionated heparins and low molecular weight heparins also have anti-inflammatory properties. Thus, heparins may represent another anti-inflammatory therapeutic tool even though the mechanisms of action responsible for their anti-inflammatory effects are not yet fully understood [203]. Recent improvements in the understanding of the pathogenic mechanisms have led to the identification of novel potential targets and therapies that might be used as new potential immunomodulatory approaches in APS and CVD such as B-cell targeted therapies, complement inhibition, inhibition of costimulation, intracellular pathway inhibition, and anticytokine therapies [204].

4.5. Sjögren's Syndrome. This is an autoimmune epithelitis that affects the exocrine glands with a functional impairment that usually presents as persistent dryness of the eyes and mouth [205, 206]. Its clinical spectrum extends from an autoimmune exocrinopathy to a systemic involvement with vasculitis and diverse extraglandular systemic manifestations (40–50%). This includes CVD although with lower prevalence as mentioned above [207, 208]. Chronic systemic inflammation is a risk factor for developing AT, however, and contrary to what is expected, the prevalence of CVD associated with AT is not appreciably increased in patients with SS. This probably is characterized by chronic but milder inflammation as Ramos-Casals et al. showed [205]. In fact, Akyel et al. [209] found endothelial dysfunction in SS patients although their carotid IMT was comparable to the healthy

control group. It should be noted that the CV risk in patients with SS is rising as a result of the population affected by the disease (i.e., postmenopausal women) [43, 210]. Vaudo et al. [211] found a high rate of subclinical AT due to changes in the carotid arterial wall studied/seen by femoral and carotid ultrasonography. All these findings (i.e., Table 4) suggest that a functional impairment of the arterial wall may sustain early phases of atherosclerotic damage in SS. A combined effect of disease-related chronic inflammatory and immunological factors appears to support dysfunction of endothelium and vascular smooth muscle cells, respectively. Table 4 contains the most frequent traditional and nontraditional risk factors related to CVD and SS. The management of CVD in SS patients must be directed toward rigorous intervention of modifiable risk factors as well as nontraditional risk factors, warranting a routine evaluation of autoantibodies and other SS-related factors. Pérez-De-Lis et al. [210] found a protective role of AMs in CVD and SS patients since these drugs show an association with a lower frequency of HTN, T2DM, and dyslipidemia. So, in the future, it will be necessary to analyze the incidence of CVD and the role of the different risk factors listed in Table 4 prospectively for the development of such complications.

4.6. Systemic Sclerosis. There are two major disease presentations: the microvascular and macrovascular involvement. The vasculopathy of SSc typically affects the small arteries and capillaries (i.e., microvascular occlusive disease with vasospasm and intimal proliferation) while macrovascular disease has been demonstrated by carotid ultrasonography, ankle brachial blood pressure index, and peripheral angiography [48, 50, 52] due to fibrosis, thickening, and chronic proliferation of the intimal layer as well as transmural lymphocytic infiltrate without evidence of atherosclerotic plaque [48, 53]. However, recently, the evidence has demonstrated increased atherosclerosis, including CAC, higher prevalence of subclinical CAD, and higher carotid IMT [46, 212]. Patchy fibrosis is the most important feature in the myocardium, especially when it is localized in subendocardial regions. This fibrosis usually accompanies LVDD [59, 60], but it is symptomatic in 10% of the cases [213]. There have been reported MI or myocardial perfusion defects with coronary arteries which suggests that the etiology of infarction may be due to microvascular disease rather than coronary AT although we must recognize that the latter is higher in patients with SSc [214, 215]. Patients with SSc have a reduced coronary flow reserve [216, 217], which is associated with higher coronary events [218, 219]. Other authors have reported ectasia, spasm, and coronary artery stenosis [56, 57]. Arrhythmias and conduction disturbances are characteristic of cardiac involvement in SSc as hypertrophy and heart failure contractility [58, 60] have been reported. Ultrasonography evaluation is also used to evaluate the carotid arteries and has been proven to be a useful marker for the assessment of subclinical AT and a strong predictor of subsequent MI and CVA [77, 216, 220]. In addition, once SSc has been diagnosed and established, attention to treatment of the vascular component is critical. While the traditional

approach has been solely to use vasodilator therapy, new investigations are underway to develop novel therapies, to prevent further vascular injury, and to stimulate vascular repair. Some of the current treatment approaches include the following: prostacyclin analogs, endothelin antagonists, phosphodiesterase inhibitors, immunosuppressive therapy, and tyrosine kinase inhibitors [221].

4.7. Spondyloarthropathies. Since spondyloarthropathies are also chronic autoimmune-autoinflammatory diseases associated with accelerated atherosclerosis, the patients with spondyloarthropathies also have a higher risk of cardiovascular disease than the general population. Ankylosing spondylitis has been associated with increased mortality rate compared to the general population, which is, in great part, the result of cardiovascular complications. Also, subclinical atherosclerosis, manifested by the presence of endothelial dysfunction and increased carotid intima-media wall thickness and carotid plaques, has been observed in patients with psoriatic arthritis and ankylosing spondylitis. In patients with ankylosing spondylitis, TNF-alpha blockade was associated with improvement of insulin resistance, markers of metabolic syndrome, and biomarkers of endothelial dysfunction [222-232].

5. Conclusions

AT and ADs share several mechanisms. The excessive CV events observed in patients with ADs are not fully explained by classic risk factors. Several novel risk factors contribute to development of premature vascular damage. Therefore, a complex interaction between traditional and disease-specific traits converges into a shared proatherogenic phenotype in this population. Until additional research and disease-specific risk prediction tools are available, current evidence supports aggressive treatment of disease activity and careful screening for and management of modifiable traditional risk factors in patients with ADs. The finding and understanding of complex interactions between predisposing factors (i.e., genetic, environmental factors, and ADs per se) will allow us to better describe and assess the broad spectrum of CV subphenotypes in ADs and their treatments.

Conflict of Interests

The authors have indicated that they have no conflict of interests regarding the content of this paper.

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Research Article

Comparison of Two Assays to Determine Anti-Citrullinated Peptide Antibodies in Rheumatoid Arthritis in relation to Other Chronic Inflammatory Rheumatic Diseases: Assaying Anti-Modified Citrullinated Vimentin Antibodies Adds Value to Second-Generation Anti-Citrullinated Cyclic Peptides Testing

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Determination of anti-citrullinated peptide antibodies (ACPA) plays a relevant role in the diagnosis of rheumatoid arthritis (RA). To date, it is still unclear if the use of several tests for these autoantibodies in the same patient offers additional value as compared to performing only one test. Therefore, we evaluated the performance of using two assays for ACPA: second-generation anti-citrullinated cyclic peptides antibodies (anti-CCP2) and anti-mutated citrullinated vimentin (anti-MCV) antibodies for the diagnosis of RA. We compared three groups: RA (n=142), chronic inflammatory disease (CIRD, n=86), and clinically healthy subjects (CHS, n=56) to evaluate sensitivity, specificity, predictive values, and likelihood ratios (LR) of these two assays for the presence of RA. A lower frequency of positivity for anti-CCP2 was found in RA (66.2%) as compared with anti-MCV (81.0%). When comparing RA versus other CIRD, sensitivity increased when both assays were performed. This strategy of testing both assays had high specificity and LR+. We conclude that adding the assay of anti-MCV antibodies to the determination of anti-CCP2 increases the sensitivity for detecting seropositive RA. Therefore, we propose the use of both assays in the initial screening of RA in longitudinal studies, including early onset of undifferentiated arthritis.

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1. Introduction

Rheumatoid arthritis (RA) is a chronic inflammatory disorder that involves synovial joints and may develop extraarticular manifestations [1]. Frequently, the diagnosis of RA may pose some difficulties in primary care, particularly during early disease, and this disease may inappropriately be confused with other rheumatic diseases [2]. In this context, a relevant tool to support the diagnosis is the presence of autoantibodies associated with the disease. Although the detection of rheumatoid factor [3] is useful to support the diagnosis and it is detected in 75% of patients with RA, a limitation of this autoantibody is its low specificity, being frequently observed in other rheumatic disorders, chronic infections, and even in healthy elderly people [3]. Different assays are currently used to detect antibodies against cyclic citrullinated antigens as well as noncyclic citrullinated peptides. Therefore, the term anti-citrullinated peptide antibody (ACPA) is commonly used in these days. Assays to identify antibodies against citrullinated cyclic peptides are commonly used as a tool to support the diagnosis of RA, because it has been widely demonstrated that these autoantibodies have higher specificity as compared with the rheumatoid factor (RF). One of the most common assays is the determination of second-generation anti-citrullinated cyclic peptide antibodies (anti-CCP2). Therefore, ACPAs have been included in the most recent classification criteria for RA diagnosis [4]. Nevertheless, around 38% of patients with RA may have negative results for anti-CCP2 [5, 6].

Assays determining antibodies against human mutated vimentin (anti-MCV) have been also proposed recently as a tool for the diagnosis of RA [7, 8]. Nevertheless, still 26% of patients with RA may yield negative results with these assays [7]. To date, there are several studies comparing the performance of different assays of anti-CCP2 versus anti-VCM in the diagnosis of RA [9–11]. These studies support that detection of anti-VCM is as useful as the assays determining anti-CCP2 to distinguish RA from healthy controls [12, 13] and can help in the differential diagnosis of RA from other rheumatic disorders [14–16]. Nevertheless, currently, there are no studies in Mexican patients evaluating if the strategy of performing both tests may increase sensitivity and positive predictive value for the presence of established RA as compared to performing them individually.

Therefore, we evaluated the performance of using two ACPA assays: second-generation anti-citrullinated cyclic peptide antibodies (anti-CCP2) and anti-mutated citrullinated vimentin (anti-MCV) antibodies in established RA, and we correlated the titers observed of these autoantibodies with disease activity.

2. Patients Methods

Design. Cross-sectional study.

Clinical Setting. Adult consecutive patients with RA seen in an outpatient rheumatology clinic of a secondary-care center in Guadalajara, Mexico (Hospital General Regional 110, Instituto Mexicano del Seguro Social), were invited to participate if

they met at least four of the 1987 ACR criteria for RA [17]. They were excluded if they had a history of blood transfusion, chronic infectious diseases, including hepatitis B or C, human immunodeficiency virus, or tuberculosis. Patients with overlapping syndrome, cancer, or other associated autoimmune disorders or pregnant patients were also excluded.

These patients were compared with two distinct non-RA controls selected.

- (i) The first comparison group was constituted by patients with other rheumatic inflammatory disorders mainly including systemic lupus erythematosus (SLE, 1982 ACR criteria) [18] or ankylosing spondylitis (AS, 1984 New York modified criteria) [19]. Nevertheless, patients with systemic sclerosis (SSc) and articular manifestations were included if they met the 1980 ACR criteria [20]. All these patients were obtained from the same rheumatology clinic where patients with RA were recruited.
- (ii) The second group was constituted by clinically healthy blood donors obtained from the same hospital, without history of blood transfusion or chronic infections.

For these two comparison groups, similar inclusion and exclusion criteria described for patients with RA were applied.

- 2.1. Clinical Evaluations. A structured assessment for patients with RA was performed including disease characteristics, evaluation of disease activity according to DAS-28 [21], functioning according to the Spanish validated version of HAQ-DI [22], and treatments used.
- 2.2. ACPA Determinations. A venous blood sample was taken from all included subjects at the same time of the clinical evaluation and the serum was obtained and stored at -20° C until antibodies determination. Anti-CCP2 were determined by ELISA using a commercial kit (Axis-Shield, UK) with a cut-off value for positivity >5 U/mL and anti-MCV were determined by ELISA using also a commercial kit (ORGENTEC, Mainz, Germany) with a cut-off value for positivity >20 U/mL.

3. Statistical Analysis

Qualitative variables were expressed as frequencies and percentages and quantitative variables were expressed as means ± standard deviations. Chi-square tests were used to compare proportions among groups and Student's t-test was used to compare means between two groups. We selected as "gold standard" the 1987-ACR criteria for diagnosis of established RA. These criteria were used instead of the most recent 2010-ACR criteria because the status of positive ACPA is included within the criteria. The performance of the assays for anti-MCV and anti-CCP2, either individually or tested together, to identify RA was evaluated estimating sensitivity, specificity, and positive and negative predictive values, as well as likelihood ratios. In this study, sensitivity can be defined as the probability of positive anti-CCP2 or anti-MCV in patients with RA. Specificity was defined as the probability of negative results for these autoantibodies in patients or controls without RA. Positive predictive value (PPV+) was

Table 1: General characteristics in patients with rheumatoid arthritis.

Cl	37 410
Characteristics	N = 142
Age in years, mean \pm SD	49 ± 10.69
Women, <i>n</i> (%)	135 (95)
Disease duration (years), mean ± DE	9 ± 8.07
DAS-28, mean \pm SD	4.7 ± 1.5
DAS-28 > $3.2 n$ (%)	118 (83.1)
HAQ-DI, mean ± SD	0.91 ± 0.65
HAQ-DI > 1.25, n (%)	38 (26.6)
Treatments	
Methotrexate, n (%)	48 (33.8)
Chloroquine, n (%)	4 (2.8)
Leflunomide, n (%)	17 (12)
Azathioprine, <i>n</i> (%)	18 (14)
Etanercept, <i>n</i> (%)	8 (5.6)
Glucocorticoids, n (%)	124 (87.9)
Prednisone mg, mean ± SD	5.7 ± 1.6

SD: standard deviation, mg: milligrams.

DAS-28: disease activity score.

DAS-28: low activity \le 3.2; moderate activity >3.2 y \le 5.1; high activity >5.1. HAQ-DI: Health Assessment Questionnaire-Disability Index: S.

defined as the probability of having RA in presence of anti-CCP2 or anti-MCV. Negative predictive value was defined as the probability of not having RA in presence of a negative result for these autoantibodies. We computed 95% confidence intervals (95% CI) for the utility values for these autoantibodies. Kappa statistics was used to compute the degree of agreement in positivity between both anti-CCP2 and anti-MCV for patients with RA.

Correlation between titers of anti-CCP2 and anti-MCV and variables was examined using Spearman's correlation coefficient. The value of statistical significance was set at a P value of <0.05. All analyses were done with the SPSS program (version 8).

4. Results

One hundred and forty-two patients with RA were included and compared with 86 patients in the group of autoimmune rheumatic diseases (33 with SLE, 44 with AS, and 9 with SSc) and 56 healthy controls.

General characteristics of patients with RA are shown in Table 1. Additional data, not shown in this table, include that 83% of patients with RA had an active disease (DAS-28 index >3.2) and 26.6% had a significant degree of disability (HAQ-DI > 1.25). At the time of the evaluation, most of the patient received glucocorticoids, 56 patients (76%) used a dose of ≤5 mg, which is considered a low dose.

Concordance between the findings of the two assays, anti-CCP2 and anti-MCV, in RA is shown in Table 2. Only around 62% of the patients showed positivity for both assays, anti-CCP2 and anti-MCV, allowing for a Kappa = 0.42 value for Kappa statistics.

TABLE 2: Concordance between the results of assays for anti-CCP2 and anti-MCV in rheumatoid arthritis.

		Anti-CCP2		
		Positive n = 94 (66.2%)	Negative $n = 48 (33.8\%)$	
	Positive			
Anti-MCV	n = 115 (81.0%)	88 (61.97%)	27 (19.01%)	
111111 1110 1	Negative			
	n = 27 (19.0%)	6 (4.22%)	21 (14.78%)	

Total patients with RA assessed = 142, and values in parenthesis represent the percentage of the total 142 patients. Kappa = 0.42.

An evaluation of utility values for the strategies of testing each assay, anti-CCP2 or anti-MCV alone, or testing both assays in established RA compared with clinically healthy blood donors is shown in Table 3. The highest sensitivity was observed when both autoantibodies tests were performed (85%) followed by testing anti-MCV alone (81%), whereas the lowest sensitivity was observed when only anti-CCP2 test was performed. On the other side, specificity and PPV(+) were similar with the three strategies, and the NPV(-) increased substantially, if both assays were negative.

The utility values for the strategies of performing only anti-CCP2 or anti-MCV or both of these assays in established RA compared with other rheumatic inflammatory diseases are shown in Table 4. The highest sensitivity was again observed when both assays were performed (85%) and the lowest sensitivity was attained when using only anti-CCP2 (66%). The highest specificity was observed when only anti-VCM was performed (96%). PPV(+) values were higher with the anti-MCV assay alone (97%), whereas the highest NPV(-) was observed when both assays were negative (79%).

5. Discussion

In our study, we observed that the assay for anti-MCV antibodies showed more sensitivity and specificity than the assay for anti-CCP2 antibodies to distinguish established RA patients from other systemic inflammatory rheumatic diseases. Using the strategy of performing both assays, we obtained an increase in sensitivity in comparison with using either assay individually. In our study, the Kappa between both assays indicates that determination of both tests should be complementary and consequently increases the utility of both tests in the clinical armamentarium without decreasing specificity.

Previous studies have reported, for anti-CCP2, specificities greater than 90% [23–25], similar to our findings where we found a specificity of 92% for CIRD and 94% for CHS, this assay being very useful to exclude people who do not have RA.

Nevertheless, in terms of a screening test, a higher sensitivity is extremely relevant; therefore, strategies to increase the values of sensitivity are required to establish an earlier diagnosis and opportune reference to the rheumatologist. To this regard, in the present study, the utilization of an assay for anti-CCP2 exclusively had only 66% of sensitivity,

Table 3: Utility values of anti-CCP2, anti-MCV, or any of these assays in rheumatoid arthritis in comparison with clinically healthy subjects (CHS).

Utility values of the assays for anti-CCP2 and anti-MCV results	Anti-CCP2	Anti-MCV	Anti-CCP2 or anti-MCV
Sensitivity % (95% CI)	66 (58–74)	81 (73-87)	85 (78–91)
Specificity % (95% CI)	94 (84-99)	94 (84-99)	94 (84–99)
Positive predictive value % (95% CI)	97 (91–99)	97 (93–99)	97 (93–99)
Negative predictive value % (95% CI)	51 (41-61)	65 (53–75)	70 (58-81)
LR+	11.69 (3.87-35.32)	14.31 (4.75-43.07)	15.05 (5-45.28)
LR-	0.36 (0.28-0.46)	0.20 (0.14-0.28)	0.16 (0.11-0.23)
Prevalence	73 (66–79)	73 (66–79)	73 (66–79)

LR+: positive likelihood ratio; LR-: negative likelihood ratio.

4

Table 4: Utility values of anti-CCP2, anti-MCV, or any of these assays in rheumatoid arthritis in comparison with other chronic inflammatory rheumatic diseases (CIRD).

Utility values of the assays for anti-CCP2 and anti-MCV results	Anti-CCP2	Anti-MCV	Anti-CCP2 or Anti-MCV
Sensitivity % (95% CI)	66 (58–74)	81 (73–87)	85 (78–90)
Specificity % (95% CI)	92 (84-97)	96 (90-99)	92 (84–97)
Positive predictive value % (95% CI)	93 (86-97)	97 (93–99)	94 (89–98)
Negative predictive value % (95% CI)	62 (53–71)	75 (66-83)	79 (70–86)
LR+	8.13 (3.96-16.7)	23.22 (7.62-70.77)	10.47 (5.13-21.36)
LR-	0.37 (0.29-0.47)	0.20 (0.14-0.28)	0.16 (0.11-0.24)
Prevalence	62 (67–89)	62 (68-89)	62 (56-68)

LR+: positive likelihood ratio; LR-: negative likelihood ratio.

whereas when both assays, anti-CCP2 and anti-MVC, were done in the same patients, the sensitivity increased to 85%, with an improvement in the utility of these assays as a tool for clinicians. Regarding specificity of anti-CCP2, some studies have shown a wide variability ranging from 40% to 83% [26, 27], the frequency of negatives being a limitation to establish the diagnosis in RA. Genetic factors may contribute to these differences in sensitivity, characteristic of the study population, including variables such as disease duration or severity of the disease, and characteristics of assays used to detect these autoantibodies [28], although, in our study, anti-MCV antibodies were more sensitive than anti-CCP2 antibodies for RA and these findings have been reported by others [29]. To this regard, around 1 of 5 patients with established RA had a negative anti-MCV test result. Therefore, the question arises if the utility value of the test could be increased by using both assays. We observed that using both assays in the same patients the sensitivity increases to 85% with an LR+ of 10.47 in comparison to other CIRD, constituting an excellent support in the clinical armamentarium for RA.

Several factors could contribute to explaining why we observed that the anti-VCM assay was more sensitive than the anti-CCP2 assay. One of them is that vimentin contains 43 arginine residues. Each arginine residue can potentially be citrullinated by peptidylarginine deiminase (PAD) resulting in a variety of citrullinated epitopes. In contrast, in the anti-CCP2 test only a few epitopes are presented [30–32].

Some authors reported recently that combining determinations of anti-MCV, anti-CCP2, and RF increases the sensitivity [15]. Nicaise-Roland et al. [29] described, in a cohort of patients with early RA and undifferentiated arthritis, an

increase in sensitivity when two tests are associated. Therefore, these data support our findings implying gains in clinical utility when two assays for ACPA are applied in the same patient. Our study, however, revealed that still 6% of controls without any rheumatic disorders had positive anti-CCP2 or anti-MCV antibodies; these data are relevant because the presence of a positive antibody without clinical manifestations is insufficient to support the presence of disease, although we ignore it if these patients would have an increase in risk for a CIRD in the future. Cohort studies will help to identify the evolution of these patients with positive anti-MCV.

Some limitations of the study due to its cross-sectional nature are that we were unable to identify if controls without rheumatic disorders who depicted positivity to one or both autoantibodies will have progression to a CIRD in the future; nevertheless, this hypothesis should be tested in cohort models, increasing the number of patients. On the other side, we did not apply these tests to specific subgroups of patients, such as RA with extra-articular manifestations, undifferentiated arthritis, or early RA, where the performance of these diagnostic tests may have substantial variations to those observed in defined RA. Another limitation was that we did not include an assay for testing anti-CCP3. Anti-CCP3 assays rely upon additional epitopes not present in the anti-CCP2 antigen sequence [33, 34]. Szekanecz et al. evaluated the sensitivity of cyclic citrullinated antibodies second-generation (anti-CCP2) and third generation (anti-CCP3 and anti-CCP3.1); the diagnostic sensitivity of anti-CCP2 was 74.8%, anti-CCP3 was 78.8%, and anti-CCP3.1 was 83.0%; the specificity of anti-CCP2 was 95.7%, anti-CCP3 was

96.6%, and anti-CCP3.1 98.3% [35]. However, Shidara et al. show no evident increase in utility values when comparing anti-CCP3 and anti-CCP2 assays; the sensitivity of anti-CCP2 was 89.5%, whereas; the sensitivity of anti-CCP3 was 91.5% and specificity was 87.7% [36]. An assay for anti-CCP3 may provide an increase in sensitivity as compared to that observed with the assay for anti-CCP2 used in this study.

In conclusion, using both assays, anti-CCP2 and anti-MCV, increases the sensitivity for the presence of RA as compared to performing only one assay; therefore, this strategy should be included in the clinical armamentarium to improve the value of these assays as screening test.

Ethical Approval

The Institutional Research Committee of the Hospital approved Project number R-2009-1301-57. All the included patients and controls signed a voluntary informed consent. This protocol followed the guidelines of the Helsinki declaration.

Conflict of Interests

All the authors declare that there is no conflict of interests to disclose.

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Research Article

Renal Transplantation in Systemic Lupus Erythematosus: Outcome and Prognostic Factors in 50 Cases from a Single Centre

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Background. End-stage renal disease (ESRD) is an important cause of morbidity and mortality in patients with systemic lupus erythematosus (SLE). Objectives. To analyze the outcome and prognostic factors of renal transplantation in patients with ESRD due to SLE from January 1986 to December 2013 in a single center. Results. Fifty renal transplantations were performed in 40 SLE patients (32 female (80%), mean age at transplantation 36 ± 10.4 years). The most frequent lupus nephropathy was type IV (72.2%). Graft failure occurred in a total of 15 (30%) transplantations and the causes of graft failure were chronic allograft nephropathy (n = 12), acute rejection (n = 2), and chronic humoral rejection (1). The death-censored graft survival rates were 93.9% at 1 year, 81.5% at 5 years, and 67.6% at the end of study. The presence of deceased donor allograft (P = 0.007) and positive anti-HCV antibodies (P = 0.001) negatively influence the survival of the renal transplant. The patient survival rate was 91.4% at the end of the study. Recurrence of lupus nephritis in renal allograft was observed in one patient. Conclusion. Renal transplantation is a good alternative for renal replacement therapy in patients with SLE. In our cohort, the presence of anti-HCV antibodies and the type of donor source were related to the development of graft failure.

1. Introduction

Systemic lupus erythematosus (SLE) is the prototype of systemic autoimmune disease characterized by widespread immunologic abnormalities and multiorgan involvement including the skin, joints, lungs, heart, central and peripheral nervous system, and kidney [1]. In fact, SLE may be considered as a syndrome rather than a single disease [2].

Considering renal involvement, 40% of the SLE patients have lupus nephritis at some stage of their disease [3]. However, the prevalence of lupus nephritis varies around the world with higher rates observed in some ethnic groups, including Mestizos [4], African American, Hispanics living in the United States, and Asian compared with Caucasian [5].

Lupus nephritis is an important cause of morbidity and mortality in patients with SLE [6–8]. Of the different pathological classes, diffuse proliferative glomerulonephritis (class IV) has the worst prognosis, and end-stage renal disease (ESRD) develops in a range from 3.5 to 17% [5, 9–11]. Ethnicity, male sex, younger age, high activity histopathologic degree, interstitial fibrosis, impaired renal function at presentation, arterial hypertension as well as delay in treatment, and poor compliance are some of the unfavorable prognostic factors for ESRD in patients with lupus nephritis [12].

Recent surveys indicate that renal transplantation is associated with good outcomes in patients with ESRD due to lupus nephritis that are, in general, similar to transplant recipients with ESRD due to other causes [13, 14]. Of note,

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some factors of the recipient have been associated with poor outcome such as the black race, the positivity of anti-phospholipid antibodies (aPL), the peritoneal dialysis, the poor clinical conditions at the time of transplantation, and the poor treatment compliance [13, 14]. In addition, longer pretransplantation dialysis period was associated with more acute rejection in a series of Chinese SLE patients [15]. Recurrent lupus nephritis after kidney transplantation occurs in a range from 0% to 30% according to the clinical or histopathologic definition [16–18] but graft loss occurs because recurrent lupus nephritis is rare [13, 14, 19].

The objective of this study was to analyze the outcome and prognostic factors of renal transplantation in patients with ESRD due to SLE from our center.

2. Methods

2.1. Patients. We examined the medical records of patients diagnosed as having SLE whose cause of ESRD (defined as the need of chronic dialysis therapy or kidney transplantation) was primarily lupus nephritis, who required renal transplantation from January 1986 to December 2013. All patients have been systematically assessed at the Department of Autoimmune Diseases and the Department of Nephrology and Renal Transplantation of Hospital Clinic. All patients fulfilled four or more of the 1982 revised classification criteria for SLE of the American College of Rheumatology [20]. In all cases, histological class of lupus nephritis was defined according to the International Society of Nephrology/Renal Pathology Society (ISN/RPS) 2003 classification system [21].

2.2. Variables. From the patients' records, we have documented the following data: gender, age at onset of SLE, onset of clinical renal disease, and time between SLE diagnosis and lupus nephritis and between lupus nephritis and onset of dialysis. Antinuclear antibodies and aPL status, including anti-cardiolipin antibodies (aCL) and lupus anticoagulant (LA), anti-hepatitis B (HBV) and C virus (HCV), and antihuman immunodeficiency virus (HIV) antibodies, were also collected. Finally, SLE treatment prior to ESRD, duration and modalities of dialysis prior to transplantation, date of transplantation, age at transplantation and time between lupus nephritis and transplantation, donor source, posttransplantation immunosuppressive therapy used (especially the use of prednisone, mycophenolic acid, cyclosporine A, and tacrolimus), follow-up time after transplantation, lupus relapse rate and graft, and patient survival were recorded. Regarding immunosuppressive treatment, it was the same for SLE and no SLE patients. Cyclosporine A, tacrolimus, and mycophenolic acid were used according to the transplant era. Induction therapy with anti-lymphocytesantibodies was used according to the anti-HLA immunological risk.

We determined flare-ups of lupus activity and recurrence of lupus nephritis by clinical and laboratory variables. Graft failure was defined as the need to restart chronic dialysis therapy or retransplantation. 2.3. Statistical Analysis. Qualitative variables are shown by frequency distributions. Quantitative variables are summarized as a mean \pm standard deviation (SD). Kolmogorov Smirnov test was used for evaluation of normality. A comparison of demographic and clinical characteristics between groups (i.e., graft failure and functioning graft) was performed using Mann-Whitney U-test and for categorical data Fisher's exact test was used. Patient and graft survival rates were calculated with Kaplan-Meier survival curves. Patient deaths with a functioning graft were censored for the graft survival analysis. All statistical tests were two sided and assessed at P=0.05 significance level. Statistical analyses were performed using SPSS software, version 20.0.

3. Results

In the above mentioned period, a total of 3274 renal transplantations were performed in our hospital, 50 (1.5%) of them in 40 SLE patients (32 female (80%)). Overall, 29 transplantations were from a deceased donor whereas 21 were from living donor. In 34 (68%) cases, a first transplantation was performed and in twelve (24%) and four (8%) cases, a second and a third transplantation were performed, respectively. The main demographic and clinical characteristics, histological class of lupus nephritis, immunologic features, and treatments are described in Table 1.

3.1. Renal Graft Survival Rates. The death-censored graft survival rates were 93.9% at 1 year, 81.5% at 5 years, and 67.6% at the end of the study (Figure 1). Clinical recurrence of lupus nephritis in renal allograft was observed in only one patient in form of membranous glomerulonephritis and chronic allograft nephropathy. Graft failure occurred in a total of 15 (30%) transplantations and the causes of graft failure were chronic allograft nephropathy (n = 12), acute rejection (n = 2), and chronic humoral rejection (n = 1).

3.2. Patient Survival Rates. The patient survival rates were 97.9% at 1 and 5 years and 91.4% at the end of the study. Four patients died at 17.6, 11, 10, and 9.4 years of the first renal transplantation, respectively. The first case was a woman who received three renal transplantations, dying as a result of Pseudomona aeruginosa sepsis. The second deceased patient was a woman with cirrhosis and HCV chronic infection who received two renal transplantations, dying as a result of E. coli sepsis. The third patient developed a coronary artery disease and died as a complication of this pathology. Finally, the forth one was a man who died because of a dilated myocardiopathy.

3.3. Comparison between Patients with Graft Failure versus Those with Functioning Grafts. When patients with graft failure versus functioning graft at time of the study were compared, we did not find significant differences in gender, age at SLE diagnosis, dialysis modality, and age at transplantation (Table 2). Of note, time on dialysis was longer in patients with graft failure (73.9 \pm 60.6 versus 35.7 \pm 35.4, P = 0.011). Conversely, the mean elapsed time between diagnosis

TABLE 1: Demographic and clinical characteristics, histological and immunologic features, and treatments used in the cohort of SLE transplanted patients.

Gender female 32 (80%) Ethnicity 38 (95%) Caucasians 38 (95%) Hispanics 2 (5%) Age at SLE diagnosis (years) 36 ± 10.4 Time between SLE diagnosis and lupus nephritis (months) 28.4 ± 65.1 Time between lupus nephritis and onset of dialysis (months) 50 ± 49.4 Time between diagnosis of lupus nephritis and transplantation (months) 71.4 ± 41 Histological diagnosis at onset of lupus nephritis: 118 ± 69 Type IV 26 (72%) Type III 3 (8%) Type V 2 (5%) Type VI 1 (3%) Interstitial nephritis 1 (3%) Thrombotic microangiopathy 1 (3%) Unknown 4 (10%) Number of transplantation 34 (68%) Second transplantation 12 (24%) Third transplantation 29 (58%) Living donor 29 (58%) Living donor 29 (58%) Living donor 21 (42%) HLA identical siblings 4 (19%) Other genetically related 13 (62%)	Demographic characteristics	
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Anti-phospholipid antibodies 12 (63%) Treatments Cyclosporine/tacrolimus 19/27 Azathioprine/mycophenolic acid 6/38 Sirolimus 3 ATG/OKT3/Basiliximab/no induction 23/1/9/17		
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Cyclosporine/tacrolimus19/27Azathioprine/mycophenolic acid6/38Sirolimus3ATG/OKT3/Basiliximab/no induction23/1/9/17		12 (63%)
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Sirolimus 3 ATG/OKT3/Basiliximab/no induction 23/1/9/17		
ATG/OKT3/Basiliximab/no induction 23/1/9/17		
Graft failure (%) 15 (30%)		
		15 (30%)

Quantitative variables are presented as mean \pm standard deviation and qualitative variables as number (percentage). Treatments are presented as number of transplantations.

SLE: systemic lupus erythematosus; ATG: antithymocyte globulin; OKT3: orthoclone

of lupus nephritis and start of dialysis was higher in those patients with functioning grafts (88.7 \pm 80.6 versus 39.0 \pm 45.5, P=0.038). Graft failure was significantly higher in patients receiving a kidney from a deceased donor compared

to living donors (P = 0.007, OR 10.0, 95% confidence interval [CI] 1.62–62.85) (Table 2).

As posttransplant immunosuppression therapy, all patients received prednisone and different immunosuppressive therapies (Table 2). The election of the different immunosuppressive treatment was related to the working protocol used in this moment in nephrology and renal transplant unit. Although the differences in the outcome could be related to a multifactorial origin, the majority of patients with graft failure were in the cyclosporine era. In fact, the majority of renal transplantations with graft failure were transplanted before 1998 (53% versus 17%; P=0.036).

No patient had antibodies against HIV. Positive anti-HCV antibodies were detected in 22 (44%) patients; one of them was simultaneously positive for hepatitis B virus (chronic infection). The number of patients with HCV positive serology was significantly higher in the group of patients who had graft failure, whereas in 12 of them, the transplant outcome was toward the graft failure. Studies of association between graft loss and the presence of HCV positive serology showed a positive association (P = 0.001, OR 12.5 CI 95% [2.50–63.34]) (Table 2). When association studies were performed considering the type of donor source (deceased or living donor) and HCV positive serology, both remained as statistical significant prognostic factor of graft failure.

3.4. Retransplantation Cases. The retransplantation cases were analyzed separately from the main group. Overall 16 additional transplantations were performed (7 from a deceased donor and 9 from a living donor). In all cases, the initial lupus nephropathy was type IV. There were 6 graft failures whose causes were chronic allograft nephropathy (n=5) and acute rejection (n=1). In one patient with negative aPL and chronic allograft nephropathy, renal arterial and venous thrombosis involving medium-sized vessel wall were observed.

3.5. Anti-phospholipid Antibodies and Renal Transplantation. Nineteen patients (48%) had at least two aPL determinations, 12 (63%) of them being positive (5 with IgG aCL plus LA, 4 with IgG aCL only, 2 with IgM aCL plus LA, and one with LA plus IgM plus IgGaCL), and only two of them had antiphospholipid syndrome. Within this group, one of the patients that previously received two renal transplantations suffered graft loss due to intraparenchymal graft thrombosis. In another case, a patient suffered the loss of two consecutive grafts due to thrombotic microangiopathy. In both patients, previous studies were negative for aPL, starting to be positive just before the third renal transplant.

4. Discussion

In the present study, we have found a graft survival rate of 93.9% at 1 year, 81.5% at 5 years, and 67.6% at the end of the study and the patient survival rates were 97.9% at 1 and 5 years and 91.4% at the end of the study. These observations are similar to those reported in other recent studies from other

Table 2: Comparison of demographic features, clinical characteristics and treatment between SLE patients with graft failure and functioning graft.

	Graft failure ($n = 15$)	Functioning graft ($n = 35$)	P
Gender female (%)	14 (93%)	27 (77%)	0.169
Age at diagnosis SLE (years)	22.4 ± 10	22.8 ± 11	0.758
Age at renal Tx (years)	41.3 ± 10.2	38.7 ± 12.0	0.280
Time SLE-nephritis (months)	17 ± 42.6	34.9 ± 75	0.412
Time nephritis dialysis (months)	39 ± 45.5	88.7 ± 80.6	0.038
Time on dialysis (months)	73.9 ± 60.6	35.7 ± 35.4	0.011
Time nephritis-Tx (months)	114.6 ± 64.2	120 ± 73.3	0.880
Dialysis before renal Tx (%):			
HD	14 (93.3%)	19 (76.0%)	0.168
CAPD	2 (13.3%)	7 (28.0%)	0.251
HD and CAPD	1 (6.7%)	3 (12.0%)	0.516
Tx date (years)	1998 ± 7	2004 ± 6	0.036
Donor source (%):			
Cadaveric	13 (86.7%)	16 (45.7%)	0.007
Living donor	2 (13.3%)	19 (54.3%)	_
Immunosuppressive regimen at Tx (grafts) (%):			
Cyclosporine A	10 (66.6%)	9 (25.7%)	0.006
Mycophenolic acid	8 (53%)	31 (88.6%)	0.003
Tacrolimus	4 (27%)	23 (66%)	0.012
Positive anti-HCV antibodies (patients) (%)	12 (80%)	10 (28.6%)	0.001
Positive aPL antibodies (%)	1 (6.7%)	11 (31.4%)	0.058

Quantitative variables are presented as mean ± standard deviation and qualitative variables as number (percentage).

SLE: systemic lupus erythematosus; Tx: transplantation; HD: hemodialysis; CAPD: continuous ambulatory peritoneal dialysis; HCV: hepatitis C virus; aPL: anti-phospholipid antibodies.

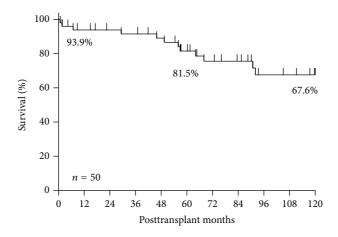


FIGURE 1: Death-censored graft survival rates at 1, 5, and 10 years.

single centers including patients from different ethnicities [22–27]. The main cause of graft failure was chronic allograft nephropathy, which is similar to data previously reported for SLE patients and also for non-SLE transplant recipients [28].

4

Currently, graft and patient survival of SLE patients undergoing renal transplantation are similar to those found in renal transplant recipients from other causes. These concepts are supported by the results of the European Transplant Registry and by a cohort of patients in the United States (United States Renal Data System) [13, 29]. However, other

authors describe different results with lower graft survival and increased mortality in patients with SLE [30]. This difference may be explained at least partly, by methodological differences between studies in terms of prospective or retrospective design, inclusion criteria, control group, and different time of renal transplantation or recruitment period. Moreover, a retrospective study analyzed 8001 patients with SLE and renal transplantation showed that graft and patients survival were higher in those patients who received a preemptive renal transplantation compared with those who were treated with

hemodialysis previously (hazard ratio [HR] 0.69; 95% CI 0.55–0.86, P < 0.01 versus HR 0.52; 95% CI 0.38–0.70, P < 0.01, resp.) [31]. In fact, in the current series, time on dialysis was significantly shorter in patients with functioning graft. Thus, as in other diseases with ESRD, renal transplantation is considered the procedure of choice for renal replacement therapy in patients with SLE [31].

In our series, relapsing lupus nephritis was found only in one case (2%). The recurrence rate of lupus nephritis was reported initially to be around 1-4% [32, 33]. However, immunofluorescence and electron microscopy studies performed in renal biopsies of SLE transplanted patients detected a rate of recurrent lupus nephritis of 30% [19, 34, 35]. However, it does not seem to negatively affect allograft or patient survival [19, 34]. Interestingly, Norby et al. [17] found a recurrence of lupus nephritis in 54% of renal biopsies from 41 SLE patients with renal transplant. However, the majority of them were subclinical in form of histological class I or II. Of note, 83% of the transplanted kidneys presented with signs of chronic allograft nephropathy, regardless of the presence or absence of lupus nephritis. Similar results of recurrence of lupus nephritis have been described in a Chinese kidney transplant cohort of 32 SLE patients [22].

Our results showed that factors that negatively influenced the survival of the renal transplant were the presence of deceased donor allograft (P=0.007), positive anti-HCV antibodies (P=0.001), and a longer time on dialysis before transplantation (P=0.011). In retrospective studies performed on databases, the deceased donor allograft recipients have worse outcomes compared with living allograft recipients [30] and African American and Caucasian Americans have similar allograft failure rates [36].

A particular feature of this series is the high number of patients with HCV infection, mainly located in the group of transplant failure, showing a significant positive association with the lower graft survival (OR 12.5, 95% CI 2.50-63.34), in the same manner as that described in non-SLE patients [37, 38]. Recent evidence documents that the concomitant HCV infection in patients with lupus nephritis is associated with worse renal outcome, higher rate of progression to ESRD, and reduced patient survival [39]. In a retrospective study involving 1624 patients with positive serology for HCV undergoing kidney transplant, Batty et al. [40] found a higher mortality (HR 1.23; 95% CI 1.01–1.49, P = 0.04) and higher rate of hospitalization in patients positive for HCV compared with patients serologically negative. A recent systematic review collecting 18 series described the negative impact of HCV infection in the outcome of renal transplantation, with increased mortality (HR 1.69; 95% CI 1.33–1.97, P < 0.0001) and graft loss (HR 1.56; 95% CI 1.22-2.004, P < 0.0001) [41]. However, in the last two studies [40, 41], lupus nephropathy was not specifically analyzed. Although the intimate pathogenic mechanisms by which HCV induces a negative impact on renal graft remain to be known, there is some evidence attributing to plasmatic viremia and anti-HCV antibodies themselves a possible pathogenic role impairing the kidney function or inducing the development of chronic nephropathy allograft [37, 42].

The reason why HCV recipients are overrepresented in this cohort of patients is probably related to the high rate of repeated transplantations. Twenty-two transplants in HCV positive recipients were distributed between 13 patients: 5 patients with one, 7 patients with two, and one patient with three transplants. By contrast within the 28 transplants in HCV negative recipients, there were 26 patients with one transplant and one patient with two transplants. Many of those HCV positive patients initiated dialysis therapy before the HCV screening test was available.

In our series, the use of mycophenolic acid, tacrolimus, and negative aPL determinations seem to be related with better renal graft survival, supporting the possible multifactorial origin of the improved performance. Moreover, thanks to methodological advances in transplantation procedure, the use of mycophenolic acid and tacrolimus in recent years partly explain the significant differences found in our series, thus, supporting the benefit of their use.

As shown in our series, coronary artery disease was one of the causes associated with mortality in the outcome. Recent studies demonstrate a reduction in cardiovascular risk with the administration of fluvastatin in patients with lupus recipients of kidney transplantation [43]. Two more patients died because of sepsis, probably related to immunosuppressive treatment.

Thrombotic events have been reported more frequently in renal transplantation recipients with aPL worsening their functional prognosis [14, 23]. In a recent study, the presence of LA at the time of renal transplantation was associated with a high rate of allograft nephropathy associated with antiphospholipid syndrome and poor transplantation outcomes [44]. In the current series, aPL determinations were available in 19 patients, because the systematic screening in the renal transplant unit was carried out only in recent years. In the present series, the allograft failure was related to thrombosis and thrombotic microangiopathy associated with the presence of aPL in two cases; therefore their detection as well as their repetition in the time, despite their negativity, should be recommended in the pretransplantation period.

Current study had some limitations. Due to the retrospective design of our analysis, some points such as the role of activity of SLE in the graft failure or the role of sociodemographic and environmental factors such as educational level, socioeconomic status, or smoking could not be analyzed. Moreover, the limited number of SLE patients who received kidney transplantation is the reason why some significant associations should be considered with caution as indicated by the wide range of confidence intervals. In the data collected, the number of patients with aPL determinations performed before or at the time of kidney transplantation was low; therefore the association between these antibodies and the thrombotic complications was weak and not significant.

Renal transplantation is a good alternative for renal replacement therapy in patients with SLE, but the existence of HCV positive serology and a thrombotic disease associated with the aPL could be related to the development of graft failure. In our series, the patient and graft survival rates as well as factors associated with these end points are similar to that of ESRD caused by other diseases.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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Research Article

Low Levels of CD36 in Peripheral Blood Monocytes in Subclinical Atherosclerosis in Rheumatoid Arthritis: A Cross-Sectional Study in a Mexican Population

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Patients with rheumatoid arthritis (RA) have a higher risk for atherosclerosis. There is no clinical information about scavenger receptor CD36 and the development of subclinical atherosclerosis in patients with RA. The aim of this study was to evaluate the association between membrane expression of CD36 in peripheral blood mononuclear cells (PBMC) and carotid intima-media thickness (cIMT) in patients with RA. *Methods*. We included 67 patients with RA from the Rheumatology Department of Hospital Civil "Dr. Juan I. Menchaca," Guadalajara, Jalisco, Mexico. We evaluated the cIMT, considering subclinical atherosclerosis when >0.6 mm. Since our main objective was to associate the membrane expression of CD36 with subclinical atherosclerosis, other molecules related with cardiovascular risk such as ox-LDL, IL-6, and TNF α were tested. *Results*. We found low CD36 membrane expression in PBMC from RA patients with subclinical atherosclerosis (P < 0.001). CD36 mean fluorescence intensity had negative correlations with cIMT (P = -0.578, P < 0.001), ox-LDL (P = -0.427, P = 0.05), TNF α (P = -0.729, P < 0.001), and IL-6 (P = -0.822, P < 0.001). *Conclusion*. RA patients with subclinical atherosclerosis showed low membrane expression of CD36 in PBMC and increased serum proinflammatory cytokines. Further studies are needed to clarify the regulation of CD36 in RA.

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1. Introduction

Rheumatoid arthritis (RA) is a chronic autoimmune disease with systemic complications and early cardiovascular death [1]. RA patients are prone to develop atherosclerosis at a relatively young age.

Atherosclerosis and inflammation in RA share several mechanisms in their pathogenesis including proinflammatory cytokine expression, infectious agents, dyslipidemia, and autoantibodies [2–8].

Type B scavenger receptors (SR), like CD36, are molecules possibly involved in the pathogenesis of atherosclerosis. During atherogenesis, blood monocytes are recruited into the intima and subintima layers of blood vessels; were they internalize oxidized low density lipoproteins (ox-LDL) through SR (CD36). This process results in the activation of monocytes and their differentiation into macrophages and foam cells. As a consequence, matrix metalloproteinases, proinflammatory cytokines, and chemoattractants enhance inflammatory infiltrates and vascular remodeling [9, 10]. CD36 has a critical role in the atherosclerotic plaque development [11–14]. However, their role in cardiovascular complications of RA has not been studied.

The aim of this study was to evaluate the association between membrane expressions of CD36 in peripheral blood mononuclear cells (PBMC) with carotid intima-media thickness (cIMT) in patients with RA without known traditional cardiovascular risk factors.

2. Methods

2.1. Patients. We recruited RA patients that met ACR 1987 criteria [15], from the Hospital Civil "Dr. Juan I. Menchaca" at Guadalajara, Jalisco, Mexico. Patients with known cardiovascular risk factors such as history of myocardiopathy, hypertension, diabetes mellitus, hyperlipidemia, malignancy, thyroid, renal or hepatic disease, smokers and steroid treatment >10 mg/day were excluded.

A structured questionnaire was applied to each patient to evaluate demographical and clinical variables. Physical examination, joint assessment, and venous blood drawn were performed at the visit.

- 2.2. Clinical Assessment. Disease activity was evaluated using Disease Activity Score 28 (DAS28) and C-reactive protein (CRP).
- 2.3. cIMT. It was assessed according to the recommendations defined by the Mannheim carotid intima-media thickness and plaque consensus (2004–2006–2011) [16] by a single operator using a high-resolution B-mode ultrasound (Philips Saronno, Italy) with a 9 MHz transducer. Two segments from the common carotid artery (CCA), one from the carotid bifurcation (BF), and two from the internal carotid artery (ICA) were evaluated. Mean cIMT values were calculated for each segment. Patients were classified according to the cIMT with a cut-off point of 0.6 mm.

2.4. Laboratory Assessment. Serum was obtained by centrifugation of whole blood at 2,000 rpm for 15 minutes; aliquots with serum were stored at -70°C for no longer than 6 months. Erythrocyte sedimentation rate (ESR) was measured using Wintrobe method and CRP by immunoturbidimetry (assay range 0.3–161 mg/L, Randox laboratories limited); total cholesterol (TC), triglycerides (Tg), high density lipoprotein cholesterol (HDL-c), and low density lipoprotein cholesterol (LDL-c) were measured by routine methods. Cardiovascular risk ratio was calculated using the atherogenic index of plasma (AIP) which was defined as TC/HDL-c. Anticyclic citrullinated peptide (CCP) antibodies (intra-assay variation coefficient (VC) < 9% and interassay VC < 11%, Axis-Shield Diagnostics Ltd.), serum interleukin (IL)-6 (intra-assay VC 5.1%-7.7% and interassay VC 6.5%-9.3%, Invitrogen), tumor necrosis factor (TNF) α (intra-assay VC 4.2%-5.2% and interassay VC 4.6%-7.4%, R&D Systems), and ox-LDL (intraassay VC 3.9%-5.7% and interassay VC 9.0%-11.0%, ALPCO Diagnostics) were measured by enzyme-linked immunosorbent assay (ELISA).

The flow cytometric analysis was performed using fluorescein isothiocyanate- (FITC-) conjugated mouse monoclonal antibodies against human CD36 and PE conjugated anti-human CD14 (BioLegend). PBMC were obtained by density gradient centrifugation using a lymphocyte separation solution. The cells were washed twice with phosphate buffered saline (PBS) and fixed with 1% paraformaldehyde for 20 minutes at 4°C. After being washed with PBS, 5×10^6 cells in $50 \,\mu$ L PBS were incubated with FITC or PE-conjugated monoclonal antibodies for 30 minutes at 4°C. The cells were then washed twice before being assayed with a flow cytometer (Beckman Coulter, Epic XL, Miami, FL, USA) and analyzed with the software WinMDI 2.9.

- 2.5. Statistical Analyses. Values are presented as mean \pm standard deviation (SD) and percentages as appropriate. Between-group differences were estimated by independent-sample Student's t-test. Chi-square test (or Fisher's exact test) was used to compare categorical variables. Spearman's correlation coefficient was calculated for cIMT, DAS28, CRP, anti-CCP, IL-6, and TNF α . All data were analyzed using SPSS 18.0 software (SPSS Inc., Chicago, IL) and replicated using the software Stata 12.0 (StataCorp LP, Texas, USA), considering a two-tailed level of P < 0.05 statistically significant.
- 2.6. Ethics. Protocol was approved by the IRB committee (register number 1068/10) of the Hospital Civil "Dr. Juan I. Menchaca" of the Benemérita Universidad de Guadalajara.

3. Results

Sixty-seven patients were included in this study; 60 (89.5%) were female, with a mean (SD) age of 44.2 (11.9) years old; 29 (43.28%) had evidence of increased cIMT. Table 1 shows the comparison of RA subgroups with and without increased cIMT. No statistical differences in age, disease duration, and disease activity were observed between higher and lower cIMT groups. The increased cIMT group (>0.6 mm) showed

Table 1: Characteristics and comparison of RA subgroups with and without increased cIMT.

Variable	Study	groups	P
variable	$cIMT \le 0.6 mm$	cIMT > 0.6 mm	1
	n = 38	n = 29	
Age, years	42.58 ± 11.43	47.74 ± 12.54	0.14
RA characteristics			
Disease duration, years	4.52 ± 4.46	3.40 ± 5.50	0.47
DAS28, units	2.73 ± 0.98	3.48 ± 1.12	0.03
Lipid profile			
TC, mg/dL	176.39 ± 34.83	239.78 ± 44.31	< 0.001
Tg, mg/dL	136.87 ± 58.22	195.33 ± 63.95	0.002
HDL-c, mg/dL	51.87 ± 15.34	36.74 ± 8.40	< 0.001
LDL-c, mg/dL	109.00 ± 24.50	111.45 ± 27.74	0.75
VLDL-c, mg/dL	27.79 ± 10.91	32.85 ± 16.10	0.17
ox-LDL, mg/dL	55.62 ± 5.38	219.48 ± 98.58	< 0.001
AIP, TC/HDL-c	3.66 ± 1.26	6.77 ± 1.72	< 0.001
Serological profile			
ESR, mm/h	24.03 ± 19.67	21.14 ± 9.03	0.52
RF, IU/mL	97.18 ± 101.12	134.18 ± 133.94	0.61
CRP, mg/L	3.83 ± 2.61	13.29 ± 6.31	< 0.001
TNFα, pg/mL	64.72 ± 9.28	104.75 ± 17.49	< 0.001
IL-6, pg/mL	29.03 ± 3.43	99.45 ± 11.29	< 0.001
Anti-CCP, U/mL	73.22 ± 65.92	154.62 ± 97.70	0.004
Flow cytometry			
CD36, MFI	170.43 ± 38.80	67.09 ± 27.50	< 0.001
DMARDs			
Methotrexate, n (%)	36 (94.7)	29 (100)	0.14
Time of use, years	4.51 ± 4.42	3.30 ± 5.27	0.06
Chloroquine, n (%)	21 (55.3)	15 (51.7)	1.00
Sulfasalazine, <i>n</i> (%)	9 (23.7)	4 (13.8)	0.52
Azathioprine, n (%)	6 (15.8)	4 (13.8)	1.00
Corticosteroids, n (%)	3 (7.9)	1 (3.5)	0.45

RA: rheumatoid arthritis; cIMT: carotid intima-media thickness; DAS28: disease activity score; TC: total cholesterol; Tg: triglycerides; HDL-c: high density lipoprotein cholesterol; LDL-c: low density lipoprotein cholesterol; VLDL-c: very low density lipoprotein cholesterol; AIP: atherogenic index of plasma; ESR: erythrocyte sedimentation rate; RF: rheumatoid factor; CRP: C-reactive protein; TNFα: tumor necrosis factor alpha; IL: interleukin; anti-CCP: anticyclic citrullinated peptides; MFI: mean fluorescence intensity; DMARDs: disease-modifying antirheumatic drugs.

Qualitative variables are expressed as frequencies (%); quantitative variables are expressed as means \pm standard deviations (SD). Comparisons between proportions were computed using Chi-square or Fisher exact test. Comparisons between medians were computed with unpaired Student's t-test.

higher serum levels of TC (P < 0.001), Tg (P = 0.002), ox-LDL (P < 0.001), and AIP (P < 0.001) and lower serum levels of HDL-c (P < 0.001) compared with the cIMT group (<0.6 mm). Serum levels of CRP, TNF α , IL-6, and anti-CCP also were higher in the increased cIMT group (P < 0.001).

3.1. CD36 PBMC Membrane Expression. RA patients with increased cIMT showed lower levels of CD36 compared with no increased cIMT (67.09 \pm 27.50 versus 170.43 \pm 38.80, P < 0.001).

The PBMC membrane expression of CD36 MFI was significantly lower in patients with moderate and high disease activity ($n = 22, 64.31 \pm 16.72$), when compared to patients

with low disease activity ($n = 11, 129.78 \pm 13.73$) or in remission ($n = 34, 158.2 \pm 13.66$) (P < 0.05).

3.2. Correlations Coefficients between cIMT, Clinical, and Laboratory Characteristics of RA Patients. Correlation coefficients between cIMT and characteristics of RA patients are shown in Table 2. cIMT was negatively correlated with CD36 MFI and HDL-c and positively correlated with age, TC, Tg, AIP, anti-CCP, TNF α , IL-6, CRP, and ox-LDL.

Figure 1 showed a negative correlation between CD36 MFI with TNF α (r=-0.729, P<0.001) and IL-6 (r=-0.822, P<0.001). In data not shown, we observed a negative correlation of CD36 MFI with ox-LDL (r=-0.841, P<0.001).

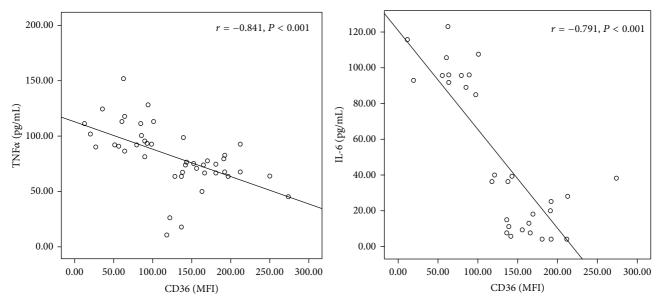


FIGURE 1: Correlation between serum TNFα, IL-6, and CD36 MFI.

TABLE 2: Correlation coefficients between cIMT and characteristics of the groups evaluated.

Baseline variable	cIMT	cIMT (mm)		
Daseille variable	r	P		
Age, years	0.564	< 0.001		
Disease duration, years	-0.063	0.65		
DAS28, units	0.159	0.26		
TC, mg/dL	0.331	0.03		
Tg, mg/dL	0.393	0.009		
HDL-c, mg/dL	-0.316	0.04		
LDL-c, mg/dL	0.285	0.06		
VLDL-c, mg/dL	0.270	0.07		
ox-LDL, mg/dL	0.457	0.007		
AIP, TC/HDL-c	0.687	0.01		
ESR, mm/h	-0.180	0.24		
RF, IU/mL	-0.001	0.99		
CRP, mg/L	0.579	0.001		
TNFα, pg/mL	0.552	0.002		
IL-6, pg/mL	0.681	< 0.001		
Anti-CCP, U/mL	0.393	0.05		
CD36	-0.578	< 0.001		

cIMT: carotid intima-media thickness; RA: rheumatoid arthritis; DAS28: disease activity score; TC: total cholesterol; Tg: triglycerides; HDL-c: high density lipoprotein cholesterol; LDL-c: low density lipoprotein cholesterol; VLDL-c: very low density lipoprotein cholesterol; AIP: atherogenic index of plasma; ESR: erythrocyte sedimentation rate; RF: rheumatoid factor; CRP: C-reactive protein; TNF α : tumor necrosis factor alpha; IL-6: interleukin 6; anti-CCP: anticyclic citrullinated peptide antibodies; MFI: mean fluorescence intensity. Spearman r test.

4. Discussion

4

In this study, we showed that RA patients with subclinical atherosclerosis showed low membrane expression of CD36

in PBMC and increased serum proinflammatory cytokines (Table 1). The CD36 PBMC membrane expression was negatively correlated with cIMT, ox-LDL, TNF α , and IL-6 (data not shown). We described a positive correlation between age, TC, Tg, ox-LDL, AIP, CRP, TNF α , IL-6, and anti-CCP antibodies with cIMT (Table 2).

In endothelial cell cultures exposed to IL-6 and TNF α , upregulation of the scavengers receptors- (SR-) A and ox-LDL receptor- (LOX-) 1 was shown but not CD36 expression. Endothelial cells stimulated with human sera rich in IL-6 and TNF α from RA patients; the CD36 expression increased and was not modified by IL-6 or TNF α antagonists. This suggests that a different factor present in the serum of these patients, like ox-LDL, may be responsible for the upregulation of CD36 [17].

TNF α promotes atherosclerosis through the inhibition of cholesterol efflux, favoring the cholesterol uptake by CD36 and other SR via protein kinase pathway. In THP-1 cells in the presence of ox-LDL, TNF α impaired the cholesterol efflux by downregulation of ATP-binding cassette (ABCA) proteins [18].

Boyer et al. showed the downregulation of membrane expression and mRNA levels of CD36 in culture of fresh PBMC from healthy donors in the presence of human recombinant TNF α . In other experiment incubating PBMC with a humanized TNF α blocker (Adalimumab), the membrane and mRNA CD36 increased [19]. The authors concluded that different pathways were involved in the regulation of CD36. When TNF α was used, the signaling was mediated by a reduction in activated peroxisome proliferator-activated receptor gamma, whereas Adalimumab increased CD36 through redox signaling.

In our report, the membrane CD36 in PBMC was decreased in RA patients with higher cIMT; besides, a negative correlation between TNF α and membrane CD36 MFI was found. These support the findings observed in

endothelial cells and PMBC cultures reported by Boyer et al. [19]. However, these results must be corroborated by further studies using similar approaches as described before.

In our patients, another possible explanation for the low levels of CD36 might be the proteolytical cleavage by ADAM17, which might result in more soluble CD36 [20]. It has been reported the protective role of the CD36 polymorphism, G573A, in plaque thickness in patients with early coronary artery disease [21].

In a more detailed analysis of our results, we looked for the influence of disease duration and treatment. We found that, RA patients with normal cIMT had longer disease duration and lower levels of TNF α and IL-6 (Table 1) probably due to the benefit of prolonged use of antirheumatic drugs in the prevention of subclinical atherosclerosis [22]. *In vitro* studies using methotrexate (MTX) favor the cholesterol efflux through activation of adenosine A2 receptor, which in turn prevents the foam cell differentiation and atherosclerosis plaque formation [23, 24]. MTX might downregulate serum TNF α in RA [25]. A large study that enrolled more than 8,000 patients using synthetic DMARDS compared with anti-TNF α users (11,000 approximately) showed a reduction in cardiovascular risk in both groups, even though the reduction was greater in the anti-TNF α treated patients [26, 27].

Based on our results, low PBMC CD36 membrane expression showed a negative correlation with cIMT, ox-LDL, TNF α , IL-6, and DAS28. From the clinical standpoint, the interaction between these factors might reflect the importance of CD36 in the development of atherosclerosis in RA.

5. Conclusion

RA patients with subclinical atherosclerosis showed low membrane expression of CD36 in PBMC and increased serum proinflammatory cytokines. Translation of the results from these studies to the clinical field is difficult since the functional role of CD36 depends on the target cell. Further studies are needed to validate our findings and clarify the downregulation of CD36 in RA.

Conflict of Interests

The authors declare that they do not have conflict of interests.

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Clinical Study

Diagnosis of Latent Tuberculosis in Patients with Systemic Lupus Erythematosus: T.SPOT.TB versus Tuberculin Skin Test

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Early studies in patients with systemic lupus erythematosus (SLE) reported increased incidence of tuberculosis. The tuberculin skin test (TST) is the technique of choice to detect latent tuberculosis infection (LTBI) but has several limitations. *Objectives*. We compared TST and the newer T.SPOT.TB test to diagnose LTBI in SLE patients. *Methods*. In this observational cohort study conducted between August 2009 and February 2012, we recruited 92 patients from those attending the SLE clinic of our university hospital. Data recorded were epidemiological and sociodemographic characteristics. Laboratory analyses included TST and T.SPOT.TB tests. *Results*. Of the patients studied, 92% were women with an average age of 42.7 years. Overall, the degree of correlation between the two tests was low (Kappa index = 0.324) but was better in patients not receiving corticosteroids (CTC)/immunosuppressive (IS) therapy (Kappa = 0.436) and in those receiving hydroxychloroquine (Kappa = 0.473). While TST results were adversely affected by those receiving CTC and/or IS drugs (P = 0.021), the T.SPOT.TB results were not. *Conclusion*. Although the TST test remains a useful tool for diagnosing LTBI in SLE patients, the T.SPOT.TB test is perhaps better employed when the patient is receiving CTC and/or IS drugs.

1. Introduction

SLE is an autoimmune disease of unknown aetiology, which can affect any organ and system [1]. Due in part to this and the IS treatment administered, the patients with SLE have a high risk of acquired infections, which constitute one of the principal causes of death in this group of patients [2, 3]. To date, there have been several studies published on subjects with SLE that have shown an increased incidence of tuberculosis (TB) in the lung and nonlung tissue, compared to the general population [4–12]. Among the different risk factors implicated in the development of TB is the use of CTC.

Hence, it is recommended that the diagnosis of LTBI is made, even in the general population, before initiating treatment [13].

The Mantoux test (or the TST tuberculin skin test or the purified protein derivative (PPD)) remains the classical technique in the detection of LTBI but has several limitations including the higher probability of false negatives in immune-compromised patients and, as well, false positives not only in those vaccinated with BCG (*Bacillus* Calmette-Guérin) but also in those who had had a previous infection with nontuberculosis *Mycobacterium* [14].

Newer techniques of LTBI detection, based on the determination of interferon gamma release assays (IGRAs), have been used in different types of patients and different geographic areas in order to evaluate their usefulness. According to a meta-analysis and systematic review of the recent literature [15], the calculated specificity of T.SPOT.TB in the diagnosis of LTBI was approximately 98% (95% CI: 86.8 to 99.9%) and 89% for the TST (95% CI: 84.6 to 92%). But this meta-analysis had some limitations, including a low number of studies evaluated in calculating the specificity of the IGRAs. In another meta-analysis published earlier in the nonvaccinated population [16], the sensitivity of T.SPOT.TB was 90% (95% CI: 86 to 93%) and 77% for the TST (95% CI: 71 to 82%). The sensitivity was calculated based on studies composed of patients with confirmed TB, and the conclusion was that the measurement of T.SPOT.TB had greater sensitivity than Quantiferon-TB Gold (QTF-2G) which was indicated as being more useful in immune-compromised patients.

To date, there have been only 2 articles comparing QTF-2G [17, 18] with TST for the diagnosis of LTBI in patients with SLE. The inconvenience of both studies is that they were performed in areas where vaccination with BCG was already in effect. This limits the extrapolation of the data to our country where it has not been recommended by the majority of the autonomous governments of several regions of Spain [14]. There have not been comparisons between the efficacy of IGRAs such as Quantiferon-TB Gold In-Tube (QTF-3G) or the T.SPOT.TB versus TST. There is no information available on the patients being treated for LTBI based on the results obtained or the usefulness of the new IGRAs in standard clinical practice. Finally, there are no studies in our geographical area of Europe (i.e., Spain) that evaluated the usefulness of IGRAs in patients with SLE.

Hence, we proposed analysing, in patients with SLE falling within our remit of healthcare provision, the concordance between T.SPOT.TB and TST in the diagnosis of LTBI. The secondary objective was to generate a protocol for the diagnosis of LTBI in these patients.

2. Patients and Methods

The study was cross-sectional, observational between August 2009 and February 2012. Following written informed consent, 92 patients with SLE were recruited from those attending the Clinic of the Systemic Autoimmune Disease of the Hospital Universitario Virgen de las Nieves (Granada, Spain). The patients needed to have fulfilled 4 or more diagnostic criteria of the American College of Rheumatology (ACR). Those patients <18 years of age and those judged to be mentally unable to provide independent consent had the consent obtained from the parents or guardians. The study was approved by the ethics committee of the hospital and the data were coded to maintain anonymity.

At the baseline clinical visit, a personal history was taken. Information sought included zone of residence, risk factors for TBL (including profession, contact history, and family status) BCG vaccination, age, gender, months since diagnosis of the disease (disease duration), other associated

immunosuppressant diseases, current treatment for SLE, history of TST, or previous treatment for LTBI. Laboratory tests performed included full blood screening, urine analysis, antinuclear antibody (ANA), C3, C4, lymphocyte populations, TST and booster (to the patients initially nonresponsive to TST and repeated within 7–20 days), T.SPOT.TB, and chest X-ray. The Systemic Lupus Erythematosus Disease Activity Index (SLEDAI) and Systemic Lupus International Collaborating Clinics (SLICC) organ damage index were determined. Patients diagnosed with LTBI, and for whom treatment was indicated [19], had the appropriate treatment initiated, provided existing active TB was not present.

2.1. Definition of Variables

- (i) TST was considered positive according to the criteria of the American Thoracic Society [19] when >5 mm and the patient was receiving IS treatment or >15 mg prednisone for >1 month or >10 mm in the rest of the cases.
- (ii) T.SPOT.TB positive, negative, or indeterminate were according to the criteria of our laboratory, using standard techniques (Oxford Immunotec, Oxford, UK). A typical result would be expected to have few or no spots in the Nil control and >20 spots in the Positive Control. In cases where the negative (Nil) control had ≤10 spots, the result was defined as positive if Panel A-Nil and/or Panel B-Nil had ≥8 spots. If the Nil control had >10 spots or Positive Control had <20 spots, the result was considered indeterminate. If the above criteria were not met, the result was defined as negative. (Available at http://www.oxfordimmunotec.com/USpageInsert.)</p>
- (iii) Patients were considered immunocompromised if receiving treatment with the following drugs: mycophenolate, methotrexate, tacrolimus, leflunomide, azathioprine, cyclophosphamide, and/or CTC at whatever dose.
- (iv) The two tests were considered concordant when the same results were obtained for both of them.
- (v) The diagnosis of TBL was considered when any of the tests were positive (TST or T.SPOT.TB).
- (vi) Prednisone dose was considered physiologic at <7.5 mg/day [13].
- (vii) Normal levels of dsDNA according to our local laboratory values were $0-30\ UI/mL$.

3. Materials and Methods

The TST was performed with an injection in the ventral surface of the forearm, of 0.1 mL PPD (variant RT-23), at a dose of 5 UT; the result is to be read within 72 hours. The TST was performed by trained personnel.

The IGRA technique used was the T.SPOT.TB (Oxford Immunotec) which is a technique that counts the T effector cells that respond to stimulation by antigens of *Mycobacterium tuberculosis* (ESAT-6 and CFP10). The technique was

applied and monitored by qualified personnel of the Clinical Analysis Laboratory of our hospital.

3.1. Statistical Analyses. Descriptive analyses of the principal variables included calculated means and standard deviation for the quantitative variables and absolute and relative frequencies for the qualitative variables. Bivariate analyses were performed to evaluate the variables associated with the diagnosis of LTBI with the two tests employed (TST and T.SPOT.TB). Quantitative variables following a normal distribution were analysed with Student's t-test or the Mann-Whitney test for those variables nonnormally distributed. The qualitative variables were analysed with Pearson's χ^2 test or the Fisher test. Significance level was set at P < 0.05.

The degree of concordance between the two tests was determined with the Kappa index. The results of the tests were evaluated using the classification of Landis and Koch in which a value of $\kappa < 0.20$ would be poor, 0.21–0.40 weak, 0.41–0.60 moderate, 0.61–0.80 good, and 0.81–1.00 very good agreement.

The diagnostic precision of the study was measured as the total accuracy value.

The SPSS statistics package (version 19) was used throughout.

4. Results

4.1. Description of the Patient Cohort; Results of TST and T.SPOT.TB. 92 consecutive patients were included in the study with SLE, of whom 92% were female. The mean age was 42.7 years (range: 14–77 years). The demographic, clinical, and laboratory variables are summarised in Table 1.

Of the 92 patients, the T.SPOT.TB was positive in 5 (5%), indeterminate in 4 (4%), and negative in 83 (90%). The TST was positive in 6 patients (7%) and negative in 86 (94%) (Table 2). Positive LTBI (whether with TST or with T.SPOT.TB) was diagnosed in 9 patients (10%). As such, the prevalence of LTB in our SLE patients in the study was 10%.

Diagnostic precision or efficiency (total accuracy) of the evaluation was 92%.

The degree of concordance between the two tests in the overall study population was low, according to the Kappa index ($\kappa = 0.324$). When this concordance was analysed only in those patients not treated with CTC or IS drugs, the values improved ($\kappa = 0.436$), as well as in those receiving hydroxychloroquine ($\kappa = 0.473$) (Table 3).

During the period of study, we diagnosed 9 patients with LTBI. We did not identify any patients with active TB. There were 3 patients (33%) who received treatment for LTBI, of whom 2 (22%) needed to have their medication suspended because of digestive intolerance, nausea, and epigastric discomfort. No severe adverse effects of grades III-IV was recorded. Of the patients diagnosed as having LTBI (n=9), 1 (11%) did not wish to receive treatment, 2 (22%) were lost to the study having moved out of the area, and 3 (33%) did not begin treatment due to decision by the attending physician, one for having active chronic liver disease due to HCV and another due to being T.SPOT.TB

negative. One patient was TST positive, without any personal history of risk or X-ray findings of fibrotic tracts suggestive of prior infection. These 3 patients had not been receiving IS treatment or CTC for several years.

4.2. Univariate Analyses. Of the patients, 64% were receiving CTC or other IS drugs; 24% received CTC alone, and 40% received both. Comparing the CTC-alone group with the combination therapy group, the latter had greater organ damage (P=0.05) and were predominantly women (P=0.023) but with no statistically significant differences with respect to TST or T.SPOT.TB. We did not find significant differences between those patients receiving daily doses of prednisone, above and below 7.5 mg dose. As such, we considered only two groups in the statistical analyses, that is, those with and those without IS treatment.

The results of TST were affected in patients receiving CTC and/or IS; that is, in this group of patients there was a greater number of TST negative, with only 17% of cases being positive (OR: 10.30; 95% CI: 0.011–0.866; P=0.02). Further, the patients with TST negative had been receiving IS (P=0.048) and CTC (P=0.008) treatment for a longer period of time. The rest of the variables analysed did not significantly influence the TST outcome (Table 4).

The results of T.SPOT.TB were not affected by IS (except for a prolonged treatment with mycophenolate) or CTC. However, age had a significant influence; that is, older patients were diagnosed with LTBI in more occasions with T.SPOT.TB than with TST (P=0.002) (Table 5). Conversely, we found that having an initial positive TST was associated with a greater probability of T.SPOT.TB being positive (P=0.033). Indeterminate T.SPOT.TB results were related to a longer time to diagnosis (duration) of the disease (P=0.028) and SLICC organ damage index (P=0.002) (Table 6).

There were no statistically significant associations between TST/T.SPOT.TB results and IS therapies such as tacrolimus (P = 0.71/P = 0.73), leflunomide (P = 0.68/P = 0.71), azathioprine (P = 0.57/P = 0.60), and cyclophosphamide (P = 0.79/P = 0.81).

Finally, we observed that the patients receiving hydroxy-chloroquine had a higher grade of concordance between the two tests (P = 0.007).

5. Discussion

Tuberculosis is an important public health problem world-wide. In the European Union (EU) it continues to be an unresolved issue, with considerable differences between countries and, over the past few years, the rates of multiresistant infections have increased [20]. Overall levels within the EU are improving. However, despite known underreporting in Spain, there are considerable differences between autonomous regions of Spain with respect to control of the disease [21].

The prevalence of LTB in our study was 10%, which coincides with the percentage of patients with risk factors for tuberculosis (9.8%). Our study was conducted in a zone considered low with respect to incidence of TB within

TABLE 1: Clinical and laboratory characteristics of the SLE patients studied.

Clinical characteristics	
Age, years, mean ± SD	42.71 ± 14.88
Females, n (%)	85 (92.4)
SLE diagnosis duration, months (IQR)	132 (60–216)
Risk factor for LTBI, <i>n</i> (%)	9 (9.8)
BCG vaccinated, n (%)	
Nonvaccinated	90 (97.8)
Vaccinated	2 (2.2)
Treatment regimen, n (%)	
<7.5 mg prednisone	39 (42.4)
>7.5 mg prednisone	18 (19.6)
IS drugs	37 (40.2)
Hydroxychloroquine	79 (85.9)
SLEDAI, mean \pm SD	3.33 ± 2.73
Laboratory findings	
dsDNAn levels, median (IQR)	14.50 (4.77–44.75)
$C3 \text{ mg/dL}$, mean $\pm SD$	96.97 ± 21.45
$C4 \text{ mg/dL}$, mean $\pm SD$	16.50 ± 7.64
Lymphocyte cells/uL, mean ± SD	1527.65 ± 585.26
CD4 cells/uL, ±SD	644.82 ± 283.29
CD4 (%)	
≤200	2.3
200–500	26.1
≥500	71.6
CD8 cells/uL, ±SD	495.67 ± 256.89
B cells/uL, median (IQR)	119.80 (65.35–215.40)
NK cells/uL, median (IQR)	167.50 (110.50-229.90)

TABLE 2: Results of TST and T.SPOT.TB.

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Results of TST	R	Results of T.SPOT.TB		
Results of 131	Negative Positive Indeterminate			
Negative	79	3	4	86
Positive	4	2	0	6
Total	83	5	4	92

TABLE 3: Correlation between TST and T.SPOT.TB tests.

SLE patients	Kappa value
All patients	0.324
Patients not receiving IS/CTC	0.436
Patients receiving hydroxychloroquine	0.473

Europe [22] and represents the first study of its kind in a nonvaccinated population of SLE patients.

In our group of patients with SLE, CTC (irrespective of the dose) and other IS drugs negatively affect the results of the TST, which results in an underdiagnosis of the disease when only the TST test is employed. We have observed this event principally with CTC, mycophenolate, and methotrexate, these patients having a 10-fold higher probability of a negative TST. No statistically significant differences with

other IS drugs (tacrolimus, leflunomide, azathioprine, and cyclophosphamide) were noted, probably due to the limited number of patients in the study. The use of CTC can cause anergy at low doses due to the alterations that are produced, principally, on cellular immunity and including, in isolated cases, humoral immunity [23]. On the other hand our results showed that positive TST was correlated with positive T.SPOT.TB, indicating the reliability of the TST. The test continues to be the test of choice for LTBI detection in patients with non-IS medication-related lupus. Our results suggest that T.SPOT.TB could be the diagnostic tool of choice for diagnosis of LTBI in patients with IS and also demonstrated greater usefulness than TST in older patients. These results need to be confirmed in further studies with a higher number of SLE patients selected from a geographic area with an incidence of tuberculosis similar to ours.

In studies published to date, there has been an increase in indeterminate T.SPOT.TB results in patients with SLE receiving IS [24]. The percentage of indeterminate values in our study was 4.3% and was similar to the 2.5% observed in the study by Yilmaz et al. [17] but much lower than the 32.4% observed by Takeda et al. [18]. This high value was considered to have resulted from the high levels of SLEDAI, lymphopenia, and the presence of the disease. In our series of patients, the percentage of indeterminate values was related

TABLE 4: TST positive versus TST negative patients. Univariate analyses.

Clinical and laboratory findings	TST positive $(n = 6)$	TST negative ($n = 86$)	P value
Age, years, mean ± SD	49.50 ± 14.69	42.23 ± 14.86	0.25
Patients with risk factors for LTBI, <i>n</i> (%)	2 (33)	7 (8)	0.10
SLE duration, median (IQR)	90 (21–237)	144 (60–225)	0.72
SLEDAI, mean \pm SD	2.83 ± 3.37	3.37 ± 2.7	0.64
SLICC, median (IQR)	0 (0-1)	0 (0-1)	0.78
dsDNAn, UI/mL, median (IQR)	29 (2.45-61.25)	13.50 (4.77–42.75)	0.71
Prednisone $> 7.5 \text{ mg/d}, n \text{ (\%)}$	0 (0)	18 (32)	0.68
Immunosuppressed patients, n (%)	1 (17)	58 (98.3)	0.021
Hydroxychloroquine treatment, n (%)	4 (66)	75 (87)	0.19
Steroid dose, mg, mean ± SD	0.83 ± 2.04	4.09 ± 4.92	0.11
Steroid cumulative dose, mg, mean ± SD	2275 ± 4056.32	19019.35 ± 22249.92	0.001
Cumulative steroids/disease duration, mg/year, mean ± SD	309.06 ± 742.74	1696.47 ± 1433.26	0.021
Mycophenolate dose, mg, mean \pm SD	0	267.55 ± 538.20	0.001
Mycophenolate cumulative dose, mg, mean ± SD	0	643743.02 ± 1329836.44	0.001
Cumulative mycophenolate/disease duration, mg/year, mean \pm SD	0	76986.98 ± 160990.33	0.001
Methotrexate dose, mg, mean ± SD	0	1.30 ± 3.33	0.001
Methotrexate cumulative dose, mg, mean \pm SD	0	336.98 ± 801.21	0.001
Cumulative methotrexate/disease duration, mg/year, mean \pm SD	0	49.35 ± 132.52	0.001

TABLE 5: T.SPOT.TB positive versus T.SPOT.TB negative patients. Univariate analyses.

Clinical and laboratory findings	T.SPOT positive $(n = 5)$	T.SPOT negative ($n = 87$)	P value
Age, years, mean ± SD	62.40 ± 12.75	41.57 ± 14.25	0.002
Patients with risk factors for LTBI, n (%)	1 (20)	8 (9.2)	0.41
SLE disease duration SLE, median (IQR)	174 (135–357)	126 (60–207)	0.10
SLEDAI, mean \pm SD	2.4 ± 2.5	3.39 ± 2.75	0.43
SLICC, median (IQR)	0 (0-0.75)	0 (0-1)	0.53
dsDNAn, UI/mL, median (IQR)	13.70 (2.05–33)	14.50 (3.72–45.50)	0.65
Daily prednisone $> 7.5 \text{ mg}, n \text{ (\%)}$	1 (20)	17 (19.5)	0.53
Immunosuppressed patients, n (%)	2 (40)	57 (65.5)	0.56
Hydroxychloroquine treatment, n (%)	4 (80)	75 (86.2)	0.54
Steroid dose, mg, mean \pm SD	3 ± 4.47	3.93 ± 4.89	0.67
Steroid cumulative dose, mg, mean \pm SD	18486 ± 18460.34	17895.22 ± 22196.28	0.94
Cumulative steroids/duration of disease, mg/year, mean ± SD	1076.41 ± 1099.36	1636.42 ± 1454.14	0.40
Mycophenolate dose, mg, mean ± SD	216 ± 482.99	252.06 ± 529.19	0.88
Mycophenolate cumulative dose, mg, mean ± SD	4800 ± 10733.12	636067.81 ± 1324014	0.001
Cumulative mycophenolate/disease duration, mg/year, mean ± SD	23.52 ± 52.61	76100.72 ± 160264.94	0.001
Methotrexate dose, mg, mean \pm SD	0	1.29 ± 3.32	0.38
Methotrexate cumulative dose, mg, mean \pm SD	216 ± 482.99	320.69 ± 794	0.77
Cumulative methotrexate/disease duration, mg/year, mean \pm SD	1.05 ± 2.36	48.72 ± 131.88	0.42

to the greater time since diagnosis (duration of the disease) and higher levels of SLICC. However, we did not observe association with the activity of the disease despite having a homogeneous population comparable to that described in other studies. This leads us to believe that our cohort was well controlled, with a mean SLEDAI around 3. We did not find association between a high activity and low TST reaction, as had been described earlier by Pascual-Ramos et al. [25] whose study indicated that the inactive-disease patients present greater TST reaction than the active-disease

patients. In their study, in contrast to ours, the mean level of SLEDAI was around 7.

In analysing the levels of lymphocyte populations in our patients, we observed that the levels of CD4 and CD8 were maintained stable despite the high percentage of lymphocytopenia recorded (58.1%) and, as such, a response to T.SPOT.TB was possible. In contrast to previous studies in patients with SLE [17, 18] in which an ELISA assay was used, our study employed a technique in which the polymorphonuclear cells were separated from the peripheral

TABLE 6: T.SPOT.TB indeterminate versus T.SPOT.TB determinate results. Univariate analyses.

Age years mean + SD	Indeterminate T.SPOT.TB ($n = 4$)	Determinate T.SPOT.TB ($n = 88$)	P value
1.5c,) care, mean = 0.	55.50 ± 13.17	42.13 ± 14.76	0.079
Patients with risk factors for LTBI, n (%)	1(25)	8 (9)	0.34
SLE disease duration, median (IQR)	318 (117–351)	138 (60–207)	0.028
SLEDAI, mean ± SD	2.25 ± 1.25	3.38 ± 2.78	0.42
SLICC, median (IQR)	1 (1–1.75)	0 (0-1)	0.002
dsDNAn, UI/mL, median	13.5 (6.77–332.75)	14.50 (3.72-43.50)	0.85
Prednisone > 7.5 mg/d, n (%)	0 (0)	18 (33.3)	0.31
Immunosuppressed patients, n (%)	3 (75)	56 (63.6)	0.64
Hydroxychloroquine treatment, n (%)	2 (50)	77 (87.5)	0.94
Steroid dosage, mg, mean ± SD	2.62 ± 2.05	3.94 ± 4.93	0.59
Steroid cumulative dose, mg, mean ± SD	35745.62 ± 27062.79	17117.40 ± 21498.45	0.09
Steroid cumulative dose/disease duration, mg/year, mean \pm SD	1766.47 ± 1248.49	1598.69 ± 1451.84	0.82
Mycophenolate dose, mg, mean \pm SD	0	261.47 ± 533.49	0.001
Mycophenolate cumulative dose, mg, mean \pm SD	0	629112.50 ± 1317998.72	0.001
Mycophenolate cumulative dose/disease duration, mg/year, mean ± SD	0	75237.27 ± 159546.95	0.001
Methotrexate dose, mg, mean \pm SD	1.25 ± 2.5	1.22 ± 3.28	0.98
Methotrexate cumulative dose, mg, mean \pm SD	150 ± 300	322.50 ± 793.78	99.0
Cumulative methotrexate dose/disease duration, mg/year, mean \pm SD	13.63 ± 27.27	47.61 ± 131.30	09.0

blood to guarantee that, in the detection assay, a normalised number of cells (i.e., cells per unit volume) were used; this refinement is more useful in patients with immune systems alterations [26].

CTC use in low and moderate doses results in slight reductions in the T lymphocytes in the peripheral circulation (more CD4 than CD8). The consequence is a delayed hypersensitivity response and unlinked cutaneous anergy [27]. This event could affect the TST result, but the outcomes of the T.SPOT.TB are not affected by cutaneous anergy.

Hydroxychloroquine, widely administered in patients with SLE, has an immune-modulatory effect and, as has been highlighted in other studies, is a protective factor against infections [28]. In our study, this role is highlighted as the concordance between TST and T.SPOT.TB in patients receiving hydroxychloroquine, that is, a higher correlation between the two tests in this group of patients.

The overall concordance between T.SPOT.TB and TST in our patients with SLE was low. These findings are similar to those previously published [17, 18]. However, when the patients are segregated with respect to treatment with IS or CTC, those not receiving this treatment have an improved concordance, an event that needs to be confirmed in further studies. In this aspect, our results are different from those published [17] in which the concordance improved when patients treated with IS and CTC are included in the overall analysis. This could be due to differences between populations studied, for example, vaccination of 97.4% in some studies versus only 2.2% in ours. One difficulty with this study is that the use of TST for the diagnosis of LTBI is inappropriate in populations with higher percentage of vaccination (97.4%), due to the number of false positives being higher.

Studies conducted in zones similar to ours in which the prevalence of TB is similar to ours [13] have demonstrated how the treatment with CTC, including that at a dose of 7.5 mg/day, increased the risk of TB. Based on these data, and taking into account that CTC treatment is employed in the great majority of patients with SLE and that many of them have been on treatment over many years, we propose a standard procedure for the outpatient clinic. This focusses on a screening test for LTBI in the evaluation of all patients with a recent diagnosis of SLE. For a diagnostic protocol of LTBI in patients with SLE, many of whom will have been on treatment for several years, we propose the following.

- (1) For patients without IS or CTC, we would initially perform a TST. If this was positive and there is no history of vaccination, we would treat the LTBI. If the TST was negative, we would administer a booster over two weeks and, in the case of repeated negativity, the diagnosis of LTBI is excluded.
- (2) In patients receiving CTC or IS we propose to proceed directly to T.SPOT.TB and make clinical decisions based on the results.

One of the principal limitations of our study, and the diagnosis of LTBI, is that there is no "gold standard" test to compare the results. Hence, we need to compare the different

techniques employed in each specific population to evaluate the usefulness. Another limitation is the number of patients. Due to the low incidence of TB in our geographic area and the low incidence of SLE in the general population, the number of patients recruited into the study was limited. This limitation would be reduced if the study was multicentred and included geographic areas with incidences of TB similar to ours. However, the multicentred studies carry other limitations too.

6. Conclusions

Based on our findings, we conclude that, in patients with SLE who are not on treatment with CTC or other IS drugs, the TST test continues to be a useful technique for the diagnosis of LTBI in our (Spanish) environment. In case the patient is receiving CTC (irrespective of dose) and/or other IS drugs, the result of the TST can be affected, increasing the number of false negatives. In these cases, T.SPOT.TB test would be the diagnostic technique of choice. Neither SLE by itself nor its activity appears to influence the TST result, the IS treatment being responsible for alterations in these results. Finally, in the patient with lupus, greater damage to organs and time of clinical evolution of the disease (disease duration) have a higher risk of indeterminate T.SPOT.TB resulting, perhaps, from deterioration of the cellular immune system.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

Authors' Contribution

Maria Del Mar Arenas Miras contributed to study design, recruitment of patients, patient management, interpretation of the data, drafting the paper, final version of the paper, and overall responsibility for the integrity of the study. Carmen Hidalgo-Tenorio contributed to study design, patient management, interpretation of the data, drafting the paper, and collaboration in the final version. Pilar Jimenez-Gamiz contributed to laboratory analyses and interpretation of the data. Juan Jiménez-Alonso contributed to patient management, drafting the paper, and overall responsibility for the integrity of the study.

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Research Article

Commercial Bovine Proteoglycan Is Highly Arthritogenic and Can Be Used as an Alternative Antigen Source for PGIA Model

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Rheumatoid arthritis (RA) is the most common systemic autoimmune disease. It affects mainly the joints, causing synovitis, cartilage destruction, and bone erosion. Many experimental models are used to study the mechanisms involved in immunopathogenesis and new therapies for this disease. Proteoglycan-induced arthritis (PGIA) is a widely used model based on the cross-reactivity of injected foreign (usually human) PG and mice self-PG. Considering the complexity of the extraction and purification of human PG, in this study we evaluated the arthritogenicity of bovine PG that is commercially available. Bovine PG was highly arthritogenic, triggering 100% incidence of arthritis in female BALB/c retired breeder mice. Animals immunized with bovine PG presented clinical symptoms and histopathological features similar to human RA and other experimental models. Moreover, bovine PG immunization determined higher levels of proinflammatory and anti-inflammatory cytokines in arthritic mice compared to healthy ones. As expected, only the arthritic group produced IgG1 and IgG2a antibodies against PG. Thus, commercial bovine PG can be used as an alternative antigenic source to PGIA for the study of many RA aspects, including the immunopathogenesis of the disease and also the development of new therapies.

1. Introduction

Rheumatoid arthritis (RA) is a chronic inflammatory disease that affects around 0.3 to 1% of the world population, with lower prevalence in developing countries [1]. It is considered the most common systemic autoimmune disease that usually affects the small joints, especially fingers. It may also involve larger joints, including shoulders, elbows, knees, and ankles. The inflammatory process in the joint is characterized by synovitis, cartilage destruction, and bone erosion. There is still no consensus on the autoantigens involved in this disease. Currently, it is known that some autoantigens such as

cartilage components, chaperone proteins, enzymes, nuclear proteins, and citrullinated proteins might be involved [2, 3]. Among several cell types found in the inflamed joint, CD4+ T-cells' subsets are considered the most important cells involved in synovitis and RA development [4]. Activated macrophages are also a very relevant source of inflammatory mediators, including proinflammatory cytokines [5]. TNF- α and IL-1, for example, promote the accumulation of inflammatory cells in the joints and the synthesis of other cytokines, chemokines, and matrix metalloproteinases [6]. Many cytokines, including IL-8, TNF- α , and IFN- γ , have been detected in synovial fluid. These cytokines, especially

TNF- α , activate resident synovial cells that by producing proteolytic enzymes mediate the destruction of joint cartilage, ligaments, and tendons. Recently, the presence of IL-17 at the site of inflammation and its synergistic effect with TNF- α , exacerbating the inflammatory process, have been evidenced [7]. The participation of B cells in RA has been more investigated in recent years. The production of autoantibodies and cytokines, presentation of autoantigens to T cells, and ectopic lymphoid organogenesis are their possible roles [8]. Regulatory T cells have also been widely studied in both human and experimental arthritis because of their therapeutic and prophylactic potential [9].

There are several experimental models of arthritis being used to elucidate the mechanisms involved in the immunopathogenesis of RA. Also, the animal models are essential to study new therapy targets for this disease. Historically, the first experimental models of arthritis, which are called adjuvant-induced arthritis (AIA), were based on the inoculation of mycobacterial components suspended in mineral oil. Later, it was discovered that this model could be improved by using pristane, which is a purified component of mineral oil. The disease caused by pristane was more similar to human RA and this model has been widely used [10-12]. After that, there was an increased interest in experimental models based on the inoculation of cartilage components such as type II collagen and proteoglycan. These models presented clinical, immunological, histopathological, and genetic characteristics typical from human RA and, for that reason, they were considered the best models to study mechanisms and possible treatments for arthritis [13, 14]. In the 90s, the first arthritis transgenic models were described. By using immunogenetic tools, Keffer et al. [15] observed a spontaneous arthritis in mice overexpressing human TNF- α transgene. In this study, the animals developed a chronic inflammatory polyarthritis that evidenced the critical role of TNF- α in the immunopathogenesis of RA. Currently, collagen-induced arthritis (CIA) is a very reliable and reproducible experimental model that is being widely used for the study of all aspects of arthritis, including the immunopathogenesis of RA, the development of new drugs from natural extracts, the new molecular targets for treatment, and also gene therapy [16-19].

The experimental model chosen for this study was based on the immunization of BALB/c mice with proteoglycan (PG). Proteoglycan-induced arthritis (PGIA) was elegantly described by Glant et al. [13]. Briefly, the systemic autoimmune arthritis in this model is induced by intraperitoneal inoculation of BALB/c or C3H mice with PG isolated from various sources. Many genetic and immunological aspects of PGIA have already been studied in this model. For example, epitopes recognized by the arthritogenic T cells and the contribution of various cytokines such as IFN-y, IL-4, and IL-12 were determined [20-22]. Although human cartilage is the preferable source of PG, its extraction and purification is a complex and laborious process that includes a variety of biochemical steps. Besides, ethical issues and rules involving the utilization of biological samples from human and animals contribute to complicate PG purification. In this scenario, we investigated the possible arthritogenicity of bovine PG

in BALB/c mice. We considered that this evaluation could be very beneficial to researchers that are not able to purify human PG. Commercial availability of bovine PG could not only facilitate the experimental model implementation but also facilitate the comparison of results obtained by different laboratories.

2. Materials and Methods

2.1. Animals. Female BALB/c retired breeder (beyond the reproductive age) mice were removed from breeding colonies by the age of 8–11 months and purchased from CEMIB (Campinas, SP, Brazil). They were maintained in the Department of Microbiology and Immunology facility under controlled conditions of luminosity (12 h light/12 h dark) and temperature (22 \pm 2°C). Mice were allocated in ventilated cages with sterile pine shavings and received sterile food and filtrated water ad libitum. The manipulation of the animals was in compliance with the local ethics committee (Protocol number 257-CEEA).

2.2. Arthritis Induction and Score Evaluation. As previously described [23], with minor modifications, a dose (100 μ L) containing 100 µg of bovine proteoglycan extracted from nasal septum (Sigma Aldrich, St. Louis, MO, USA) and 1 mg of emulsified (micelle form) dodecyl dioctadecyl ammonium bromide (DDA) adjuvant (Sigma Aldrich, St. Louis, MO, USA) was intraperitoneally injected three times with 21day interval for arthritis induction. After the third injection, arthritis score was daily evaluated until euthanasia (70 days after the first immunization). Arthritis severity was determined using a standard visual scoring system based on the degree of swelling and redness ranging from 0 to 4 for each paw. The following system was used: 0 = normal; 1 = mildswelling in the paw or one joint; 2 = moderate swelling and redness in the paw and one or more joints; 3 = pronounced swelling and redness in the paw, all joints, and ankle; 4 = severe swelling and redness of the entire paw and ankle and movement limitation. This classification resulted in a total score that ranged from 0 to 16 for each animal.

2.3. Histopathological Analysis. After euthanasia, mice paws were collected and fixed in 10% formalin phosphate buffer for at least seven days at room temperature. The samples were thoroughly demineralized in 10% Titriplex EDTA disodium salt (Merck Millipore, Darmstadt, Germany) for one to two months. The decalcified tissues were trimmed, dehydrated in graded ethanol, and embedded in paraffin. Serial sections (5 μ m) were cut and mounted on glass slides precoated with 0.1% poly-L-lysine (Sigma Aldrich, St. Louis, MO, USA). Histological assessment was carried out following routine hematoxylin and eosin (HE) staining. The images were acquired by a digital camera attached to the optical microscope (Nikon, Kurobanemuko, Otawara, Japan).

2.4. Immune Responses Evaluation. For cellular immune response, spleens were collected after euthanasia and the cells resuspended in RPMI medium containing gentamicin

and fetal calf serum. The cells were stimulated with ConA $(5 \,\mu\text{g/mL})$ and PG $(50 \,\mu\text{g/mL})$. After 48 hours incubation at 37°C/5% CO₂, the supernatants were collected for detection of IL-2, IL-6, TNF- α , IL-17, IFN- γ , IL-5, and IL-10. These cytokines were quantified using enzyme linked immunosorbent assay (ELISA), according to the manufacturer's instructions (BD Biosciences, San Jose, CA, USA, and RD Systems, Minneapolis, MN, USA). For humoral immune response, blood samples were collected by facial vein two days before each dose and seven days after the third dose of PG+DDA. 70 days after the first immunization, the blood was collected by cardiac puncture. The sera were obtained by blood centrifugation (6000 rpm for 15 minutes at 25°C). Briefly, Maxisorp plates (Nunc, Life Technologies, USA) were coated with 5 μg/mL of bovine PG (Sigma Aldrich, St. Louis, MO, USA) and nonspecific protein binding was blocked with 0.1% bovine serum albumin in phosphate buffered saline. Subsequently, plates were incubated with serum samples diluted 1:1000. Biotinylated anti-mouse IgG1 and IgG2a antibodies (BD Biosciences, San Jose, CA, USA) were used to detect heterologous anti-PG antibodies. Plates were then incubated with streptavidin (RD Systems, Minneapolis, MN, USA) and revealed by adding H₂O₂ and orthophenylenediamine (Sigma Aldrich, St. Louis, MO, USA).

2.5. Statistical Analysis. Results were presented as mean \pm standard deviation for parametric variables and the comparison among the groups was performed by t-test. For nonparametric variables, the results were presented as median and the comparison between the groups was performed by Mann-Whitney's test. Paired t-test was performed for antibody production. All data were analyzed using SigmaPlot software version 12.0 (Jandel Corporation, USA) and P < 0.05 was considered significant.

3. Results

- 3.1. Arthritis Incidence and Clinical Score. As expected, animals from control group did not develop experimental arthritis. However, all animals immunized with three doses of bovine PG+DDA adjuvant developed the disease (Figure 1(a)). Arthritis onset was observed at day 51 and total clinical score increased in the arthritic group until day 70 (Figure 1(b)). Moreover, the median of the maximum score in the arthritic group was statistically significant in comparison to the healthy control group (Figure 1(c)).
- 3.2. Histopathological Analysis. Figure 2 shows the differences among the clinical scores observed in mice hind paws and forepaws during arthritis development. HE stained paw sections revealed important histological changes in the arthritic joints compared to the healthy ones. According to the scoring system, all animals from control group presented score 0 and there was no signal of inflammation in these animals (Figures 2(a) and 2(a')). The joint structure was preserved and characterized by a well-defined synovial space, cartilage presence, thin synovial membrane, and compact bone (Figure 2(a")). Mice from arthritic group

presented a variety of scores, ranging from 1 to 4 in each paw. Score 1 was characterized by only one inflamed joint (head arrows; Figures 2(b) and 2(b')). No differences were observed in histological sections from paws with score 1; that is, all animals presented well preserved joint structures (Figure 2(b")). Score 2 was characterized by the presence of two or more affected joints in the paw (Figures 2(c) and 2(c')). In this score, there was an inflammatory cell infiltrate and a slight thickening of the synovial membrane. However, it was still possible to observe the presence of the synovial space and well-preserved cartilage and bone tissue (Figure 2(c'')). Score 3 was characterized by the inflammation of multiple joints including the ankle (lines; Figures 2(d) and 2(d')). In this score, there was an inflammatory cells infiltrate that characterizes the initial pannus formation, which is the inflammatory tissue that invades the synovial space and promotes cartilage destruction and bone erosion (Figure 2(d")). However, bone tissue was still preserved in this score. Score 4 was characterized by accentuated erythema and edema throughout the foot and ankle, involving all joints, with consequent movement impairment (Figures 2(e) and 2(e')). Inflammation and joint destruction were evident and were characterized by pannus formation, synovial membrane thickening, cartilage destruction, and bone erosion in paws with score 4 (Figure 2(e'')).

- 3.3. Production of Cytokines. Compared to the control group, spleen cells from arthritic mice produced significantly higher levels of IL-2 and the proinflammatory cytokines TNF- α , IL-6, IFN- γ , and IL-17 when restimulated *in vitro* with the specific antigen (Figures 3, 4, and 5). Interestingly, arthritic animals also produced significant levels of IL-5 and IL-10 anti-inflammatory cytokines in response to *in vitro* stimulation with PG (Figure 6). Results from nonstimulated cultures showed that there was spontaneous production of all cytokines in the arthritic animals, but not in the healthy ones (Figures 3, 4, 5, and 6). However, polyclonal stimulation of spleen cells with ConA triggered significant increase only in IL-6, IL-17, and IL-10 production by spleen cells from the arthritic group compared to the control one.
- 3.4. Production of Anti-PG Antibodies. The experimental arthritis induced by bovine PG determined production of both IgG1 and IgG2a anti-PG antibodies, with higher production of IgG1 (Figure 7). The levels of these specific antibodies increased significantly and progressively after the first immunization with PG+DDA (day 1). After reaching the maximum level around day 41, antibody production was maintained until euthanasia at day 70. As expected, control animals that were not immunized with PG+DDA did not produce specific antibodies against bovine PG (data not shown).

4. Discussion

There are several experimental models of rheumatoid arthritis that contribute to understand the mechanisms involved in this disease [24]. Experimental arthritis models induced

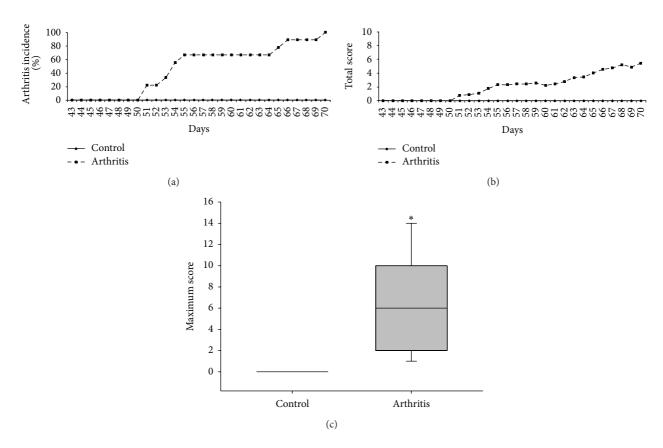


FIGURE 1: Arthritis incidence (a) total clinical score (b) and maximum clinical score (c) in mice with bovine proteoglycan-induced arthritis. Female BALB/c retired breeder mice were immunized with three doses of bovine PG associated with DDA adjuvant, 21-day interval. Clinical score was daily evaluated after the third immunization. $^*P < 0.05$ compared to control.

by cartilage components have been extensively studied, primarily the induction of arthritis by collagen and proteoglycan (PGIA). Considering the clinical and histopathological characteristics of the disease, this model shares many similarities with human arthritis. The development of arthritis in PGIA is attributed to a cross-reaction against foreign PG and mice self-PG [25]. In this experimental model, the disease is usually triggered by injections of human PG associated with a strong adjuvant. The PG can be extracted from the cartilage of various origins, but human PG is considered the most arthritogenic one. In this context and considering that PG purification is a complex and laborious process, we determined the arthritogenicity of a commercial source of bovine PG. This evaluation was done by immunization of BALB/c retired breeders with three doses of bovine PG emulsified with DDA. In spite of the advanced age of these animals, no spontaneous arthritis was observed. According to Besenyei et al. [26], approximately 0.5 to 1.0% of retired breeder BALB/c mice can develop the disease spontaneously.

Immunization with the commercial bovine PG was very effective to induce arthritis. A 100% incidence was observed in the majority of the experiments as has been described with human PG [13, 23]. In terms of clinical disease, we observed slightly lower scores than the ones described for human PG. However, this finding was equally described by

other authors that employed bovine PG [23, 27]. In spite of this, the histopathological analysis revealed the presence of very typical arthritic histological alterations as inflammatory infiltrates, synovial membrane thickening, pannus formation, cartilage destruction, and bone erosion. These features are very similar to the ones described by other authors in PGIA and also in human arthritis [13, 28]. This parallelism indicates that bovine PG can be further explored as another source of antigen to study arthritis. The efficacy of this bovine PG to induce murine arthritis is probably related, among other things, to the adopted adjuvant. As nicely described by Hanyecz et al. [23], the arthritogenicity of bovine PG was significantly incremented when it was combined with DDA. We also believe that the employment of BALB/c retired breeders contributed a lot to this achievement. According to Tarjanyi et al. [29], these old animals are very prone to arthritis development.

Immunization with this commercial product also induced significant production of IgG1 and IgG2b antibovine PG antibodies. Even though we were not able to assess a possible cross-reactivity of these antibodies with murine PG, we believe that it exists and is underlying the arthritogenicity of bovine PG to mice. This assumption is mainly based on structural and comparative biochemical studies and on arthritogenicity for mice. In this context,

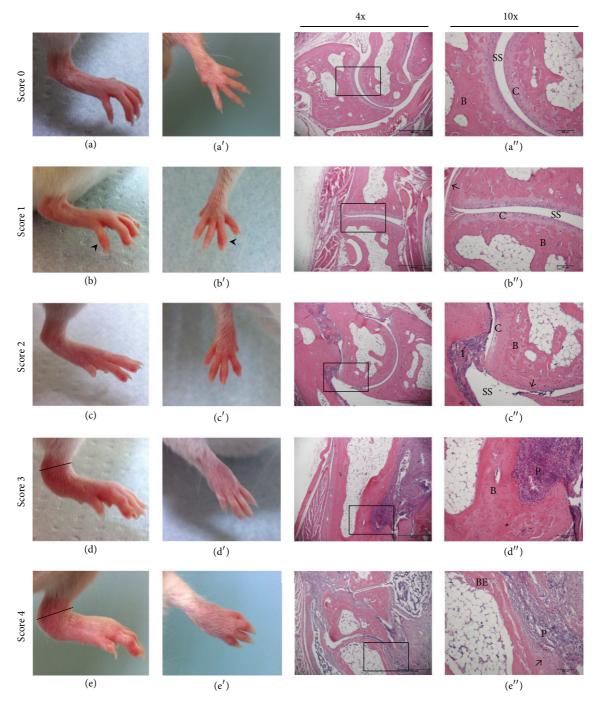


FIGURE 2: Representative clinical scores of hind paws (first column) and forepaws (second column) and histological sections of mice joints (third and fourth columns) with arthritis induced by bovine PG. Female BALB/c retired breeder mice paws were collected 70 days after the disease induction. The rectangles represent the regions highlighted in the fourth column. Head arrows indicate single joint inflammation; lines indicate ankle thickening; filled arrows indicate the synovial membrane. SS: synovial space; C: cartilage; B: bone; I: inflammatory infiltrate; P: pannus; BE: bone erosion.

Walcz et al. [30] demonstrated that murine and bovine PG core protein share 72.5% homology. The arthritogenic potential of distinct PG sources was checked in mice. Interestingly, arthritogenicity or its absence was associated with the ability to induce or not, respectively, the production of cross-reactive antibodies [31].

An aspect that deserves further elucidation is the degree of glycosylation present in this commercial PG. It has been strongly emphasized that PG deglycosylation is fundamental to achieve arthritogenicity [13, 32]. However, we believe that this preparation is not devoid of polysaccharides. This hypothesis is based on references specified by the company

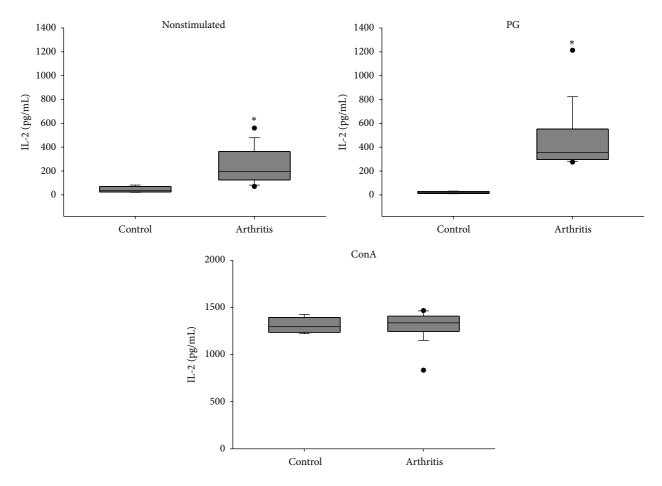


FIGURE 3: IL-2 production by spleen cells from BALB/c retired breeder mice with bovine proteoglycan-induced arthritis. Spleen cells were *in vitro* stimulated with PG and ConA and incubated for 48 hours. $^*P < 0.05$ compared to the respective control.

that commercializes the product and also in information described by authors that utilized this product. According to Tham et al. [33], this commercial product contains 86% of chondroitin sulfate, 8% protein, 6% keratan sulfate, and less than 1% hyaluronic acid and it was able to enhance the survival of neural stem cells. In the central nervous system, chondroitin sulfate proteoglycan (CSPG) is the most prevalent PG and CS removal with chondroitinase reduces neural stem cells proliferation and neurogenesis. Also, according to Antonopoulos et al. [34], PG isolated by urea procedure is probably found in PG subunits instead of PG complexes form due to its gel chromatographic pattern. PG subunits could expose the G1 domain and the link protein, which are highly arthritogenic [27, 35]. Antonopoulos et al. [34] also demonstrated that urea did not cause PG degradation. It is possible to think that this organic compound could interfere in PG structure and protein solubility exposing some core protein epitopes and, therefore, become able to induce experimental arthritis.

Results from cytokine production by spleen cells in vitro stimulated with PG showed that arthritic animals, but not

healthy ones, produced high levels of IL-2, TNF- α , IL-6, IFNγ, and IL-17. Spleen cells from arthritic mice were already producing higher levels of IL-2 than the healthy ones. Also, addition of PG to the cultures determined a significant increase in the production of this cytokine in the arthritic group. As a very good correlation has been established between IL-2 level and T-cell proliferation index, in either up- [36] or downregulation [37], our results indicate the occurrence of a specific proliferative process in the spleen. The higher production of TNF- α , IL-6, IFN- γ , and IL-17 was expected and corroborates with their arthritogenic potential observed in humans [38] and in animal models [24]. The production of IL-6 and TNF- α is related to the immunopathogenesis and maintenance of RA. These cytokines are also responsible for hyperalgesia caused by mechanical stimulus in this disease. According to Schaible et al. [38], these proinflammatory cytokines act on nerve cells responsible for the nociceptive stimuli during joint movement. These authors showed that drugs which neutralize the action of TNF- α promoted reduction of pain and inflammation in rats with adjuvant-induced arthritis. A similar result was found concerning IL-6 neutralization.

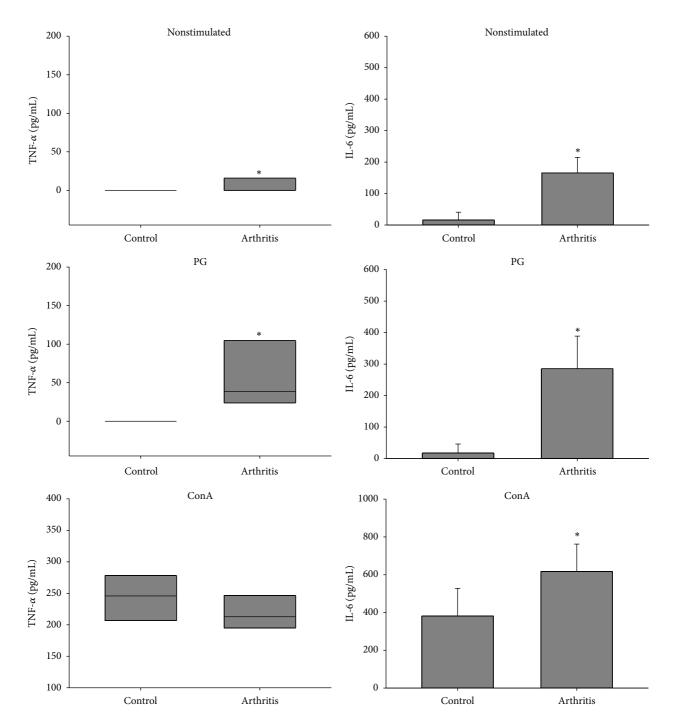


FIGURE 4: TNF-α and IL-6 production by spleen cells from BALB/c retired breeder mice with bovine proteoglycan-induced arthritis. Spleen cells were *in vitro* stimulated with PG and ConA and incubated for 48 hours. $^*P < 0.05$ compared to the respective control.

Thus, drugs whose action mechanisms are based on TNF- α , IL-6, and IL-1 neutralization have been extensively studied and some of them such as TNF- α and IL-6 are already used for the treatment of RA clinical symptoms [39].

Many studies have considered the balance between the production of IL-17 and IFN- γ as the key to understand the main immunopathogenic mechanisms involved in arthritis development. Considered a major proinflammatory cytokine

in human arthritis and in most experimental models, IL-17 plays an important role in the establishment, maintenance, and progression of this disease [40–42]. Regarding this, studies have shown that the absence of IL-17 decreased the clinical symptoms of arthritis in different experimental models [43, 44]. The role of IL-17 in PGIA is not clearly evaluated yet. However, it has been suggested that in this case the IFN- γ is more important than IL-17 in the establishment

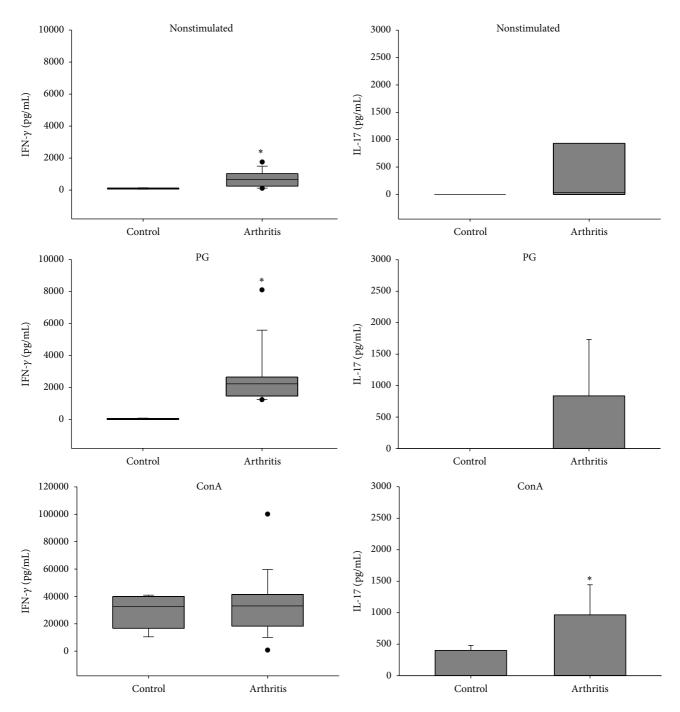


FIGURE 5: IFN- γ and IL-17 production by spleen cells from BALB/c retired breeder mice with bovine proteoglycan-induced arthritis. Spleen cells were *in vitro* stimulated with PG and ConA and incubated for 48 hours. *P < 0.05 compared to the respective control.

of the disease. Doodes et al. [21], using knockout mice, showed that IFN- γ is essential for PGIA triggering in an IL-17 independent manner. The IFN- γ represents a paradox in autoimmune arthritis. Although its pathogenic effect is well described, recent studies showed a protective effect of this cytokine in arthritis. Alzabin and Williams [45] carefully reviewed the role of effector T cells in autoimmune arthritis. By analyzing the results of several experimental models, the authors demonstrated the protective role of IFN- γ .

The administration of this cytokine that is, theoretically, proinflammatory, decreased clinical signals in different arthritis models. For example, genetically modified animals which were not able to produce IFN- γ presented an exacerbated collagen-induced arthritis [46]. However, it has been also reported that animals that did not produce this cytokine were less susceptible to PGIA [47].

The specific *in vitro* stimulation of spleen cells also triggered production of anti-inflammatory cytokines such

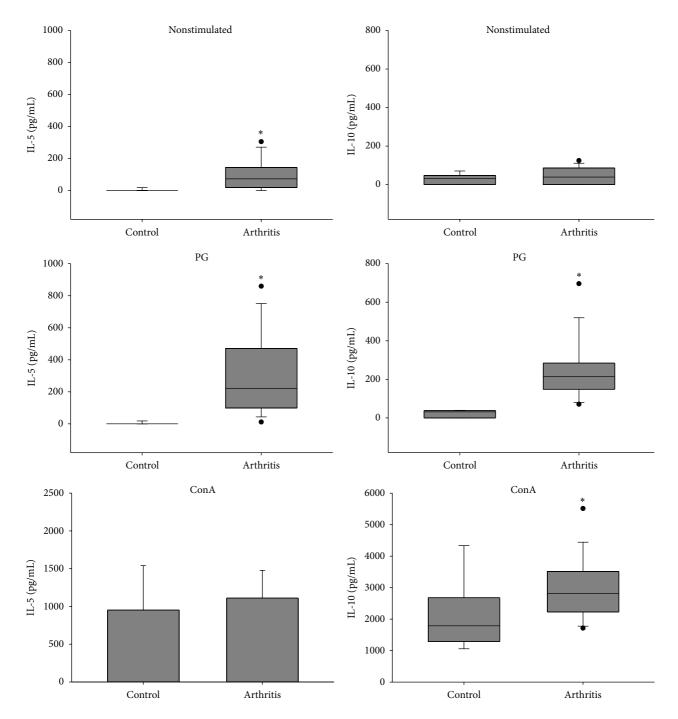


FIGURE 6: IL-5 and IL-10 production by spleen cells from BALB/c retired breeder mice with bovine proteoglycan-induced arthritis. Spleen cells were *in vitro* stimulated with PG and ConA and incubated for 48 hours. $^*P < 0.05$ compared to the respective control.

as IL-5 and IL-10. Although RA is considered a disease characterized by predominant Th1 pattern, studies indicate that Th2 cytokines such as IL-4 and IL-10 also contribute to the immunopathogenesis of the disease and may also be related to the stage of disease development [48]. According to Gerli et al. [49], there is a high production of IL-4 and IL-10 by T cells from peripheral blood of patients in earlier stages of arthritis, but this production decreases significantly

in later stages, contributing to disease progression and joint destruction in the chronic phase. Our results are, therefore, similar to the mixed Th1/Th2 pattern already shown in humans and in PGIA model [31]. An interesting aspect was observed in nonstimulated spleen cell cultures from arthritic animals when compared to control group. The arthritic group produced detectable levels of IFN- γ , TNF- α , IL-6, IL-17, IL-5, and IL-10 even in the absence of the specific

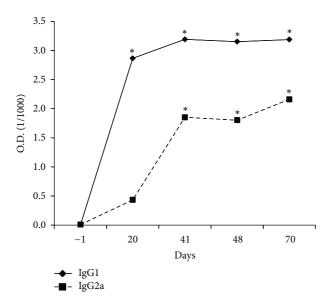


FIGURE 7: IgG1 and IgG2a serum levels from BALB/c retired breeder mice with bovine proteoglycan-induced arthritis. Blood samples were obtained two days before each PG+DDA immunization (days -1, 20, and 41), seven days after the third immunization (day 48), and after euthanasia (day 70). *P < 0.05 compared to day -1 of the same group.

stimulus. This spontaneous production, which might be more properly called endogenous production, could result from the intense immune response activation and cytokine secretion by effector cells that are significantly occurring.

Some interesting results mainly related to IL-17 were also detected in spleen cell cultures stimulated with ConA. In this case, we highlight the fact that the production of this cytokine after polyclonal stimulation was very similar to that induced by specific antigen stimulation. This finding is different from the ones usually obtained after polyclonal activation. The stimulation with mitogens is usually associated with induction of significantly higher cytokine production than the specific stimulus. However, recently, Doodes et al. [21] observed that the production of IL-17 and IFN-γ in response to specific stimulus is extremely high, reaching levels greater than 2000 pg/mL in the PGIA model. Similarly high levels of IL-17 were observed in human studies. Leipe et al. [50] evaluated the importance of IL-17 in autoimmune arthritis and found that purified T cells from the peripheral blood of patients, in the early stage of the disease, produced very high levels of this cytokine. Furthermore, analysis of the production of IL-17 by mononuclear cells from peripheral blood of healthy individuals, in response to different mitogens, revealed that the level of this cytokine in response to ConA did not exceed 500 pg/mL [51].

5. Conclusions

Our results indicate that this commercial bovine PG is highly arthritogenic for BALB/c retired breeder mice. In addition, the disease induced by this reagent presents clinical symptoms and histopathological features that are very similar to those found in other arthritis models and also the human

corresponding pathology. Taken together, these results suggest that this bovine PG can be used as an alternative source in PGIA for the study of many aspects of RA, including the immunopathogenesis of the disease and also the development of new therapies.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

Acknowledgments

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Research Article

Prediction of Methotrexate Clinical Response in Portuguese Rheumatoid Arthritis Patients: Implication of MTHFR rs1801133 and ATIC rs4673993 Polymorphisms

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Objective. Methotrexate (MTX), the most used drug in rheumatoid arthritis (RA) treatment, showing variability in clinical response, is often associated with genetic polymorphisms. This study aimed to elucidate the role of methylenetetrahydrofolate reductase (MTHFR) C677T and aminoimidazole carboxamide adenosine ribonucleotide transformylase (ATIC) T675C polymorphisms and clinicopathological variables in clinical response to MTX in Portuguese RA patients. Methods. Study included 233 RA patients treated with MTX for at least six months. MTHFR C677T and ATIC T675C polymorphisms were genotyped and clinicopathological variables were collected. Statistical analyses were performed and binary logistic regression method adjusted to possible confounding variables. Results. Multivariate analyses demonstrated that MTHFR 677TT (OR = 4.63; P = 0.013) and ATIC 675T carriers (OR = 5.16; P = 0.013) were associated with over 4-fold increased risk for nonresponse. For clinicopathological variables, noncurrent smokers (OR = 7.98; P = 0.001), patients positive to anti-cyclic citrullinated peptide (OR = 3.53; P = 0.004) and antinuclear antibodies (OR = 2.28; P = 0.045), with higher health assessment questionnaire score (OR = 2.42; P = 0.007), and nonsteroidal anti-inflammatory drug users (OR = 2.77; P = 0.018) were also associated with nonresponse. Contrarily, subcutaneous administration route (OR = 0.11; P < 0.001) was associated with response. Conclusion. Our study suggests that MTHFR C677T and ATIC T675C genotyping combined with clinicopathological data may help to identify patients whom will not benefit from MTX treatment and, therefore, assist clinicians in personalizing RA treatment.

1. Introduction

Rheumatoid arthritis (RA) is a chronic disease characterized by an inflammation of the joints with an autoimmune profile and the most widely used disease modifying antirheumatic drug (DMARD) for RA treatment is methotrexate (MTX) [1]. Despite MTX cost-effectiveness, clinical response to MTX varies widely [2]. The factors that are possibly influencing

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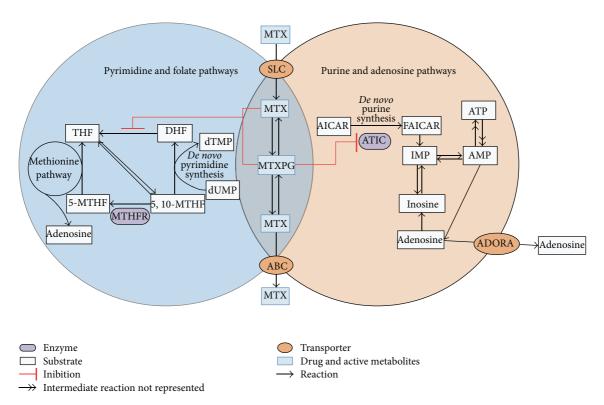


FIGURE 1: Methotrexate action mechanism. Left panel represents the intervention of MTX in *de novo* pyrimidine synthesis, folate, and methionine pathways by the inhibition of key enzymes. Right panel shows the effect of MTX in *de novo* purine synthesis and adenosine pathway by ATIC inhibition. 5-MTHF: 5-methyltetrahydrofolate; 5,10-MTHF: 5,10-methylenetetrahydrofolate; ABC: ATP-binding cassette; ADORA: adenosine receptor; AICAR: 5-aminoimidazole-4-carboxamide ribonucleotide; AMP: adenosine monophosphate; ATIC: 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase; ATP: adenosine triphosphate; DHF: dihydrofolate; dTMP: deoxythymidine monophosphate; dUMP: deoxyuridine monophosphate; FAICAR: 5-formamidoimidazole-4-carboxamide ribonucleotide; IMP: inosine monophosphate; MTHFR: methylenetetrahydrofolate reductase; MTX: methotrexate; MTXPG: methotrexate polyglutamate; SLC: solute carrier; THF: tetrahydrofolate.

disease course and therapeutic outcome can be classified into (1) clinicopathological variables, which can be divided into patient-related variables (age, gender, ethnicity, and comorbidities), disease-related variables (duration, activity, disability, and biomarkers), and treatment-related variables (compliance, dose, and previous drugs used) [3–9], and (2) genetic factors, such as genetic polymorphisms implicated in key MTX pathway genes [2, 10–15]. Several studies have been performed in order to evaluate the influence of clinicopathological variables in clinical response to MTX [3, 5, 7, 16, 17]; nevertheless, there is no consensus on which factors can be used as predictors [18]. Pharmacogenomics has raised great interest and, in fact, some studies have attempted to clarify the influence of genetic variations on clinical response to MTX [19].

MTX is an antifolate drug, with antiproliferative and antiinflammatory effects, by inhibition of folate and adenosine pathways and also inhibition of purines and pyrimidines synthesis (Figure 1) [16, 20, 21]. Methylenetetra- hydrofolate reductase (MTHFR), an enzyme involved in folate pathway, is responsible for the conversion of 5,10-methylenetetrahydrofolate (5,10-MTHF) to 5-methyltetrahydrofolate (5-MTHF) that acts as a carbon donor for the remethylation of homocysteine into methionine [22]. On the other hand, methionine can be transformed into S-adenosyl methionine (SAM) and then to S-adenosyl homocysteine (SAH), which can be reversibly hydrolyzed into adenosine and homocysteine [23]. Despite the fact that MTHFR is not directly inhibited by MTX or by its polyglutamated forms (MTXPG), its expression levels seem to influence MTX effect by modifying the folate status [16]. Additionally, it is known that aminoimidazole carboxamide adenosine ribonucleotide (AICAR) transformylase (ATIC), an enzyme involved in the *de novo* purine synthesis pathway responsible for the conversion of AICAR into formyl-AICAR (FAICAR), is directly inhibited by MTXPG, causing intracellular accumulation of AICAR [16]. AICAR and its metabolites can then inhibit two enzymes, adenosine deaminase (ADA) and adenosine monophosphate deaminase 1 (AMPD1), which are involved in adenosine metabolism, thus leading to increased intracellular concentrations of adenosine and its consequent release to the extracellular space [21]. This release contributes to the anti-inflammatory effects of MTX since adenosine is a potent anti-inflammatory agent [21].

Several studies have demonstrated that the occurrence of variations on clinical response to MTX could be explained by genetic polymorphisms in *MTHFR* and *ATIC* genes [11, 13–16, 24–28]. The most studied polymorphism in *MTHFR* is C677T

(rs1801133), which is responsible for a substitution of an alanine to a valine, leading to a thermolabile form of MTHFR with reduced activity [29]. In fact, it has been suggested that *MTHFR* 677T allele is related to MTX nonresponse in RA [13, 24]. Similar to MTHFR, some authors have studied the role of the T675C (rs4673993) polymorphism in *ATIC*, of which the *ATIC* 675C allele has been associated with improved clinical *status* and, consequently, with clinical response to MTX [14, 26].

The pattern of MTX therapeutic outcome is considered to be a major factor for the motivation of researchers and clinicians to enroll patients in pharmacogenetic studies, mainly by comparative studies within different populations. Therefore, the aim of this study was to elucidate the association of clinical response to MTX with MTHFR C677T and ATIC T675C polymorphisms, in Portuguese RA patients.

2. Methods

2.1. Characterization of the Studied Population. This study was developed as a retrospective study in a cohort of consecutive Caucasian patients (≥18 years) with RA treated with MTX for at least six months and was conducted between January 2009 and December 2012 at São João Hospital Center (Porto, Portugal). After diagnosis, patients were classified according to the 1987 criteria of the American College of Rheumatology (ACR) and reclassified according to the 2010 criteria of ACR and the European League Against Rheumatism (EULAR) [30]. All patients were initially treated with 10 mg per os (PO)/week of MTX in monotherapy. This dose was increased 5 mg at each three weeks if patients did not meet EULAR criteria for response, that is, if presenting a disease activity score in 28 joints (DAS28) > 3.2. At three months, if patients were still without response, the administration route was changed from PO to subcutaneous (SC) maintaining the MTX dose. If within three months, using SC at the maximum tolerable doses, patients did not meet the response criteria, MTX therapy was associated with other synthetic DMARDs. After three more months, if patients continued without response in two successive evaluations and did not present any contraindication, MTX therapy was discontinued or associated with biological DMARDs. The adjustment of MTX therapy also occurred when patients developed MTX-related toxicity. Due to the well-known protective effect of folic acid supplementation for the prevention of toxicity occurrence, in particular for gastrointestinal disorders [31–33], this drug was prescribed once a week to all patients and their regular compliance was registered.

Patients were excluded from the study if not treated with MTX for at least six months and if there was history of drug abuse, recent pregnancy, or desire to become pregnant. The study procedures were considered according to the ethical standards of the Helsinki Declaration by the local Ethical Committee (reference 33/2009) and all patients provided a signed informed written consent.

2.2. Data Collection and Variable Definition. Clinicopathological data were collected from individual clinical records

by clinicians during patients' regular hospital visits and include variables possibly influencing disease state and clinical response to MTX, which were selected based on either the literature review and/or the clinical significance [3, 5, 7, 16, 17, 33]. These variables included (1) patient-related variables: age, gender, menopause, body mass index (BMI), smoking, number of pack years (NPY), and comorbidities; (2) disease-related variables: diagnosis age, duration, rheumatoid factor (RF), anti-cyclic citrullinated peptide (anti-CCP), antinuclear antibodies (ANAs), DAS28, and health assessment questionnaire (HAQ); and (3) treatment-related variables: symptomatic (corticosteroids and nonsteroidal anti-inflammatory drugs (NSAIDs), supplements (folic acid), other concomitant DMARDs, and MTX administration characteristics (dose, treatment duration, and administration route).

NPY was calculated by the formula: (number of cigarettes smoked per day \times number of years smoking)/20. Comorbidity was defined as the presence of diabetes mellitus, hypertension, dyslipidemia, and/or cardiac disorders beyond RA. DAS28 was calculated as described by Prevoo et al. [34]. Daily corticosteroid therapy dose was considered in prednisolone equivalents.

MTX clinical response was recorded at the time of each visit. Nonresponse was defined if patients presented a DAS28 > 3.2 in two consecutive evaluations despite the use of MTX either in monotherapy or combined with other DMARDs. Therefore, at least six months of MTX therapy was required to define which patients had nonresponse to MTX. Response to MTX was defined when patients presented a DAS28 \leq 3.2.

2.3. Sample Collection and Processing. Whole blood samples were obtained with standard venipuncture technique using ethylenediaminetetraacetic acid (EDTA) containing tubes and genomic deoxyribonucleic acid (DNA) extracted with QIAamp DNA Blood Mini Kit according to the manufacturer instructions (QIAGEN, Hilden, Germany). Total genomic DNA was quantified and its purity and integrity were analyzed using the NanoDrop 1000 Spectrophotometer v3.7 (Thermo Scientific, Wilmington, DE, USA).

2.4. MTHFR C677T and ATIC T675C Genotyping. MTHFR C677T and ATIC T675C polymorphisms were selected based on the role of MTHFR and ATIC in MTX action pathway, upon the putative alteration of these proteins levels and the consequent implication in MTX clinical response [13, 14, 24, 26, 29].

Genotyping protocols were adjusted from those proposed by Sadananda Adiga et al. [35] for *MTHFR* C677T and Hinks et al. [27] for *ATIC* T675C.

MTHFR C677T polymorphism was genotyped by polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) techniques. PCR amplification was performed for a final volume of 50 μL containing 0.3 μM of each primer (forward: 5'-TGA AGG AGA AGG TGT CTG CGG GA-3'; reverse: 5'-AGG ACG GTG CGG TGA GAG TG-3'), 1x DreamTaq Green master mix (Thermo Scientific, Vilnius, Lithuania), and 50–100 ng of genomic DNA. The PCR conditions consisted of initial denaturation at 94°C

during 5 minutes followed by 30 cycles with denaturation for 1 minute at 94°C, annealing for 1 minute at 57°C, extension for 15 seconds at 72°C, and a final extension at 72°C during 10 minutes. RFLP was performed at 37°C, overnight, using HinfI (Thermo Scientific, Vilnius, Lithuania). Individuals with the CC genotype presented 1 fragment with 198 base pairs (bp), whereas individuals with the TT genotype presented 1 fragment with 175 bp.

ATIC T675C polymorphism was genotyped using Taq-Man SNP Genotyping Assay (C_362264_10) from Applied Biosystems (Foster City, CA, USA) with fluorogenic binding probes. Reactions were performed on an Applied Biosystems 7300 Real Time PCR System (Applied Biosystems, Foster City, CA, USA) with a 5 μ L final volume mixture containing 1x TaqMan Genotyping Master Mix (Applied Biosystems, Foster City, CA, USA), 900 nM of each primer, 200 nM of probes labeled with either FAM or VIC, and 10 ng of extracted DNA. Thermal cycling conditions were 10 minutes at 95°C followed by 40 cycles of 15 seconds at 95°C and 1 minute at 60°C. Allelic discrimination was performed by measuring endpoint fluorescence using ABI PRISM Sequence Detection System (Version 1.2.3, Applied Biosystems, Foster City, CA, USA).

For quality control, 10% of the samples were randomly selected for a second analysis and 10% percent of cases were confirmed by automated sequencing in a 3130xl Genetic Analyzer using the Kit BigDye Terminator v3.1 (Life Technologies, Foster City, CA, USA). Results were 100% concordant.

2.5. Statistical Analysis. Statistical analyses were performed using the IBM SPSS Statistics for Windows, Version 20.0 (IBM Corp., Armonk, NY, USA), considering a statistically significant probability (*P*) value of 5% or less. The chi-square test was used to assess the association between the groups (response *versus* nonresponse) and the different categorical variables. Odds ratio (OR) and the correspondent 95% confidence intervals (CI) were calculated as a measure of the association between the categorical variables. For the comparison of quantitative variables two sample *t*-tests and nonparametric Mann-Whitney *U* tests were applied.

Multivariate analysis with binary logistic regression was used to identify which genetic variables (*MTHFR* C677T and *ATIC* T675C genotypes) and clinicopathological variables could predict risk for occurrence of nonresponse to MTX. This analysis was performed adjusting to potential confounding variables in three steps: (1) patient-related variables; (2) patient- and disease-related variables; and (3) patient-, disease-, and treatment-related variables.

3. Results

3.1. Characterization of the Studied Population. Table 1 reports the clinicopathological variables of population enrolled in the study, that includes follow-up data from a total of 233 patients (196 females and 37 males), with a mean age of 52 ± 11.9 and disease duration of 8.0 (range: 0.5-53.0) years. Considering MTX therapy, the median treatment duration was 28.0 (range: 6.0-230.0) months

with a median dose of 15.0 (range: 2.5-25.0) mg/week. Furthermore, 201 patients (86.3%) administered MTX by PO administration route and 32 (13.7%) by SC administration route. Nonresponse to MTX was observed in 128 (54.9%) patients and the mean for DAS28 was 4.2 ± 1.3 .

3.2. Clinicopathological Variables and Clinical Response to MTX. Table 2 represents the relation between clinicopathological variables and clinical response to MTX. In accordance with patient-related variables, our results showed that early age of diagnosis (P < 0.001) and noncurrent smokers (OR = 0.32; P = 0.004) were statistically significant associated with nonresponse to MTX. Concerning disease-related variables, our results demonstrated that positivity to anti-CCP (OR = 2.28; P = 0.007) and ANAs (OR = 1.98; P = 0.024) was statistically significant associated with nonresponse to MTX. Additionally, higher number of tender joints count (TJC) (P = 0.007) and swollen joints count (SJC) (P = 0.008)and higher health assessment questionnaire (HAQ) score (P = 0.006) were statistically significant associated with nonresponse to MTX. Considering the treatment-related variables, our results revealed that NSAIDs users (OR = 3.09; P < 0.001) were associated with nonresponse to MTX. In addition, attending to MTX administration characteristics, higher MTX doses (P < 0.001) were associated with nonresponse to MTX, while SC administration route (OR = 0.32; P = 0.004) was statistically significant associated with response to MTX.

3.3. MTHFR C677T and ATIC T675C and Clinical Response to MTX. The frequencies of MTHFR C677T (rs1801133) genotypes were 105 CC (45.1%), 99 CT (42.5%), and 29 TT (12.4%), while for ATIC T675C (rs4673993) they were 110 TT (47.2%), 99 TC (42.5%), and 24 CC (10.3%). In our population, the minor allele for MTHFR C677T was T and for ATIC T675C was C (see Figure S1 in Supplementary Materials available online at http://dx.doi.org/10.1155/2014/368681). Considering distribution between responders and nonresponders, results showed significant differences for MTHFR C667T (P = 0.049) and ATIC T675C (P = 0.025) genotypes.

Table 3 and Figures S2 and S3 represent the relation between genetic variables and clinical response to MTX. In accordance with MTHFR C677T polymorphism, our results showed that MTHFR 677TT was statistically significant associated with about 3-fold increased risk for nonresponse to MTX when compared to MTHFR 677CC (OR = 3.08; P = 0.015) and MTHFR 677C carriers (OR = 2.91; P = 0.015). Regarding ATIC T675C polymorphism, we observed that ATIC 675CC was associated with response to MTX when compared to ATIC 675TT (OR = 0.32; P = 0.016) and ATIC 675T carriers (OR = 0.30; P = 0.007).

3.4. Multivariate Analysis and Clinical Response to MTX. Multivariate analysis with binary logistic regression was used to identify which clinicopathological and genetic variables (MTHFR C677T and ATIC T675C genotypes) could predict risk for the occurrence of nonresponse to MTX (Table 4).

Table 1: Clinicopathological variables of population enrolled in the study.

	Value
Patient-related	
Male, <i>n</i> (%)	37 (15.9)
Female, <i>n</i> (%)	196 (84.1)
Postmenopausal, n (%)	96 (49.0)
Current smokers, <i>n</i> (%)	32 (13.7)
NPY*, median (IQR)	19.5 (0.8–120.0)
Comorbidity**, n (%)	126 (54.1)
Disease-related	
Diagnosis age, mean \pm SD, years	40.3 ± 13.2
Disease duration, median (IQR), years	8.0 (0.5–53.0)
RF positive, <i>n</i> (%)	131 (56.2)
Anti-CCP positive, <i>n</i> (%)	175 (75.1)
ANAs positive, <i>n</i> (%)	66 (28.3)
DAS28, mean \pm SD	4.2 ± 1.3
Individual variables—DAS28	
TJC (out of 28), median (IQR)	4.0 (0.0-27.0)
SJC (out of 28), median (IQR)	3.0 (0.0-24.1)
ESR, median (IQR), minutes (1st hour)	18.0 (1.0-92.0)
Global health on VAS, median (IQR)	48.0 (0.0-100.0)
HAQ score, median (IQR)	1.25 (0.0–2.9)
$HAQ \leq 0.5, n (\%)$	39 (16.7)
Treatment-related §	
Symptomatic	
Corticosteroids, <i>n</i> (%)	188 (80.7)
Daily dose in prednisolone equivalents, median (IQR), mg	5.0 (0.0-20.0)
NSAIDs, <i>n</i> (%)	170 (73.0)
Supplements	
Folic acid $^{\#}$, n (%)	118 (50.6)
DMARDs	
Methotrexate monotherapy, n (%)	146 (62.7)
Combined methotrexate therapy—synthetic DMARDs, <i>n</i> (%)	59 (25.3)
Combined methotrexate therapy—biological DMARDs, <i>n</i> (%)	28 (12.0)
Methotrexate administration characteristics	
Dose, median (IQR), mg/week	15.0 (2.5–25.0)
Treatment duration, median (IQR), months	28.0 (6.0-230.0)
<i>Per os</i> administration route, n (%)	201 (86.3)
Subcutaneous administration route, n (%)	32 (13.7)

ANAs: antinuclear antibodies; Anti-CCP: anti-cyclic citrullinated peptide; BMI: body mass index; DAS28: disease activity score 28; DMARDs: disease modifying antirheumatic drugs; ESR: erythrocyte sedimentation rate; HAQ: health assessment questionnaire; IQR: interquartile range; NPY: number of pack years; NSAIDs: nonsteroidal anti-inflammatory drugs; RF: rheumatoid factor; SD: standard deviation; SJC: swollen joints count; TJC: tender joints count; VAS: visual analog scale.

This analysis was performed in three steps adjusting to potential confounding variables. In the first step, patient-related variables were considered and our results demonstrated that MTHFR 677TT (OR = 2.64; P = 0.040) and ATIC 675T carriers (OR = 3.20; P = 0.022) were associated with about 3fold increased risk for nonresponse to MTX. In a second step,

beyond patient-related variables, disease-related variables were added and results confirmed that MTHFR 677TT (OR = 3.23; P = 0.025) and ATIC 675T carriers (OR = 4.63; P = 0.007) were associated with nonresponse to MTX. In a third step, beyond patient- and disease-related variables, treatment-related variables were added and the obtained

^{*}NPY = (number of cigarettes smoked per day × number of years smoking)/20.

**Comorbidity was defined as the presence of diabetes mellitus, hypertension, dyslipidemia, and/or cardiac disorders beyond rheumatoid arthritis.

[§]Drugs coadministered with methotrexate when clinical response to methotrexate was recorded.

^{*}Patients in compliance with folic acid supplementation.

Table 2: Relation between clinicopathological variables and clinical response to methotrexate.

Characteristic	Response $(n = 105)$	Nonresponse ($n = 128$)	P value
Patient-related			
Male, n (%)	19 (51.4)	18 (48.6)	Reference
Female, n (%)	86 (43.9)	110 (56.1)	0.402
Premenopausal, n (%)	39 (39.0)	61 (61.0)	Reference
Postmenopausal, n (%)	47 (49.0)	49 (51.0)	0.160
Age, mean \pm SD, years	55.1 ± 11.6	49.3 ± 11.5	<0.001
BMI, median (IQR), Kg/m ²	26.2 (18.5–43.1)	26.3 (18.4–38.9)	0.574
Noncurrent smoker*, n (%)	83 (41.3)	118 (58.7)	Reference
Current smoker, <i>n</i> (%)	22 (68.8)	10 (31.2)	0.004^{a}
NPY**, median (IQR)	20.1 (1.5–120.0)	14.0 (0.8–40.0)	0.269
Noncomorbidity, n (%)	51 (47.7)	56 (52.3)	Reference
Comorbidity***, n (%)	54 (42.9)	72 (57.1)	0.462
Disease-related			
Diagnosis age, mean \pm SD, years	42.1 ± 13.3	39.1 ± 12.8	0.081
Disease duration, median (IQR), years	8.0 (1.0-53.0)	8.0 (0.5–38.0)	0.164
RF negative, n (%)	42 (41.2)	60 (58.8)	Reference
RF positive, n (%)	63 (48.1)	68 (51.9)	0.293
Anti-CCP negative, n (%)	35 (60.3)	23 (39.7)	Reference
Anti-CCP positive, <i>n</i> (%)	70 (40.0)	105 (60.0)	0.007^{b}
ANAs negative, n (%)	83 (49.7)	84 (50.3)	Reference
ANAs positive, <i>n</i> (%)	22 (33.3)	44 (66.7)	0.024 ^c
DAS28, mean ± SD	4.0 ± 1.5	4.3 ± 1.2	0.089
Individual variables—DAS28			
TJC (out of 28), median (IQR)	3.0 (0.0–27.0)	5.0 (0.0-20.0)	0.007
SJC (out of 28), median (IQR)	2.0 (0.0-24.0)	4.0 (0.0-23.0)	0.008
ESR, median (IQR), minutes (1st hour)	19.0 (1.0-88.0)	17.0 (1.0–92.0)	0.509
Global health on VAS, median (IQR)	47.0 (0.0–100.0)	49.0 (0.0-100.0)	0.516
HAQ score, median (IQR)	1.1 (0.0-2.9)	1.5 (0.0–2.6)	0.006
Treatment-related §			
Symptomatic			
Noncorticosteroids, n (%)	21 (46.7)	24 (53.3)	Reference
Corticosteroids, n (%)	84 (44.7)	104 (55.3)	0.810
Non-NSAIDs, n (%)	41 (65.1)	22 (34.9)	Reference
NSAIDs, n (%)	64 (37.6)	106 (62.4)	< 0.001 ^d
Supplements			
Folic acid nonregular users, n (%)	52 (45.2)	63 (54.8)	Reference
Folic acid regular users, <i>n</i> (%)	53 (44.9)	65 (55.1)	0.963
Methotrexate administration characteristics			
Dose, median (IQR), mg/week	15.0 (2.5–25.0)	20.0 (7.5–25.0)	< 0.001
Treatment duration, median (IQR), months	28.0 (6.0-230.0)	29.0 (6.0–209.0)	0.204
<i>Per os</i> administration route, n (%)	83 (41.3)	118 (58.7)	Reference
Subcutaneous administration route, n (%)	22 (68.8)	10 (31.2)	0.004^{e}

^{*} Noncurrent smokers include the never smokers and the ex-smokers.

^{**}NPY = (number of cigarettes smoked per day × number of years smoking)/20.

***Comorbidity was defined as the presence of diabetes mellitus, hypertension, dyslipidemia, and/or cardiac disorders beyond rheumatoid arthritis.

[§]Drugs coadministered with methotrexate when clinical response to methotrexate was recorded.

P value < 0.05 is considered to be of statistical significance (highlighted in bold).

^aOR = 0.32, 95% CI: 0.14–0.71. ^bOR = 2.28, 95% CI: 1.24–4.19. ^cOR = 1.98, 95% CI: 1.09–3.58. ^dOR = 3.09, 95% CI: 1.69–5.65. ^eOR = 0.32, 95% CI: 0.14–0.71. ANAs: antinuclear antibodies; anti-CCP: anti-cyclic citrullinated peptide; BMI: body mass index; DAS28: disease activity score 28; ESR: erythrocyte sedimentation rate; HAQ: health assessment questionnaire; IQR: interquartile range; NPY: number of pack years; NSAIDs: nonsteroidal anti-inflammatory drugs; RF: rheumatoid factor; SD: standard deviation; SJC: swollen joints count; TJC: tender joints count; VAS: visual analog scale.

TABLE 3: Relation between genetic variables and clinical response to methotrexate.

	Response $(n = 105)$	Nonresponse ($n = 128$)	P value	OR (95% CI)
MTHFR C677T, rs1801133				
CC	52 (49.5)	53 (50.5)		Reference
CT	46 (46.5)	53 (53.5)	0.662	1.13 (0.65-1.96)
TT	7 (24.1)	22 (75.9)	0.015	3.08 (1.21-7.84)
CC	52 (49.5)	53 (50.5)		Reference
T carrier	53 (41.4)	75 (58.6)	0.215	1.39 (0.83-2.33)
C carrier	98 (48.0)	106 (52.0)		Reference
TT	7 (24.1)	22 (75.9)	0.015	2.91 (1.19-7.10)
ATIC T675C, rs4673993				
TT	48 (43.6)	62 (56.4)		Reference
TC	40 (40.4)	59 (59.6)	0.637	1.14 (0.66-1.98)
CC	17 (70.8)	7 (29.2)	0.016	0.32 (0.12-0.83)
TT	48 (43.6)	62 (56.4)		Reference
C carrier	57 (46.3)	66 (53.7)	0.679	0.90 (0.53-1.50)
T carrier	88 (42.1)	121 (57.9)		Reference
CC	17 (70.8)	7 (29.2)	0.007	0.30 (0.12-0.75)

Results are expressed in n (%).

P value < 0.05 is considered to be of statistical significance (highlighted in bold).

ATIC: 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase; C: cytosine; CI: confidence interval; MTHFR: methylenetetrahydrofolate reductase; OR: odds ratio; T: thymine.

TABLE 4: Multivariate logistic regression analysis and clinical response to methotrexate.

			A	djusted variables			
Genetic variables	Patient-related Patien		Patient-related	atient-related + disease-related		Patient-related + disease-related + treatment-related	
	P value	OR (95% CI)	P value	OR (95% CI)	P value	OR (95% CI)	
MTHFR C677T, rs1801133							
C carriers		Reference		Reference		Reference	
TT	0.040	2.64 (1.04-6.67)	0.025	3.23 (1.16-9.02)	0.013	4.63 (1.37-15.60)	
ATIC T675C, rs4673993							
CC		Reference		Reference		Reference	
T carriers	0.022	3.20 (1.18-8.66)	0.007	4.63 (1.51-14.12)	0.013	5.16 (1.42-18.76)	

P value < 0.05 is considered to be of statistical significance (highlighted in bold).

Adjusted variables include (1) patient-related variables (age, gender, and smoking), (2) disease-related variables (diagnosis age, disease duration, anti-CCPs, ANAs, TJC, SJC, and HAQ), and (3) treatment-related variables (folic acid supplementation, corticosteroids therapy, use of NSAIDs, other concomitant DMARDs used and MTX administration characteristics such as dose, treatment duration, and administration route). Genetic variables include *MTHFR* C677T and *ATIC* T675C polymorphisms.

ANAs: antinuclear antibodies; anti-CCP: anti-cyclic citrullinated peptide; ATIC: 5-aminoimidazole-4-carboxamide ribonucleotide formyltransferase; C: cytosine; CI: confidence interval; HAQ: health assessment questionnaire; MTHFR: methylenetetrahydrofolate reductase; NSAIDs: nonsteroidal anti-inflammatory drugs; OR: odds ratio; SJC: swollen joints count; T: thymine; TJC: tender joints count.

results showed that *MTHFR* 677TT carriers (OR = 4.63; P = 0.013) were statistically significant associated with more than 4-fold increased risk for nonresponse to MTX when compared to *MTHFR* 677C carriers. Additionally, *ATIC* 675T carriers (OR = 5.16; P = 0.013) were statistically significant associated with more than 5-fold increased risk for nonresponse to MTX when compared to *ATIC* 675CC.

Furthermore, considering clinicopathological variables, we observed that noncurrent smokers (OR = 7.98; P = 0.001), positivity to anti-CCP (OR = 3.53; P = 0.004) and ANAs (OR = 2.28; P = 0.045), higher HAQ (OR = 2.42; P = 0.007), and NSAIDs users (OR = 2.77; P = 0.018) were

statistically significant associated with nonresponse to MTX. Moreover, SC administration route (OR = 0.11; P < 0.001) was statistically significant associated with response to MTX.

4. Discussion

Despite the fact that MTX is extensively used in RA treatment, the individual clinical response to MTX is variable and, therefore, additional DMARDs are often required to achieve a low disease activity profile or even remission [2].

Previous studies revealed controversial results when clinicopathological variables were associated with MTHFR

C677T and ATIC T675C polymorphisms for clinical response to MTX. Several explanations can be proposed for such observed discrepancies, such as bias related to study design and settings, sample size/power, ethnicity, the population disease duration (early or established RA), changes in folate status, influence of less common single nucleotide polymorphisms (SNPs) in MTHFR and ATIC, polymorphisms in genes encoding to other intervenient proteins in folate, purine, pyrimidine, adenosine, and methionine pathways, and also differences in the definition of MTX clinical response [28].

Besides the potential importance of our results, we are aware of possible limitations, especially the sample size. Despite this, patient characteristics are similar to those reported in the literature [36, 37]. Our case series is a representative clinical practice cohort of established and well-defined RA patients [25, 38] and the genotypes distribution of *MTHFR* C677T and *ATIC* T675C polymorphisms is in accordance with the published literature for other Caucasian population [13, 14, 24–26, 39].

4.1. MTHFR C677T and ATIC T675C and Clinical Response to MTX. Regarding MTHFR C677T polymorphism, our results demonstrated a statistically significant association between MTHFR 677TT and nonresponse to MTX, which is in accordance with previously reported studies [13, 24]. Although MTHFR is not directly inhibited by MTX or MTXPG, its expression levels may play an important role in MTX overall effect by modifying the folate status of the cell [16]. Literature describes MTHFR 677TT as responsible for a reduction of MTHFR activity [29], leading to reduced 5-MTHF and other folate cofactors levels and, consequently, to decreased adenosine release [22, 23, 40], which can partially explain MTX nonresponse.

Regarding ATIC T675C polymorphism, our results indicate that ATIC 675T carriers presented an increased risk for nonresponse to MTX, as previously reported [14, 26]. To the best of our knowledge, there are no functional studies reporting the effect of this polymorphism in ATIC activity. Nevertheless, it can be hypothesized that the presence of ATIC 675T allele will lead to MTX nonresponse due to the increased conversion of AICAR to FAICAR (Figure 1), causing adenosine degradation and its nonrelease, hindering MTX anti-inflammatory effects. Additionally, ATIC 675T allele seems to contribute to the decrease of MTX antiproliferative effect [41]. Moreover, this polymorphism seems to be in linkage disequilibrium with ATIC C347G (rs2372536), of which ATIC 347G carriers (minor allele) have been reported as related to better response [16, 26, 42, 43]. Hence, results are consistent with ours reporting an association between ATIC 675CC (minor allele) and clinical response to MTX.

4.2. Clinicopathological Variables and Clinical Response to MTX. According to patient-related variables, multivariate analysis results demonstrated that noncurrent smokers were associated with nonresponse to MTX. Literature describes the association between smoking and decreased folate levels

which, in fact, enhance the antifolate effect of MTX and, therefore, improve clinical response to MTX [44-46]. Furthermore, cigarette nicotine seems to potentiate the immunosuppressive and anti-inflammatory effects by acting on the immunological system [47, 48]. Although some studies have demonstrated that smokers had worst response to MTX, presenting a higher disease activity and severity [6, 49], others were able to demonstrate that tobacco exposure reduced radiographic progression and favored a better functional score [50, 51]. Considering disease-related variables, our results demonstrated an association of more than 2-fold higher risk between anti-CCP and ANAs positivity and nonresponse to MTX. Anti-CCP and ANAs are autoantibodies found in RA that are strongly correlated with erosive disease, worse functional status, and higher disease activity [1, 9, 52-55] associated with nonresponse. Other studies have shown a relation between anti-CCP positivity and MTX response or presented no associations in early RA patients [56, 57]; nevertheless, our results may be explained by the fact that our series was constituted mainly by patients with established disease. To the best of our knowledge there are no studies in RA associating ANAs and MTX response. Additionally, higher HAQ was associated with more than 2-fold increased risk for nonresponse to MTX. Since higher HAQ score represents an increased disease activity it was expected, as reported by others, that these patients have worst response [56, 58]. In accordance with treatment-related variables, the concomitant use of NSAIDs was correlated with nonresponse to MTX. These results could be explained by the existence of drugdrug interactions since NSAIDs are known to alter MTX and 7-hydroxymethotrexate binding to plasmatic proteins and to impair MTX hepatic metabolism [41]. This translates into low amount of free MTX and lesser formation of active MTX metabolites in hepatocytes. Due to the importance of NSAIDs as symptomatic therapy in RA and due to contradictory results reported, further studies are required to clarify this association [56, 59]. In addition, SC administration route was statistically significant associated with MTX response. This result can be explained by the higher MTX bioavailability associated with SC administration route [60]. Consequently, this will lead to a greater tissues exposure to MTX, higher cellular polyglutamation and retention, and better response to MTX.

5. Conclusions

Our results suggested that noncurrent smoking, anti-CCP and ANAs positivity, higher HAQ, NSAIDs utilization, PO administration route, T homozygosity for *MTHFR* C677T, and T allele carrying for *ATIC* T675C can be possible predictive factors of nonresponse to MTX. Thus, the inclusion of these polymorphisms in combination with clinicopathological variables may add valuable information that may help to identify patients who will benefit from MTX treatment and assist clinicians to make better treatment decisions. Despite the potential of these findings, translation into clinical practice requires larger and multicentric studies in order to clearly endorse the importance of these polymorphisms.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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Clinical Study

Monitoring Drug and Antidrug Levels: A Rational Approach in Rheumatoid Arthritis Patients Treated with Biologic Agents Who Experience Inadequate Response While Being on a Stable Biologic Treatment

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Clinical response in patients with rheumatoid arthritis (RA) treated with biologic agents can be influenced by their pharmacokinetics and immunogenicity. The present study evaluated the concordance between serum drug and antidrug levels as well as the clinical response in RA patients treated with biological agents who experience their first disease exacerbation while being on a stable biologic treatment. 154 RA patients treated with rituximab (RTX), infliximab (IFX), adalimumab (ADL), or etanercept (ETN) were included. DAS28, SDAI, and EULAR response were assessed at baseline and reevaluated at precise time intervals. At the time of their first sign of inadequate response, patients were tested for both serum drug level and antidrug antibodies level. At the next reevaluation, patients retreated with RTX that had detectable drug level had a better EULAR response (P = 0.038) with lower DAS28 and SDAI scores (P = 0.01 and P = 0.03). The same tendency was observed in patients treated with IFX and ETN regarding EULAR response (P = 0.002 and P = 0.023), DAS28 score (P = 0.002 and P = 0.003), and SDAI score (P = 0.001 and P = 0.026). Detectable biologic drug levels correlated with a better clinical response in patients experiencing their first RA inadequate response while being on a stable biologic treatment with RTX, IFX, and ETN.

1. Introduction

Rheumatoid arthritis (RA) is a chronic inflammatory disease that can result in substantial morbidity [1–3], impaired physical activity, and poor quality of life [4, 5], leading to a reduced life expectancy by 3 to 18 years [6] and increased mortality [7–11].

The targets of biologic agents are interactions between the immune cells (mainly T lymphocytes, B lymphocytes, and macrophages), which are responsible for inflammation and structural damage in affected joints, and the signaling molecules involved in their activation. The most used approved biologic agents for the treatment of RA are tumor necrosis factor (TNF) antagonists (infliximab, adalimumab, etanercept, golimumab, and certolizumab) or products that target B cells like rituximab (a chimeric monoclonal antibody that targets CD20 B cells) or inhibitor of costimulation of T cells (abatacept). Most of these agents are very effective

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at improving the signs and symptoms and at slowing or preventing structural damage in patients with RA [12–21]. Since the introduction of biologic treatment, prognosis of the disease has been substantially improved [22, 23].

Nevertheless, despite all these therapeutic advances and their relatively expensive costs, a variable proportion of patients with several autoimmune diseases including RA and inflammatory bowel diseases (IBD), who initially benefited from biologics, eventually lost response [24–26]. For example, a study from the Swedish TNF-antagonist registry found that 44% of patients were still taking their initial therapy at five years, and 25% were no longer taking any TNF antagonist at all [25]. As for IBD, up to 50% of patients lose response to treatment (secondary nonresponders) and up to 30% do not respond at all (primary nonresponders) [27]. The rational for lack or loss of response is multifactorial: molecular structure of biologic drug, pharmacokinetics, pharmacodynamics, and development of anti-drug antibodies.

In IBD, there are several strategies to the management of secondary failure to TNF antagonists [26]. These include switching to another drug in the same or different class, increasing the dose of biologic drug, changing concomitant immunosuppressive drug, or measuring drug levels and antibodies [28–30]. Therapeutic drug monitoring seems to be the adequate approach for the biologic treatment management [28]. Testing for drug levels and antibodies in secondary nonresponders is more cost-effective when compared to empiric drug escalation [31, 32]. It identifies those patients who will benefit from dose escalation versus those who are unlikely to respond to this strategy (high titers of anti-drug antibodies) [33].

Drug immunogenicity is one of the main mechanisms behind therapeutic failure also for RA patients [34–38]. Systemic reviews and meta-analysis conclude that anti-drug antibodies are clinically relevant and lead to significant decrease of therapeutic response [39]. Dose escalation in these patients may boost anti-drug antibodies production with serious adverse events [37, 40–42]. As for nonresponders without anti-drug antibodies but with detectable serum drug levels, these may respond better when switched to a drug with different mechanisms of action [43].

2. Methods

During a period of 2 years (January 2012–January 2014), we followed up 154 patients with established RA receiving one of the following biologic agents: rituximab (62 patients), infliximab (32 patients), etanercept (45 patients), and adalimumab (15 patients) with concomitant conventional synthetic disease-modifying antirheumatic drug (csDMARD) and few cases of monotherapy. Patients were included in order of their admission to the Department of Rheumatology, "Sfanta Maria" Hospital, Bucharest, Romania. All patients were previously diagnosed with RA according to ACR 1987 criteria [44] or ACR/EULAR 2010 criteria [45] and were treated using "treat to target" strategy [46] and local guidelines for the management of active RA [47]. The study was approved by the hospital Ethics Committee and all patients gave written informed consent before the study was started.

Demographic data, clinical (number of tender and swollen joints) and laboratory (ESR-erythrocyte sedimentation rate, CRP: C reactive protein, RF: rheumatoid factor, ACPA: anticyclic citrullinated peptide, IgG type) variables were collected at baseline and at each reevaluation. RA activity was evaluated in all patients by using 3 variables: Disease activity scores (DAS28 4v), Simplified Disease Activity Index (SDAI), and European League Against Rheumatism (EULAR) response. All clinical evaluations were performed by two independent assessors. As it was proposed at OMER-ACT 9 (Outcomes in Rheumatology) meeting [48], a RA flare represents a cluster of symptoms of sufficient duration intensity to require (re)initiation, change, or increase in therapy. Nevertheless, as suggested by several reports [49], in clinical research these criteria may be difficult to apply. Since there is no definition validated, we considered the situation as RA flare when at least one of the following conditions occurred: an increase in SDAI, an increase in ESR and/or CRP not due to a concomitant infection, an increase in DAS score to moderate or high disease activity, and a lower class in EULAR response as compared to previous reevaluation. At the moment of RA flare as described before, just before a new administration, patients were tested for anti-drug antibodies and biologic drug serum levels. According to serum drug levels patients were classified in group A if their serum drug levels were detectable and in group B if their drug levels were undetectable.

Patients were excluded from testing if their RA flare was related to conventional synthetic or biologic DMARD discontinuation, or a concomitant infectious disease, also if between baseline (the moment of serum drug level testing) and next reevaluation; patients had a change in their treatment regimen (increase in glucocorticoid dose and csDMARD dose or addition of a new immunosuppressive drugs). These particular patients were excluded from the final analysis. The reevaluation and clinical responses were assessed for each biologic drug: after 6 months from drug level testing, for RTX; after 2 months, just before a new i.v. infusion, for IFX; and after 3 to 4 months, for ETN and ADL.

2.1. Detection of Serum Drug Level and Anti-Drug Antibodies. Serum drug and antidrug levels were measured by enzyme linked immunosorbent assay (ELISA), using Progenika kits (Promonitor-RTX, Promonitor-anti-RTX, Promonitor-IFX, Promonitor-anti-IFX, Promonitor-ETN, Promonitor-anti-ETN, Promonitor-ADL, and Promonitor-anti-ADL). Several assays and technologies have been approved for monitoring serum drug and antidrug level [50], but bridging ELISA seems to be the only method with the potential for routine adoption in a hospital clinical setting for patient monitoring [37, 43, 51, 52]. It has been demonstrated that antibodies against TNF antagonists are anti-idiotypic, therefore neutralizing by definition [53]. Other technologies like cellbased assays, biacore, and homogeneous mobility shift assays can characterize the functionality of anti-drug antibodies; however, the question arises whether characterization of the antibody binding activity is required, when this can be easily answered with a simple ELISA test due to the fact that the immune response detected by ELISA is neutralizing. ELISA

assays detect binding antibodies regardless of their functional activity. This method is similar for any other solid-phase methods like radioimmunoassays (RIA).

The clinical relevance of the immune response detected by ELISA is very well established and demonstrated in several studies [37, 51, 54, 55]. Promonitor kits have high accuracy for quantifying serum drug level, a pivotal importance to develop therapeutic algorithms [56].

In regards to drug levels detected by Promonitor kits, these span all clinically relevant drug concentrations (35–14400 ng/mL, 24–12000 ng/mL, 35–40000 ng/mL, and 665–240000 ng/mL for IFX, ADL, ETN, and RTX levels, resp.). ELISA tests used in this work have demonstrated an excellent correlation with other commercially available assays used for drug monitoring [56].

Cut-points of the anti-drug antibody tests are determined to be 2 AU/mL, 3.5 AU/mL, 142 AU/mL, and 340 AU/mL for anti-IFX, anti-ADL, anti-ETN, and anti-RTX antibodies, respectively. No human anti-drug antibody is currently available for anti-drug antibody screening; therefore outputs are given in arbitrary units per milliliter.

2.2. Statistical Analysis. Statistical analysis was performed using SPSS statistical software, version 20.0. The data were expressed as the mean \pm SD. All statistical tests were two-sided and were performed at an α level of 0.05. The differences between groups were analyzed by Student's t-test, Kruskal-Wallis test, or Mann-Whitney test, as appropriate. Spearman's test was used for correlations.

3. Results

3.1. Characteristics of the Cohort. The study included 154 patients with established RA. One hundred and ten of them had a clinical or laboratory condition suggesting a disease flare during the evaluated period. Since final analysis, 38 patients met the exclusion criteria (8 patients had a significant increase in their glucocorticoid dose, 12 patients had csD-MARD dose increase, 7 patients had a new csDMARD added to their treatment regimen, and 11 patients were switched to another biologic drug).

The final cohort of tested patients had the following treatment characteristics: 34.72% RTX patients (25 patients), 27.77% IFX patients (20 patients), 25% ETN patients (18 patients), and 12.5% ADL patients (9 patients). Their mean current biologic agent treatment was 41.79 ± 27.76 months in patients with RTX treatment, 34.45 ± 27.76 months with IFX, 49.38 ± 38.03 months with ETN, and 45.56 ± 23.88 months with ADL. The results showed that no detectable anti-drug antibodies were found in patients receiving RTX, ADL, and ETN. Patient's baseline characteristics are listed in Table 1.

At the moment of disease flare, 36% patients from the RTX group had undetectable drug level with 66.66% of them having moderate and high disease activity, mean DAS28 score of 3.45 ± 1.20 . SDAI was lower in patients with detectable drug levels compared to patients with undetectable drug levels, 20.0 ± 15.7 versus 21.7 ± 29.6 . There was no significant difference between groups A and B regarding both DAS28

score and SDAI (P = 0.678 and P = 0.845) nor treatment duration (27.75 \pm 13.71 versus 48.81 \pm 53.94, P = 0.294).

We found a significant difference in RTX serum level depending on ACPA status (P=0.021). ACPA presence was positively associated with detectable RTX levels (OR = 8.75; 95%CI 1.21–63.4; P=0.032) being a moderate predictor with AUC = 0.715; 95%CI: 0.5239–0.9067. This new finding supports the idea that patients positive for ACPA achieve a better clinical result being on treatment with B-cell depletion therapy. The mechanism by which these patients have higher RTX serum drug level should be studied further.

Interestingly, RTX serum level also correlated with the increased number of previous biologic agents (P=0.009, r=0.514). Sixty-two percent of patients with detectable serum RTX level had 2 anti-TNF agents as previous biologic treatment. Mention should be made that according to local guidelines, RTX is a second line biologic drug.

In the IFX treated patients, 90.90% (10 patients) of those with undetectable IFX serum level had moderate and high disease activity. Seven (63.63%) of these patients had anti-IFX antibodies. Surprisingly, anti-IFX antibodies were also found in 2 patients with subtherapeutic drug level. Twelve patients (60%) had a csDMARD associated: 8 patients had methotrexate, one patient had azathioprine, two patients had leflunomide, and one patient had sulfasalazine. Six patients did not have a csDMARD associated. Methotrexate dose range was between 7.5 mg and 20 mg/week. Our results showed that methotrexate association and the presence of anti-IFX antibodies were negatively correlated (P = 0.048, P = -0.047), confirming that methotrexate reduces IFX immunogenicity.

No anti-ETN antibodies were found in the 18 patients treated with ETN. At baseline, 77.77% of them had moderate and high disease activity evaluated by using DAS28 score and only 3 patients had undetectable drug levels. Also in this subgroup, there were 5 (27.7%) patients without a csDMARD, but all of them had detectable drug levels. Seven patients had methotrexate associated ranging from 10 mg to 20 mg/week and 6 patients had leflunomide 20 mg/day.

The group of patients treated with ADL that had a RA flare and were tested for drug levels was relatively small; 9 patients out of 15 patients enrolled in the study. Their mean DAS28 score was of 3.41. Moderate disease activity was found in 55.55% of them. No anti-ADL antibodies were detected. Only one patient had no csDMARD associated. Seven patients had methotrexate associated (10–20 mg/week, mean dose 15 mg/week) and one patient had leflunomide 20 mg/day.

3.2. Therapeutic Responses at Next Reevaluation after RA Exacerbation. During the follow-up period, patients from the final analysis remained on the same therapeutic treatment regimen regarding conventional synthetic and biologic DMARDs. Their EULAR responses are listed in Table 2.

Six months after testing the serum drug levels, RTX treated patients that had detectable drug levels at baseline (group A) and had a mean DAS28 2.93 \pm 1.20 compared to 3.27 \pm 1.47 in group B (P=0.01). Twenty-two percent of patients from group B still had high disease activity according

TABLE 1: Patient's characteristics at the moment of dosing biologic drug level.

Biologic agent	Current biologic treatment, duration, and mean	DAS28 baseline, mean	SDAI baseline, mean	csDMARD associated, no (%)	ACPA positive, no (%)	RF positive, no
RTX						
Group A	48.8 ± 53.4	3.65 ± 1.12	20.0 ± 15.7	15 (60%)	14 (56%)	16 (64%)
Group B	27.7 ± 13.7	3.45 ± 1.19	21.7 ± 29.6	8 (32%)	4 (16%)	7 (28%)
P	0.294	0.678	0.845	0.667	0.021	0.049
IFX						
Group A	40.6 ± 39.9	3.57 ± 1.25	15.2 ± 19.7	6 (30%)	4 (20%)	7 (35%)
Group B	29.3 ± 17.5	5.42 ± 1.19	43.2 ± 29.6	6 (30%)	3 (15%)	4 (20%)
P	0.379	0.003	0.026	0.582	0.515	0.064
ETN						
Group A	47.8 ± 38.5	4.14 ± 1.44	31.6 ± 31.3	10 (55.55%)	11 (61.11%)	12 (66.67%)
Group B	57.6 ± 23.7	5.25 ± 1.79	41.5 ± 40.3	3 (16.67%)	2 (11.11%)	2 (11.11%)
P	0.679	0.259	0.639	0.239	0.814	0.612
ADL						
Group A	46.7 ± 25.2	3.39 ± 1.04	10.1 ± 6.05	7 (77.78%)	4 (44.44%)	6 (66.67%)
Group B	36	3.54	32.9	1 (11.11%)	1 (11.11%)	1 (11.11%)
P	0.700	0.902	0.009	0.708	0.495	0.571

Differences between patient's baseline characteristics were tested by Student's *t*-test or chi-square test.

RTX: rituximab; IFX: infliximab; ETN: etanercept; ADL: adalimumab.

Group A: detectable drug level; Group B: undetectable drug level.

csDMARD: conventional synthetic disease modifying antirheumatic drug; ACPA: anticitrullinated peptides antibodies status; RF: rheumatoid factor status.

TABLE 2: EULAR responses at next reevaluation after first RA flare.

	EULAR response			
	No	Moderate	Good	P
RTX				
Group A	4 (16%)	5 (20%)	7 (28%)	0.038
Group B	6 (24%)	2 (10%)	1 (4%)	0.038
IFX				
Group A	2 (10%)	5 (25%)	2 (10%)	0.002
Group B	10 (50%)	1 (5%)	0	
ETN				
Group A	3 (16.67%)	5 (27.78%)	7 (38.89%)	0.023
Group B	3 (16.67%)	0	0	0.023
ADL				
Group A	2 (22.22%)	1 (11.11%)	5 (55.56%)	0.194
Group B	1 (11.11%)	0	0	0.194

Differences between EULAR responses in group A and group B were tested using Kruskal-Wallis test, for each biologic agent.

RTX: rituximab; IFX: infliximab; ETN: etanercept; ADL: adalimumab.

Group A: detectable drug level; Group B: undetectable drug level.

to DAS28 score and only 3 patients in this group obtained remission. The differences in disease activity (remission, low, moderate, and high) using DAS28 score were significant between groups A and B (P=0.003). There was also a significant difference in their SDAI evolution: mean SDAI in group A was 12.23 \pm 14.13 and in group B was 14.83 \pm 20.51 (P=0.033).

Regarding EULAR response (no, moderate, and good) in RTX treated patients there was a significant difference in the evolution of the two groups (P = 0.038). Twelve patients from group A achieved good and moderate response compared to only 3 patients from group B (Table 2).

All patients treated with IFX were reevaluated after 2 months. The difference in DAS28 evolution between group A

	Positive anti-IFX antibodies	Negative anti-IFX antibodies	P value
Disease duration, mean, and months	90.77 ± 49.56	128 ± 97.48	0.306
IFX treatment duration, mean, and months	29.77 ± 17.01	38.77 ± 34.60	0.511
DAS28 at flare and mean	5.09 ± 1.19	4.18 ± 1.67	0.189
DAS28 after 2 months and mean	5.68 ± 0.8	3.95 ± 1.49	0.006
csDMARD association and nr (%)	3	9	0.028

TABLE 3: Patient's characteristics among positive and negative anti-IFX antibodies.

Differences between patient's characteristics were tested by Student's *t*-test or chi-square test. IFX: infliximab; csDMARD: conventional synthetic disease modifying antirheumatic drug.

and group B was significant: 3.67 ± 1.24 versus 5.59 ± 1.07 (P = 0.002). None of the patients having undetectable drug level at first RA flare achieved remission or low disease activity. Clinical response was also significantly different regarding also SDAI evolution (group A mean SDAI 17.26 \pm 12.29 compared to group B mean SDAI 44.33 \pm 18.22, P = 0.001). EULAR response was better in patients having detectable drug level at flare (P = 0.002) (Table 2).

Anti-drug antibodies were detected in 45% of IFX treated patients: seven patients (35%) had undetectable IFX level and 2 patients (10%) had subtherapeutic IFX level. All patients having anti-IFX antibodies had no EULAR response at follow-up and appropriate therapeutic management was initiated. Patient's characteristics are listed under positive and negative anti-IFX antibodies (Table 3).

At follow-up, higher DAS28 score was observed in patients with undetectable ETN levels compared to those from group A (7.17 \pm 1.21 versus 3.57 \pm 1.65, P=0.003). Similar results were obtained in regards SDAI evolution: mean SDAI in group A was 19.06 versus mean SDAI in group B of 58.73 (P=0.026). Patients with detectable ETN drug levels had better EULAR response (P=0.023).

There was a relatively small number of patients treated with ADL. Mean DAS28 after 4 months of treatment from RA flare was 2.20 ± 0.38 in patients with detectable drug levels. Only one patient with undetectable drug level consequently had moderate disease activity at follow-up. No anti-ADL antibodies were found in patients treated with ADL.

4. Discussions

Current recommendation for the management of RA does not address serum biologic drug monitoring in clinical practice [46] even if biologicals possess a large pharmacokinetic variation. Thus, if a better disease control is aimed at measuring drug level seems appropriate [57].

RTX detectable drug level correlated with better clinical response at follow-up. We found a significant difference in RTX drug level at the moment of inadequate response in patients with positive and negative ACPA status. In a number of studies, serum concentration of ACPA and RF decreases during RTX treatment [58, 59], but their relation to RTX serum level has not been studied yet. As is known, there are biomarkers that seem to predict a good EULAR response: no steroid therapy, low lymphocyte count, and high RF level and BAFF levels [60]. Meanwhile, in larger observational cohort study, ACPA was a better biomarker of good EULAR

response than RF [61]. Whether RF and/or ACPA positivity predict a better clinical response to RTX still remains to be demonstrated.

In our study, IFX serum drug level at the moment of inadequate response correlated with clinical activity. There was a significant difference in patient's EULAR response at follow-up; patients that had detectable serum drug levels had a better response. The presence of anti-IFX antibodies correlated to disease activity using DAS28 score at baseline; all of the patients with anti-drug antibodies had no EULAR response at follow-up. Methotrexate dose has an impact on INF immunogenicity and appropriate therapeutic approach should be made to reduce its immunogenicity.

As is well known, ETN has the lowest immunogenicity [62] and in our study none of the patients experiencing inadequate response had anti-ETA antibodies. Even though a proportion of them did not have a csDMARD associated there were no differences in serum drug levels. The data obtained in the ADL treated group was not significantly relevant because of the number of patients. But this cannot exclude the utility of serum drug and anti-drug dosing in patients treated with ADL.

Our results showed that evaluation of drug levels in patients that experience inadequate response while being on biologics correlate to their clinical response at follow-up. Thus it can be possible to determine loss of efficacy starting from the first RA exacerbation in patients with stable biologic treatment. This approach can be used in view of a better disease control and appropriate therapeutic decision.

We acknowledge that our study cannot fully demonstrate whether biologic drug dosing is predictive for clinical response and nonresponsiveness. Further studies are essential as this may be an argument for switching to another biologic drug in RA patients.

5. Conclusion

To our knowledge, this is the first study that evaluates biologic drug levels at first inadequate response and their relation to further clinical response in patients with RA. Our study strongly supports the idea that serum drug monitoring should be considered in clinical practice during long-term use of biologic agents. It adds some evidence that immunogenicity has an impact in clinical response in patients with anti-drug antibodies. Measuring drug level and assessing immunogenicity in a RA flare might help to optimize and personalize usage of biological therapies.

Ethical Approval

Ethics Committee of the "Carol Davila" University of Medicine and Pharmacology, Bucharest Romania, approved this study.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

Authors' Contribution

Diana Mazilu and Daniela Opris contributed equally to this study.

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Review Article

Imbalance between Endothelial Damage and Repair: A Gateway to Cardiovascular Disease in Systemic Lupus Erythematosus

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Atherosclerosis is accelerated in patients with systemic lupus erythematosus (SLE) and it leads to excessive cardiovascular complications in these patients. Despite the improved awareness of cardiovascular disease and advent of clinical diagnostics, the process of atherogenesis in most patients remains clinically silent until symptoms and signs of cardiovascular complications develop. As evidence has demonstrated that vascular damage is already occurring before clinically overt cardiovascular disease develops in lupus patients, intervention at the preclinical stage of atherogenesis would be plausible. Indeed, endothelial dysfunction, one of the earliest steps of atherogenesis, has been demonstrated to occur in lupus patients even when they are naïve for cardiovascular disease. Currently known "endothelium-toxic" factors including type 1 interferon, proinflammatory cytokines, inflammatory cells, immune complexes, costimulatory molecules, neutrophils extracellular traps, lupus-related autoantibodies, oxidative stress, and dyslipidemia, coupled with the aberrant functions of the endothelial progenitor cells (EPC) which are crucial to vascular repair, likely tip the balance towards endothelial dysfunction and propensity to develop cardiovascular disease in lupus patients. In this review, altered physiology of the endothelium, factors leading to perturbed vascular repair contributed by lupus EPC and the impact of proatherogenic factors on the endothelium which potentially lead to atherosclerosis in lupus patients will be discussed.

1. Introduction

1.1. Systemic Lupus Erythematosus and Cardiovascular Disease. Systemic lupus erythematosus (SLE) is a systemic autoimmune condition mainly mediated by immune-complex induced inflammation which potentially affects any organ system during the course of the disease [1]. Although the overall survival of lupus patients has been improving in the past 5 decades, excessive mortality is unanimously evident [2]. While disease- and treatment-related complications such as renal disease and infections remain as the leading causes of death in patients with SLE, cardiovascular disease (CVD) is emerging as an increasingly common cause of mortality amongst these patients over the past 30 years [3]. While patients with SLE in general are over 2 times more likely to have CVD as compared with the general populations [4], an epidemiological study revealed that lupus patients older

than the age of 35 are >50 times more likely to develop CVD than their age- and sex-matched healthy counterparts [5]. The reasons for the high prevalence of CVD in lupus patients are multifactorial. Besides the fact that patients with SLE carry more unfavourable traditional Framingham risk factors such as hypertension, dyslipidaemia, and diabetes mellitus than their healthy counterparts, nonclassical cardiovascular risk factors, systemic inflammation and proinflammatory adipokines, and treatment-related side effects are operant [6]. While not as extensively studied as in patients with rheumatoid arthritis in larger scale studies [7-10], genetic polymorphisms potentially contributing to cardiovascular disease in patients with SLE have increasingly been identified in a number of lupus cohorts [11-16]. Thus far, genetic polymorphisms associated with premature atherosclerosis and cardiovascular disease in patients with SLE have been convincingly found in the *interferon regulatory factor 8 (IRF8)*

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[11], matrix metalloproteinase-2 (MMP-2) functional promoter [12], plasminogen activator inhibitor 1 (PAI-1) promoter [13], mannose-binding lectin-2 (MBL-2) [14], stromelysin promoter [15], and *C-reactive protein (CRP)* genes [16]. With the everincreasing knowledge in the pathogenesis of atherogenesis in SLE, more genetic polymorphisms related to CVD in patients with SLE are expected to be identified.

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1.2. Early Recognition of Atherogenesis in Patients with Systemic Lupus Erythematosus. Currently, therapeutic strategy for CVD is considered "palliative" in that drugs such as antiplatelet agents, anticoagulants, antihypertensives, and statins aim to mitigate cardiovascular risk factors and reduce the probability of future cardiovascular events [17]. In the era of preventive medicine, it is prudent to recognize atherosclerosis early in its progress so that more meticulous monitoring can be instituted and potential primary interventions can be tested, with an ultimate aim to prevent the development of clinically overt cardiovascular complications such as arrhythmias, myocardial ischaemia, and subendocardial and even full-thickness myocardial infarctions. To date, a number of modalities to detect early changes in the process of atherogenesis such as carotid intima-media thickness [18-20], coronary calcium [21–23], speckle-tracking strain echocardiogram [24, 25], and endothelium-dependent vasodilation [26–30] have been reported in patients with SLE and related autoimmune disorders such as scleroderma and systemic vasculitides [18-25]. Amongst these modalities, assessment of the endothelium has received much attention because, at present, it is strongly believed that endothelial dysfunction is one of the earliest steps involved in the process of atherogenesis [31]. Additionally, endothelial dysfunction is theoretically reversible, making it a potentially attractive site of target for preventive intervention against the development of CVD [32]. In this review, how various factors affect the physiology of the endothelium which result in the imbalance between endothelial damage and endothelial repair that lead to CVD, as evident in both murine lupus models and human disease, will be discussed. Information constituting this review was extracted from relevant original papers and review articles on PubMed between 1950 and January 2014 by using the combinations of the keywords "lupus," "cardiovascular," and "endothelial." Bibliography of the relevant articles obtained was thoroughly assessed for relevancy. References which were deemed to be relevant by the authors of this review were further hand-searched, with the useful information extracted for discussion in this paper.

2. Normal Physiology of the Endothelium and the Functions of Nitric Oxide—In Brief

The vascular endothelium is a monolayer of cells, which line the luminal surface of blood vessels of all sizes, and confers a physical barrier from potential injuries induced by various vascular toxic components in the blood such as inflammatory mediators, oxidizers, infective agents, and migrating inflammatory cells [33]. Aside from being a physical barrier, the endothelium regulates the vascular tone in response to physiological changes such as intravascular shear stress and high perfusion pressure by producing endothelium-derived relaxing factors (EDRF) which provokes vasodilation and reduces vascular resistance [34]. The EDRF was subsequently identified to be endothelial nitric oxide (NO), which is converted from the substrate L-arginine by the enzymatic action of endothelial NO synthase (eNOS) [35]. NO diffuses into the vascular smooth muscle layer and mediates cyclic GMP-mediated vasodilation. As involved in one of the earliest steps of atherogenesis, the deficiency in the production and bioavailability of NO as a result of endothelial damage lead to impairment of endothelial-dependent vasodilation, which has been proven to be an independent risk factor of cardiovascular events [36, 37].

Besides regulation of vascular tone, NO also contributes to part of the anti-inflammatory and antithrombotic properties on the endothelial level. NO has been demonstrated to reduce interleukin (IL)-1-induced VCAM-1 expression which is paralleled by the reduction of monocyte adhesion to the endothelium, in addition to repressing the production of soluble IL-6 and IL-8 [38, 39]. Recently, an *in vitro* study found that AMP-activated protein kinase, which is central to the regulation of eNOS, reduced TNF α -induced monocyte adhesion on human aortic endothelial cells and endothelial MCP-1 expression [40]. As for the antithrombotic effect of NO, it has been demonstrated that the activity of eNOS and the endothelial isoform of NO are critical regulators which suppress platelet activation and aggregation [41].

3. Assessment of Endothelial Function: The Current State

3.1. Endothelium-Dependent and Endothelium-Independent Flow-Mediated Dilation. To date, there are two established methods to assess the function of the endothelium biophysically, namely, the endothelium-dependent vasodilation, or flow-mediated vasodilation (FMD), and endothelium-independent vasodilation [42]. In brief, for measuring the FMD, subjects are asked to rest in supine position for at least ten minutes before the measurement in the same position. FMD at the brachial artery is measured using a high-resolution ultrasound system, in which the ultrasound probe is steadied by a stereotactic holding device which also permits fine positional adjustment. Reactive hyperaemia is induced by rapid inflation of a pneumatic cuff placed around the proximal forearm to pressure 50 mm Hg above the systolic blood pressure for around 5 minutes, followed by rapid deflation [42]. Change of the vessel diameter at maximum dilatation and percentage of FMD change can hence be detected by the ultrasound probe and calculated by a computer program, with the peak reactive hyperaemic blood flow at 45 to 60 seconds after cuff deflation [42]. All FMD studies are preferably performed after abstention from food and exercise, for 8 to 12 hours, and caffeine and alcohol for 24 and 48 hours, respectively [42]. Another established way to assess endothelial reactivity is to measure endothelium-independent vasodilation of the brachial artery before and after administration of nitroglycerin, which is a direct smooth-muscle relaxant without the need for nitric oxide production and release by the endothelium. After 10 to 15 minutes of rest

following completion of endothelium-dependent FMD measurement, 0.4 mg of nitroglycerin, in the form of sublingual spray or tablet, is administered. Peak vasodilation occurs between 3 and 5 minutes after nitroglycerin administration and endothelium-independent FMD can be measured, using the same method as for endothelium-dependent FMD, except that no forearm occlusion is required [43]. According to a recent meta-analysis of 13 studies, FMD but not endothelium-independent vasodilation, is reduced in patients with SLE. However, interpretation of FMD needs to be cautious especially in lupus patients of advanced age and in those who have longstanding SLE because these factors independently affect endothelial function [43].

3.2. Endothelial Progenitor Cells. Originated from the haematopoietic stem cells, the endothelial progenitor cells (EPC) are believed to participate in repairing the damaged endothelium and maintaining the integrity of vascular lining [44]. In a number of well-conducted case-control studies, EPC have been shown to be reduced in patients carrying traditional cardiovascular risk factors such as diabetes mellitus and hypertension [45, 46], as well as in those with clinical cerebrovascular and cardiovascular diseases [47, 48]. In a 1year prospective study of 519 patients with angiographyconfirmed coronary artery disease, patients with higher baseline levels of EPC (identified as CD34+CD133+CD309+ cells) were noted to be associated with reductions in risks of death from cardiovascular causes, a first major cardiovascular event, revascularization procedure, and hospitalization by 69%, 26%, 23%, and 38%, respectively, than those with lower baseline EPC levels, after adjusting for age, sex, and vascular risk factors [49].

In rheumatic disorders, EPC have been relatively well studied in scleroderma and SLE, but results are inconsistent [50–54]. The main problem of EPC studies likely stems from the absence of a consensus on the surface markers leading to identification of the true population of EPC, as well as a validated and reliable strategy to identify them. In fact, the European League Against Rheumatism (EULAR) Scleroderma Trials and Research group (EULAR/EUSTAR) has recently proposed a standard method in identifying EPC in patients with scleroderma by the use of fluorospheres and elimination of dead cells and lineage-positive population [51]. Such method resulted in a consistent finding of low levels of circulating EPC in patients with scleroderma [51]. In SLE, while most of the studies demonstrated lower circulating EPC in patients with SLE than their healthy counterparts, results are inconsistent, most likely due to different protocols adopted for identifying EPC [52-54]. Nevertheless, whether the number of circulating EPC can predict cardiovascular events in patients with SLE remains to be answered by prospective studies.

4. Altered Physiology of Endothelium in SLE

4.1. Factors Associated with Endothelial Damage. Being the hallmark of the pathogenesis of SLE, inflammation has been postulated to be one of the most important triggers of endothelial damage. Type 1 interferon (IFN) appears to

play the critical role in mediating endothelial damage in patients with SLE [55], alongside with other endothelial toxic mediators and conditions both dependent and independent of type 1 IFN including proinflammatory cytokines, costimulatory molecules, immune complexes, oxidized lipid species, oxidative stress, autoantibodies, including antiphospholipid antibodies and anti-annexin-V antibodies, and the process of neutrophil extracellular traps ("Netosis").

4.2. Type 1 Interferon. Type 1 IFN, which is central to the pathogenesis of SLE and mainly produced by the plasmacytoid dendritic cells (pDC), is increased in the majority of patients with SLE [56, 57]. pDC residing in atherosclerotic plaques produce type I IFN which locally induces adjacent CD4+ T cells to express TNF-related apoptosisinducing ligand (TRAIL) [58]. While TRAIL was demonstrated to be antiatherosclerotic in the context of chronic inflammation and deficiency of TRAIL was shown to be associated with calcification in atherosclerosis in a mouse model [59, 60], TRAIL potentially leads to plaque rupture and acute coronary event [58]. Type 1 IFN also induces myeloid dendritic cells (mDCs) in atherosclerotic plaques to produce inflammatory cytokines and matrix metalloproteinases which are capable of destabilizing plaques [61]. Platelet aggregation and thrombosis are also induced by type 1 IFN on diseased endothelium in a P-selectin-dependent fashion [62]. Indeed, SLE platelets have been demonstrated to have heightened IFN signatures which are able to activate pDC and subsequent IFNα production through the interaction between CD40 and CD40L, potentially perpetuating endothelial toxicity and vascular thrombosis by further activating platelet aggregation as a positive feedback loop [63].

IFN α has recently been shown to affect vasculogenesis by interfering the phenotypes and function of EPC [64]. How IFN α affects EPC and impairs endothelial repair will be discussed in subsequent sections.

4.3. Oxidized Low-Density Lipoproteins and Proinflammatory High-Density Lipoproteins. While epidemiological studies have demonstrated strong associations between high serum levels of circulating oxidized low-density lipoproteins (ox-LDL) and coronary artery disease in the general population [65, 66], a similar association appears to hold true for patients with SLE especially in those with cardiovascular disease and antiphospholipid antibody (APA) syndrome (APS). [67-69]. Mechanistically, ox-LDL induces the secretion of chemokines and proinflammatory cytokines such as monocyte chemotactic protein-1 (MCP-1), IL-8, and IL-6 from the endothelial cells [70]. As a consequence, T cells, monocytes, and dendritic cells are attracted to the subendothelial space of the diseased endothelium where monocytes further differentiate into macrophages that constitute the foam cells under the further stimulation of the ox-LDL [71]. Macrophages, under the influence of IFNy from the T cells, express key proinflammatory cytokines including TNF α and IL-1 which in turn aggravate the expression of adhesion molecules on the endothelium including vascular cell adhesion molecule

1 (VCAM-1), intercellular adhesion molecule 1 (ICAM-1), and E-selectin and further attracts monocytes [72]. Additionally, ox-LDL binds to CD14 of macrophages and leads to inhibition of their abilities to phagocytose and induction of CD36 expression [73]. Acting as a scavenger receptor on macrophages, activation of CD36 enhances the uptake of ox-LDL and upregulates the NF-κB expression, perpetuating local inflammatory response [73]. Interestingly, while HDL has long been advocated as the "good cholesterol" in that its level is inversely associated with cardiovascular disease and it functions to reverse LDL and phospholipid oxidation through apolipoprotein (apo A-1) and paraoxonase, respectively, the functions of HDL which can be either anti-inflammatory or inflammatory, is more pathologically relevant in atherogenesis [74]. The proinflammatory form of HDL, which is increased in acute-phase response, has been demonstrated to be able to impair LDL oxidation and the level of proinflammatory HDL was found to be significantly associated with ox-LDL levels in patients with SLE [75].

4.3.1. Atherogenic Adipokines. Amongst various atherogenic adipokines, leptin has been most extensively and systematically studied in patient with SLE, in relation to premature atherosclerosis and cardiovascular disease [76-82]. Leptin is an adipocyte-derived protein which regulates appetite, and energy intake and its expenditure [76]. Plasma leptin was shown to be increased in obese individuals and was correlated with serum C-reactive protein level, endothelial dysfunction, and cardiovascular event [77, 78]. Serum leptin levels have been demonstrated to be higher in patients with SLE as compared with those of healthy individuals [79, 80]. Recently, high serum level of leptin of ≥34 ng/dL has been shown to be associated significantly with carotid plaques with an odds ratio of 7.3 in a study of 210 female patients with SLE and 100 age-matched healthy controls [79]. In the NZB/W F1 mouse model, leptin was shown to enhance survival and proliferation of autoreactive T cells [81] and promote Th17 response through the transcription of Retinoid-Acid Receptor-related Orphan Receptor gamma t (RORyt) in CD4+ T cells [82]. While further information is required, these findings imply that targeting at leptin would be a potential strategy to combat cardiovascular disease in patients with SLE.

4.4. Oxidative Stress. Chronic inflammation of SLE leads to oxidative stress with the production of reactive oxygen species and accumulation of advanced glycation end products which are detrimental to the wellbeing of the endothelium [83]. Recently, it has been demonstrated that under the influence of IFN α , cultured lymphocytes undergo intracellular formation of the tubuloreticular structures (TRS) which signifies the presence of oxidative stress on the intracellular level. Additionally, the presence of TRS is significantly and proportionally elevated in higher disease activity of SLE [84]. Thus, it may potentially explain why a number of studies has demonstrated significant associations between clinical disease activity of SLE and various biomarkers of oxidative stress [85–87].

4.5. Costimulatory Molecules

4.5.1. CD137-CD137L. CD137 (4-1BB) belongs to the TNF superfamily which is mainly expressed on activated T cells and natural killer T cells. Its ligand, CD137L, is constitutively expressed on antigen presenting cells (APC) including B cells and dendritic cells (DC) [88, 89]. CD137 is a potent costimulatory receptor molecule and its cognate interaction with CD137L induces proliferation of activated T cells, and profound immunoglobulin production in B cells as well as maturation of DC on which CD137L is expressed [89]. Interestingly, agonizing CD137 with anti-CD137 monoclonal antibodies alleviates glomerulonephritis and improves mortality in MRL/lpr mice alongside with reduction of anti-dsDNA antibody, CD4+ T cells, and germinal centre formation [90]. In NZW/B mouse model, agonizing CD137 leads to the alleviation of lupus-like manifestations by increasing splenic CD4+CD25+ T regulatory cells [91].

Endothelial cells have also been shown to express CD137 upon activation and stimulation by proinflammatory stimuli such as TNF α [92]. The interaction between CD137 on the endothelium and CD137L expressed on monocytes enhances the former to express adhesion molecules such as ICAM-1 and VCAM-1, and the latter to migrate to vascular wall in an E-selectin and ICAM-1-dependent fashion [92–94]. Thus, CD137 activation promotes atherosclerosis early on the endothelium level. Although agonistic anti-CD137 antibody demonstrates alleviation of lupus in animal models [90, 91], its potential to cause atherosclerosis may be a relevant concern if this monoclonal antibody is to be evaluated in clinical trials for the treatment of SLE.

4.5.2. CD40-CD40L. Similar to CD137L, CD40L belongs to the TNF superfamily and is expressed on T cells [95, 96]. The CD40L gene is a SLE susceptible gene which is overexpressed in female lupus patients, partly due to the consequence of demethylation of the regulatory sequence on the inactivated X chromosome of T cells [95, 96]. CD40L and CD40 interaction between T cells and CD40-expressing endothelial cells triggers endothelial expression of adhesion molecules such as VCAM-1 [97]. While antagonizing CD40L with anti-CD40L in LDL-receptor deficient mice has been shown to cause substantial reductions of atherosclerotic lesions and their lipid content, and the amount of intralesional macrophages and T cells, as well as VCAM-1 expression on the endothelium [98], a clinical trial testing anti-CD40L in patients with SLE was unfortunately terminated prematurely due to excessive occurrence of cardiovascular events [99]. Thus, it seems unlikely that anti-CD40L will be able to protect the cardiovascular system in human SLE even though promising results in alleviating lupus nephritis was evident [99].

4.6. Proinflammatory Cytokines. Key proinflammatory cytokines which have been advocated to play a role in endothelial damage include IL-17, IFN-gamma (IFN γ), and TNF α . Expansion of the Th17 population and elevation of serum IL-17 levels have been clearly demonstrated in patients with SLE [100]. In nonlupus models, IL-17 has been implicated in the development of atherosclerotic plaques. Indeed, depleting

IL-17R by knocking out the IL-17R gene of LDL receptor-deficient atherosclerosis-prone mice reduced the size of aortic atherosclerotic plaques in these mice fed with Western-type diet [101]. In humans, T cells which produce both IL-17 and IFN γ were demonstrated to reside in the specimens of atherosclerotic plaque from patients with coronary heart disease [102]. Furthermore, in patients with acute coronary syndrome, higher number of circulating Th17 cells and levels of IL-17 as well as its related cytokines such as IL-6 and IL-23 levels were demonstrated as compared with those with stable angina and healthy individuals [102]. Nevertheless, data addressing whether IL-17 is directly related to clinical cardiovascular events are sparse.

As far as TNF α is concerned, our team has recently demonstrated that TNF α is elevated in patients with SLE with the use of the multiplex immunoassay platform, as compared with age- and sex-matched healthy individuals [103]. TNF α elevation was shown to be associated with higher coronary calcium scores in patients with SLE [104]. TNF α induces adhesion molecules expression on, and enhances the recruitment of T cells and monocytes to the endothelial cells [105]. As for IFN γ which has been discussed above, it is expressed by activated T cells and other immunocytes and it induces the macrophages to express TNF α and IL-1 which in turn aggravate the expression of VCAM-1, ICAM-1, and E-selectin and further attracts monocytes towards the diseased endothelium [72]. After all, IFN γ per se promotes oxidative stress and resultant endothelial damage [83].

4.7. Autoantibodies against ox-LDL, Phospholipids, and Annexin-V in Systemic Lupus Erythematosus. By intuition, antibodies against ox-LDL may alleviate the toxic effect of ox-LDL on the endothelium. Indeed, animal studies revealed that infusion of anti-LDL protected against atherosclerosis in hypercholesterolemic mice [106] and immunization of modified LDL, which triggered high titre of anti-ox-LDL antibodies, reduced atherosclerotic lesions in LDL-receptor deficit rabbits [107]. However, the results do not appear to be translated to human disease. While the cross-reactivity between antibodies against cardiolipin (a phospholipid species) and ox-LDL might imply an increased chance of the development of CVD in patients with SLE, the association between antiox-LDL antibodies and CVD remains inconsistent in these patients [67, 108, 109]. On the other hand, the association between antiphospholipid antibodies and CVD is undoubtedly clear. Formation of immune complexes involving β 2glycoprotein 1 has been shown to be detrimental to the vascular wall in part due to the stimulation of adhesion molecule expressions on the endothelium [110].

Annexin-V is a naturally occurring and potent phospholipid-binding anticoagulant protein which protects the endothelium from damage by inhibiting the procoagulant effects of tissue factors and binding to negatively charged phospholipids [111, 112]. In patients with SLE, besides the higher levels of anti-annexin-V antibodies, serum anti-annexin-V levels were shown to be predictive of poorer endothelial function gauged by endothelium-dependent vasodilation [111–113]. Mechanistically, it is evident that the binding of the atheroprotective annexin-V to phospholipid bilayer of the

endothelium is interfered by the anti- β 2-glycoprotein 1 anti-bodies [114].

4.8. Immune Complexes. Autoantibodies, which are characteristically abundant in SLE, form immune complexes (IC) with their respective autoantigens. Complements are subsequently fixed onto the IC in an attempt to be opsonised for removal by phagocytes. In fact, complement-associated immune complexes induce endothelial expression of adhesion molecules which enhance migration of T cells and monocytes towards the subendothelial space that initiate endothelial damage [115]. Interestingly, not all IC are detrimental to the wellbeing of the endothelium. C1q complexes are indeed atheroprotective in that they are able to trigger clearance of oxLDL by macrophages [116]. Thus, qualitative and quantitative deficiency of C1q found in patients with SLE may be implicated as a risk factor for CVD.

4.9. Neutrophil Extracellular Traps. A recent breakthrough in the research of antimicrobial mechanism by neutrophils is the discovery of the formation of neutrophil extracellular traps (NETs) [117]. NETs essentially comprise intracellular antimicrobial proteins such as LL37 and human neutrophils peptide and DNA which are microbicidal. In patients with SLE, the presence of antibodies against ribonucleoproteins and those against LL37 prime and increase the propensity of NET formation when compared to healthy individuals [118]. In addition, NETs confer strong cytotoxic signals which lead to endothelial damage and endothelial apoptosis [119]. Furthermore, NETs have been shown to activate platelets which induce thrombosis at the site of vascular injury and induce IFN α production by pDC which are activated by NETs-stimulated lupus neutrophils [120]. As a result, the tendency of NET formation in patients with SLE results in direct endothelial apoptosis and damage which are further potentiated by its effects on platelet and pDC activation, enhancing vascular thrombosis and perpetuation of the vicious cycle of endothelial dysfunction.

4.10. Factors Associated with Perturbed Vascular Repair

4.10.1. Endothelial Progenitor Cells. The serum levels of IFN α , and transcription of genes which enhance the expression of those encoding IFN α ("IFN signatures"), are upregulated in patients with SLE. IFN α plays a central role in the pathogenesis of SLE and, at the same time, it is "toxic" to the endothelium [121]. For example, EPC were demonstrated to undergo striking apoptosis after treating with IFN α , accompanied by a reduced capability to differentiate into mature endothelial cells, which were reversible by neutralizing IFN α [122]. It has been postulated that type 1 IFN leads to perturbed vascular repair by repressing the expression of angiogenic factors such as VEGF and IL-1 β on the endothelium, coupled with enhanced expression of IL-18 [123]. Very recently, angiogenic T cells (Tang), a novel subset of T cells which are functionally similar to the EPC in terms of the ability of endothelial repair, have been described in patients with rheumatoid arthritis [124]. Tang express CD3, CD31, and CD184 and their number in the peripheral blood was found to be correlated with 6

Table 1: A summary of the factors and their mechanisms which contribute to endothelial damage and impaired repair of the endothelium.

Endothelial damage	Description (ref)	
Type 1 interferon	Chiefly produced by pDC, IFN α is increased in SLE [46, 47] and it stimulates CD4+ cells residing in atherosclerotic plaque to express TRAIL which in turn enhances plaque rupture [48]. IFN α induces mDC residing in atherosclerotic plaques to express proinflammatory cytokines and MMPs which destabilize plaques and promote plaque rupture [49]. IFN α stimulates platelet aggregation and vascular thrombosis in a P-selectin dependent fashion [50].	
Type 2 interferon	Type 2 IFN is produced by a wide range of immunocytes including mDC, activated lymphocytes, and monocytes. It induces monocytes to upregulate IL-1 and TNF α which induce the expression of adhesion molecules such as VCAM-1, E-selectin, and ICAM-1 on the endothelium [59].	
Proinflammatory cytokines	Major proinflammatory cytokines, including TNF α , IL-1, IL-17, and IFN γ which are elevated in SLE, stimulate endothelial expression of adhesion molecules and lead to recruitment of atherogenesis-enhancing monocytes and T cells to the subendothelial space [59, 85]. A clinical study revealed that higher serum TNF α levels were associated with higher coronary calcium score [84], a radiological predictor of coronary artery event.	
Immune complexes	Complement-fixed immune complexes upregulate the expression of adhesion molecules on the endothelium [96] However, Clq-containing immune complexes are atheroprotective as they promote clearance of ox-LDL by macrophages [97].	
Costimulatory molecules	Endothelium expresses CD137 upon activation by proinflammatory signals such as TNF α [72]. Ligation of endothelial CD137 with CD137L expressed on monocytes induces the former to express adhesion molecules and facilitate monocyte migration to the subendothelial space [72–74]. CD40 is expressed on the endothelium, and its interaction with CD40L expressed on T cells induces expression of VCAM-1 which enhances atherosclerosis [77]. A clinical study testing anti-CD40L was however terminated due to the unexpected excessive occurrence of cardiovascular events [79].	
Oxidized lipids	Circulating ox-LDL induces endothelial secretion of MCP-1, IL-8, and IL6 which attract DC, T cells, and monocytes. Monocytes are induced to form foam cells under the further influence of ox-LDL and proinflammatory cytokines [58].	
Oxidative stress	Oxidative stress increases with higher disease activity of SLE [83]. Reactive oxygen species formed during oxidative stress lead to accumulation of glycation end products which are toxic to the endothelium [63].	
Annexin-V is a naturally occurring phospholipid-binding anticoagulant plupus patients demonstrate elevation of the anti-annexin-V antibody, where the antibodies antibodies, in particular the anti-β2-glycoprotein-1 antibodies, interferes binding between the atheroprotective annexin-V to the phospholipid endothelium [95].		
NETs	Antibodies against ribonucleoproteins and LL37 promote NET formation, which induces IFN α production by pDC as result of NETs-stimulated lupus neutrophils [99–101], NETs formation leads to activation of vascular thrombosis and endothelial apoptosis [99–101].	
Perturbation of vascular repair	Description (ref).	
Endothelial progenitor cells	IFN α induces EPC apoptosis and the ability of EPC to differentiate to mature endothelium [102, 103]. Vascular repair is impaired by the ability of IFN α to repress VEGF and IL-1 and upregulate IL-18 on the endothelium [104]. LDG is another source of IFN α apart from pDC which is elevated in patients with SLE. LDG impairs endothelial cell repair, and depletion of LDG restores the ability of EPC to differentiate into mature EPC and repair the endothelial monolayer [106]	

ref: references; pDC: plasmacytoid dendritic cells; IFN α : interferon-alpha; SLE: systemic lupus erythematosus; TRAIL: TNF-related apoptosis-inducing ligand; mDC: myeloid dendritic cells; MMP: matrix metalloproteinases; IFN: interferon; IL: interleukin; TNF α : tumour necrosis factor-alpha; VCAM-1: vascular cell adhesion molecule 1; ICAM-1: intercellular adhesion molecule 1; IFN γ : interferon-gamma; ox-LDL: oxidized low-density lipoproteins; MCP-1: monocyte chemotactic protein-1; DC: dendritic cells; NETs: neutrophil extracellular traps; LDG: low-density granulocytes.

that of the EPC in patients with rheumatoid arthritis [124]. Interestingly, the number of circulating Tang was associated positively with the positivity of antinuclear antibody and serum IFN α level and negatively with the occurrence of cardiovascular events in 103 patients with rheumatoid arthritis [124]. Since positivity of antinuclear antigen, high IFN α level and propensity to develop cardiovascular disease are evident in patients with SLE, phenotypic and functional studies of Tang in lupus patients in relation to cardiovascular disease would potentially yield exciting information of translational potential.

In animal lupus models, NZW/B mice were shown to have impaired endothelium-dependent vasorelaxation, reduction in the quantity, and increase in apoptosis of bone marrow and splenic EPC as compared with BALB/c controls. In addition, EPC from NZW/B failed to differentiate into mature endothelial cells as what C57BL/6 mice did. Type 1 IFN signatures were increased in EPC of NZW/B mice and IFN α was shown to induce apoptosis of EPC in vivo [125]. Interestingly, B6/lpr mice did not demonstrate quantitative, phenotypic, and functional abnormalities of EPC. While it gives researchers the information that B6/lpr mice might not be an ideal murine model to study endothelial physiology in lupus, lupus activity and renal dysfunction, which are more prominent in the B6/lpr mice, are not the sole contributors to endothelial dysfunction. Locally produced IFN α can induce uptake of ox-LDL into macrophages.

Besides the pDC which are the major producer of IFN α in patients with SLE, low-density granulocytes (LDGs), which are elevated in patients with SLE, have been demonstrated to produce type 1 interferon sufficiently enough to impair vascular repair [126]. In fact, depletion of LDGs instead of pDC in patients with SLE was shown to restore the capability of EPC to differentiate into normal endothelial monolayers [126].

5. Conclusion

Recognition of atherogenesis early in the pathogenesis taking place in the endothelium, exploration of the value of FMD and circulating EPC, and research for potential intervention to maintain the wellbeing of the endothelium before clinical cardiovascular disease develops are potentially useful and highly relevant in reducing cardiovascular mortality and morbidity. Type 1 IFN, which is important to the pathogenesis of SLE, appears to be crucial in initiating and perpetuating endothelial damage and impairing vascular repair through its inhibitory action in EPC. Supported by a prevalent study that high IFN signature is associated with endothelial dysfunction, high coronary calcium score and carotid IMT after controlling for traditional cardiovascular risk factors [127], suppression of type 1 IFN in selected patients with heightened IFN signature might therefore be an attractive avenue in preventing cardiovascular disease in patients with SLE. However, stronger evidence from prospective studies which advocates the association between heavy IFN signatures and development of cardiovascular disease amongst lupus patients is undoubtedly required. In addition, much more work needs to be done to further obtain and validate

available knowledge in order to translate it into potentially beneficial therapeutic and preventive interventions against cardiovascular disease in patients with SLE. Table 1 summarizes the factors and their potential mechanisms which contribute to endothelial damage and impaired endothelial repair in SLE.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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Review Article

Interleukin 6 and Rheumatoid Arthritis

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Interleukin-6 (IL-6) is a representative cytokine featuring pleiotropic activity and redundancy. A transient synthesis of IL-6 contributes to host defense against infectious agents and tissue injuries by inducing acute phase reactions and immunological and hematopoietic responses. However, uncontrolled persistent production of IL-6 may lead to the development of several immune-mediated diseases. Rheumatoid arthritis (RA) is a chronic disease with joint and systemic inflammation resulting from immunological abnormalities and it has been found that IL-6 plays a key role in the development of this disease. Clinical trials in various parts of the world of tocilizumab, a humanized anti-IL-6 receptor antibody, have proved its efficacy and tolerable safety either as monotherapy or in combination with disease-modifying antirheumatic drugs. As a result, it is currently used as a first-line biologic for the treatment of moderate-to-severe RA in more than 100 countries. Clarification of the mechanism(s) through which tocilizumab exerts its effect on RA and of the reason(s) why IL-6 is continuously produced in RA can be expected to lead to the best use of this agent for RA patients and aid in investigations into the pathogenesis of RA.

1. Introduction

Rheumatoid arthritis (RA) is characterized by synovial inflammation and hyperplasia, autoantibody production such as rheumatoid factor (RF) and anti-citrullinated protein antibody (ACPA), cartilage and bone destruction, and systemic features, including cardiovascular, pulmonary, psychological, and skeletal disorders [1]. Although its exact pathogenesis remains to be determined, a multistep progression is considered for the development of RA [1]. First, environment-gene interactions promote loss of tolerance to self-antigens that contain a citrulline residue generated by posttranslational modification. Second, the anticitrulline response is induced in T cells as well as B cells. Thereafter, localization of the inflammatory response occurs in the joint and synovitis is initiated and perpetuated by positive feedback loops and promotes systemic disorders. In this process, various cells and their products contribute to the development. For instance, as key molecules many cytokines including TNF- α , IL-1, IL-7, IL-15, IL-17A, IL-17F, IL-18, IL-21, IL-23, IL-32, and IL-33 are implicated in the pathogenesis of RA [1].

Before this century, the only drugs available for RA were nonsteroidal anti-inflammatory drugs (NSAIDs), corticosteroids, and disease-modifying antirheumatic drugs (DMARDs) including gold, chloroxine, salazosulfapyridine, and methotrexate (MTX). However, these drugs were often not effective enough to completely suppress disease activity and joint destruction. The arrival of biological agents (biologics, biological DMARD) such as TNF inhibitors, abatacept, an inhibitor of T-cell costimulation, and rituximab, an agent leading to B-cell depletion induced a paradigm shift in the treatment of RA and Treat-to-Target (T2T) treatment proved to be successful for disease remission and protection against joint destruction [2].

Dysregulated persistent production of interleukin-6 (IL-6) also plays a key role in the development of the main characteristics of RA [3–5]. In response to the supposition

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that IL-6 targeting could be a novel therapeutic strategy for RA, a humanized anti-IL-6 receptor monoclonal antibody (Ab), tocilizumab (TCZ), was developed. Subsequent clinical trials conducted all over the world have proved the efficacy and tolerable safety of TCZ and it is currently used as an innovative biologic for the treatment of RA in more than 100 countries. Moreover, TCZ was also approved for the treatment of systemic juvenile idiopathic arthritis in Japan, USA, EU, and India, and Castleman's disease in Japan and India, while recent various case reports or pilot studies of off-label use with TCZ suggest that it is widely applicable for the treatment of other immune-mediated diseases including vasculitis syndrome, adult-onset Still's disease, systemic lupus erythematosus, or others [4, 5]. In this paper, we present current evidence of the pathological role of IL-6 in the development of RA and the efficacy and safety profile of TCZ for RA and discuss future aspects of IL-6 targeting strategy for RA.

2. IL-6 and Signaling Pathway of IL-6

IL-6 is a glycoprotein with a molecular weight of 26 kDa and pleiotropic activity. It was first identified as B cell differentiation factor (BCDF) or B cell stimulatory factor 2 (BSF-2), which is a T-cell-derived soluble factor that induces the differentiation of activated B cells into Ab producing cells [6, 7]. Complementary DNA of IL-6 was successfully cloned by Hirano et al. in 1986 [8] and the resultant molecule was found to be identical to hybridoma growth factor (HGF), which derives its name from its promotion of growth of fusion cells with myeloma, to hepatocyte-stimulating factor (HSF) with its promotion of synthesis of acute phase proteins such as C-reactive protein (CRP), serum amyloid A (SAA), haptoglobin, fibrinogen, and hepcidin in hepatocytes, or to interferon (IFN) β 2 due to its IFN anti-viral activity [9–11]. Subsequent studies also revealed that IL-6 performs multiple and essential functions in immune regulation, inflammation, and even oncogenesis and could be a key mediator for the development of many chronic inflammatory or autoimmune diseases including RA [12-14].

IL-6 triggers its signaling system through binding to an 80 kDa transmembrane IL-6 receptor (IL-6R) (Figure 1) [15, 16]. After binding to IL-6R, the complex consisting of IL-6 and transmembrane IL-6R associates with signal-transducing molecule gp130, resulting in the activation of downstream signaling events via Janus kinase (JAK) in target cells [17-20]. This activation is known as classic signaling pathway. Transmembrane IL-6R is expressed on only limited cells such as hepatocytes and some leukocytes, whereas gp130 is expressed on various cells. A soluble form of IL-6R (sIL-6R) lacking the cytoplasmic region exists in serum and has a similar affinity to IL-6 as transmembrane IL-6R. The complex of IL-6 and sIL-6R can also bind to gp130, leading to the activation of signaling cascade. This process is called trans-signaling. Accumulating evidence suggests that IL-6 trans-signaling is proinflammatory, whereas classic signaling is needed for regenerative or anti-inflammatory activities [21].

JAK is a member of the tyrosine kinase family, and its phosphorylation further induces the activation of signal transducer and activator of transcription (STAT) 3 and hyperphosphorylation of mitogen-activated protein kinases (MAPKs) [22]. The activation of the former is dependent on phosphorylation at tyrosine 759 (Y759) in gp130 and the latter requires phosphorylation on any residues of Y767, Y814, Y904, and Y915, which are all encountered in the YXXQ motif context. STAT3 then stimulates the expression of several genes leading to the induction of cell growth and differentiation [23-26]. MAPK also activates several transcription factors associated with acute phase protein synthesis and cell growth. Phosphorylation of a phosphoinositol-3 kinase (PI3K) by JAK results in activation of a third pathway by IL-6, which is the PI3K protein kinase B (PkB)/Akt pathway [27]. The activated Akt then phosphorylates several downstream targets to upregulate cellular survival [28].

3. Pathological Role of IL-6 in RA

RA is a chronic, progressive inflammatory disease of the joints and surrounding tissues accompanied by intense pain, if untreated, irreversible joint destruction, and systemic complications such as fatigue, anemia, and fever [1]. RA patients typically show immunological abnormalities leading to the production of autoantibodies such as RF and ACPA.

IL-6 has been shown to contribute to the production of autoantibodies by acting on plasmablasts [29]. Historically, IL-6 was originally identified as a helper T-cell-derived soluble factor that promoted immunoglobulin secretion by activated B cells [6, 7], while recent findings indicate that IL-6 also acts as regulator of CD4+ T cell differentiation and activation. IL-6 signaling has been found to control proliferation and resistance of resting T cells against apoptosis by promoting IL-2 production and STAT3 activation. In addition, IL-6 influences T cell effector functions by promoting Th2 cell differentiation through upregulation of nuclear factors of activated T cells (NFAT)c2 and c-maf, while it blocks IFN-γ-signaling and inhibits Th1 cell differentiation [30]. Moreover and more important, in the presence of transforming growth factor (TGF)- β , IL-6 is able to promote Th17 cell differentiation through STAT3-mediated upregulation of retinoid orphan receptor (ROR)yt, while it inhibits TGF- β -induced regulatory T cell (Treg) differentiation [31, 32]. IL-6 thus promotes predominance of Th17 over Treg in the effector CD4+ T cell subsets, which is thought to play a major role in the development of RA and various other immunemediated diseases. In addition, IL-6 has been shown to promote T follicular helper cell development, which secretes IL-21, another B cell differentiation factor [33–35].

It has further been demonstrated that IL-6 is involved in local inflammation causing joint destruction by inducing endothelial cells to produce IL-8 and monocyte chemoattractant protein-1 (MCP-1) and to activate expression of adhesion molecules and recruit leukocytes to involved joints [36]. Synoviocytes can produce IL-6, while IL-6 can induce synoviocyte proliferation and osteoclast differentiation through receptor activator of NF-kappa B ligand (RANKL) expression

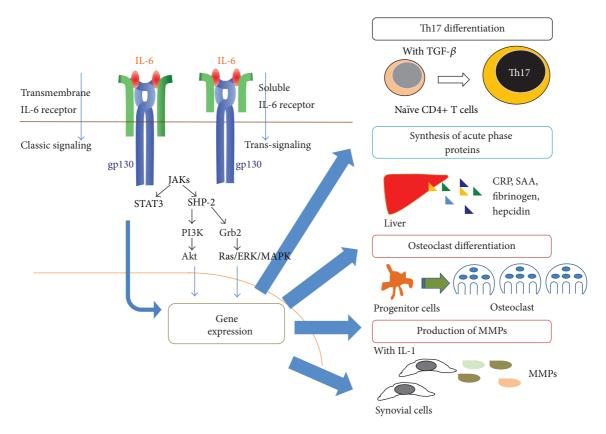


FIGURE 1: IL-6 exerts its pleiotropic activity by activation of gp130 through its binding to transmembrane or soluble IL-6 receptor. IL-6 initiates the IL-6 signaling pathway through binding to transmembrane or soluble IL-6 receptor. The resultant complex then induces homodimerization of gp130, which leads to activation of a signaling system. Transcriptional factors including STAT3 activate various gene expressions, resulting in cell differentiation or proliferation. JAKs: Janus kinases; STAT3: signal transducer and activator of transcription 3; SHP-2: SH2 domain-containing tyrosine phosphatase 2; PI3K: phosphoinositol-3 kinase; Grb2, growth factor receptor-bound protein 2; ERK: extracellular signal-regulated kinase; MAPK: mitogen activated protein kinase; Akt: protein kinase B; TGF-β: transforming growth factor beta; CRP: C-reactive protein; SAA: serum amyloid A; MMPs: matrix metalloproteinases.

[37, 38]. This stimulation by IL-6 is also associated with the development of osteoporosis and bone destruction. IL-6 and IL-1 synergistically enhance the production of matrix metalloproteinases (MMPs) from synovial cells, which may lead to cartilage and joint destruction [39]. Furthermore, enhanced angiogenesis and vascular permeability of synovial tissue are pathological features of RA resulting from the excess production of vascular endothelial growth factor (VEGF), which is also induced by IL-6 in synovial fibroblasts [40].

Systemic inflammatory signs and symptoms related to RA include fever, malaise, sleep disturbance, muscle weakness, and anemia, while laboratory findings observed in patients with RA are CRP elevation, hypercoagulability, and hypoal-buminemia. These are thought to be mostly mediated by IL-6 [5, 10, 11]. IL-6 induces hepcidin production, which blocks the action of iron transporter ferroportin 1 on gut and thus reduces serum iron and hemoglobin levels [41]. Moreover, RA patients often suffer from thrombocytosis, also mediated by IL-6, which promotes the differentiation of megakaryocytes into platelets [42].

These findings prove that IL-6 plays a key role in the induction of immunological abnormalities and in the development of joint and systemic inflammation of RA.

IL-6 was found to be elevated in serum as well as synovial fluid of patients with RA [43]. These levels correlated with disease activity of RA, while successful treatment with DMARDs or TNF inhibitors has been shown to reduce serum IL-6 concentrations [44–46]. Moreover, reduction in IL-6 levels during the first 12 months of treatment is reportedly a prognostic marker for better clinical outcome [47]. Recently, it was also shown that a decrease in serum IL-6 levels during TCZ treatment can be a predictive marker for maintenance of remission status [48]. These findings clearly point to the pathologic role of IL-6 in RA. However, it remains unknown what the exact mechanisms are through which IL-6 is continuously oversynthesized in RA and TCZ treatment leads to a reduction in intrinsic production of IL-6.

The pathological role of IL-6 in several animal models of RA was also documented. Collagen-induced arthritis (CIA) is the most well-known animal model of RA, in which injection of mice with type II collagen produces an immune response

directed at connective tissues. In the CIA model, activated T cells produce augmented amounts of both Th1 and Th17 cytokines, while deficiency of IL-6 activity through gene knockout suppresses Th17 cytokine production and clinical symptoms of arthritis [49, 50]. Similar results have been found for blockade of IL-6 signaling by using an anti-mouse IL-6R Ab [51, 52]. In this model, the proliferative response of B and T cells isolated from lymph nodes of anti-IL-6R-treated mice was significantly suppressed compared to controls. In addition, anti-IL-6R treatment led to amelioration of the histopathological features of arthritis including inflammatory synovitis and joint erosions. IL-6 gene deficiency and blockade of IL-6 activity also reduced severity of arthritis in other mouse models of RA, such as antigen-induced arthritis (AIA), an immune complex model of RA, and SKG mice which spontaneously develop autoimmune arthritis with ageing due to a spontaneous mutation in the zeta-chainassociated protein kinase-70 (ZAP-70) gene [53–57].

4. Development of Tocilizumab, a Humanized Anti-IL-6 Receptor Monoclonal Antibody

The findings described above led to the concept that IL-6 targeting might constitute a novel therapeutic strategy for RA. In response to this supposition, TCZ, a humanized anti-IL-6R monoclonal Ab of the IgG1 class, was developed [58]. TCZ blocks IL-6-mediated signal transduction through inhibition of IL-6 binding to transmembrane as well as soluble IL-6R. The first clinical evaluation of the efficacy of TCZ was conducted for the treatment of seven patients with Castleman's disease, a chronic inflammatory disease characterized by multiple lymph node swellings with massive infiltration of mature plasma cells [59]. Such patients present with severe inflammatory symptoms such as high fever, anemia, increased levels of acute-phase proteins, and hyper-yglobulinemia. After TCZ administration, the fever promptly diminished, CRP levels became normalized, and hemoglobin levels increased. The efficacy of TCZ was next proved in a clinical trial using 28 patients with Castleman's disease [60], and this resulted in its approval as an orphan drug for the Japanese market in 2005.

The further development of TCZ entailed phase I and II clinical trials of TCZ for RA performed between 2002 and 2006 with favorable results [61–63]. The first trial was a randomized, double-blind, placebo controlled, dose-escalation trial in the UK [61]. Patients treated with 5 mg/kg or 10 mg/kg TCZ showed significant improvement by week 2. The next dosing determination trial was conducted in Japan. Patients were given a placebo or TCZ (4 or 8 mg/kg every 4 weeks) and 8 mg/kg TCZ resulted in the greatest improvement [62].

5. Efficacy of Tocilizumab in Phase III Clinical Trials and Actual as in Clinical Settings

Seven phase III randomized controlled trials (RCT) were conducted to evaluate the clinical efficacy of TCZ as either monotherapy or in combination with DMARDs including MTX (Table 1) [64–70].

5.1. Tocilizumab Combination Therapy. For further assessment of the efficacy of TCZ, RCTs of TCZ combination therapy were conducted. The OPTION trial was designed to evaluate the usefulness of TCZ (4 or 8 mg/kg every 4 weeks) in combination with MTX and the results demonstrated that this combination therapy was effective for and well tolerated by patients with active RA and an unsatisfactory response to MTX [64]. The TOWARD study compared the efficacy of TCZ (8 mg/kg every 4 weeks) plus DMARDs with that of DMARDs only for inadequate responders to DMARDs [65], and the RADIATE study compared the efficacy of TCZ (4 or 8 mg/kg every 4 weeks) plus MTX with that of MTX only for inadequate responders to TNF inhibitors [66]. Both studies showed evidence of a significant reduction of disease activity in the TCZ groups. The LITHE trial demonstrated that TCZ (4 or 8 mg/kg every 4 weeks) plus MTX had superior American College of Rheumatology (ACR20), 50 and 70 responses at 52 weeks compared with controls treated with placebo plus MTX [67].

5.2. Tocilizumab Monotherapy. The AMBITION trial was designed to compare the efficacy and safety of TCZ monotherapy with those of MTX monotherapy [68]. The results showed rapid improvement in RA disease activity and a favorable risk benefit profile for TCZ compared to MTX monotherapy. The SAMURAI study, which evaluated the efficacy of TCZ monotherapy for patients with an inadequate response to DMARDs, also showed a superior efficacy of TCZ compared to DMARDs [69]. Finally, the SATORI study investigated the efficacy of TCZ monotherapy for moderate-to-severe active RA patients with an inadequate response to low doses of MTX [70]. At week 24, the ACR20 response rate was 80.3% for the TCZ group and 25.0% for the MTX group.

In summary, TCZ as either monotherapy or in combination therapy with MTX or other DMARDs was highly efficacious for RA patients (Tables 1(a) and 1(b)).

5.3. Efficacy of TCZ in Protection of Radiographic Progression of Joints. In addition to clinical efficacy of TCZ in disease activity, TCZ showed beneficial effects in radiographic progression of joints (Table 1(c)). In the SUMURAI study, the TCZ group showed statistically significantly less radiographic change in the van der Heijde-modified Total Sharp Score (TSS) than the DMARD group at week 52 [69]. Moreover, the LITHE trial proved that at 52 week, the TCZ (either 4 mg/kg or 8 mg/kg) plus MTX group showed less progression of joint damage than the MTX group, as evaluated with the Genant-modified TSS (GmTSS) method [67].

5.4. Efficacy of TCZ in Phase IIIb/IV Trials and Clinical Practice. Following the seven phase III clinical trials, several phase IIIb/IV studies were conducted. The REACTION study performed in Japan showed that by 24-week treatment with TCZ, average disease activity score (DAS) 28 of 229 patients significantly decreased from 5.70 to 3.25 and a European League Against Rheumatism (EULAR) good response and DAS remission was achieved in 57.4% and 40.7% of the patients, respectively [71]. Moreover, at week 52, radiographic

TABLE 1: Randomized phase III controlled trials of tocilizumab.

(a) Clinical efficacy of tocilizumab (Tocilizumab combination therapy)

Study	Population	Week at evaluation Treatment arms	Treatment arms		Patient number HAO (% >MCID)	Response	Response rates (%), OR (95% CI)		DAS28 < 2.6 remission rate
oran)	- Oparation	veen at evaluation	Teaming and			ACR20	ACR50	ACR70	(%), OR (95% CI)
TOWARD	DMARDs-IR	24 W	TCZ (8 mg/kg) + DMARDs	803	****09	61***	38***	21***	30***, 13.8
			DMARDs	413	34	25	6	3	3
TH YEAR	di di di	71777	TCZ (4 mg/kg) + MTX	161	$\Delta - 0.3^*$	30***	17***	rV	8, 4.3
KADIALE	Anti-11NF-11K	74 W	TCZ (8 mg/kg) + MTX	170	$\Delta - 0.4^{****}$	50***	29***	12***	30***, 21
			MTX	158	$\Delta - 0.1$	10	4	1	2
NOTEGO	The state of the s	747.60	TCZ (4 mg/kg) + MTX	214	$\Delta - 0.52^*$	48***, 2.6 (1.7–3.9)	31***, 3.8 (2.3–6.5)	12***, 7.0 (2.4–20.4)	13***, 18.8 (2.5–142)
OFILON	MIA-IK	74 W	TCZ (8 mg/kg) + MTX	205	$\Delta-0.55^{**}$	$59^{***}, 4.0$ (2.6–6.1)	44***, 6.6 (3.9–11.2)	$22^{****}, 14.2$ (5.0–40.4)	27****, 45 (6.1–332)
			MTX	204	$\Delta - 0.34$	26	11	2	1
1 1771	di VTM	78.02	TCZ (4 mg/kg) + MTX	399	09	*47*	*67	16*	30*, 4.92
LILLE	M1.A-1M	32 VV	TCZ (8 mg/kg) + MTX	398	63*	26***	36***	20***	47***,10.2
			MTX	393	53	25	10	4	8
				(b) Tocilizum	(b) Tocilizumab monotherapy				
Study	Population	Week at evaluation Treatment arms	Treatment arms	Patient number	HAQ (% ≥MCID)	Response J ACR20	Response rates (%), OR (95% CI) CR20 ACR50 ACR7		DAS28 < 2.6 remission rate (%), OR (95% CI)
AMBITION	MTX, anti-TNF	7.4 TAT	TCZ (8 mg/kg)	286	$\Delta - 0.7$	***07	44**	28***	34 ^{n.d.} , 5.83 (3.27–10.4)
AMBITION	naïve	V4 VV	MTX	284	$\Delta - 0.5$	53	34	15	12
S A MITTD A I	DM ADD, TD	747 C3	TCZ (8 mg/kg)	157	***89	78**	64***	44***	59***, 46.5
SAMONAI	DIMPADS-IN	V 2C	DMARDs	145	40	34	13	9	33
SATORI	MTY-IR	W VC	TCZ (8 mg/kg)		****29	***08	49 ^{n.d.}	$30^{ m u.d.}$	43***, 37.0
STATE OF STATE	VII - X7 I IA7		MTX	64	34	25	11	9	2

 $^*P < 0.05, ^{**}P < 0.01, ^{***}P < 0.001, ^{***}P < 0.0001.$

HAQ: health assessment questionnaire disability index; MCID: minimal clinical important difference; OR: odds ratio; CI: confidence interval; DMARDs: disease-modifying antirheumatic drugs; IR: inadequate response; TCZ: tocilizumab; TNF: tumor necrosis factor; MTX: methotrexate; n.d.: not described.

(c) Efficacy of tocilizumab in protection of radiographic progression of joints

Study	Radiographic assessment	Week at evaluation	Treatment arms	Dronortion without progression TSS < 0		Change in score (95% CI)	·CI)
Study	Natiographic assessment	ween at evaluation	meanment arms	riopordon widdon progression 133 = 0		Total score Erosion score JSN score	JSN score
CAMITDAL	AMITDAL was dow United was different Chaires	7A7 C3	TCZ (8 mg/kg)	56**	2.3**, (1.5-3.2) 0.9***, (0.3-1.4) 1.5*, (0.9-2.1)	0.9***, (0.3-1.4)	$1.5^*, (0.9-2.1)$
V IENIOIMES	an dei meijde-modined maip score	72 W	DMARDs	39	6.1(4.2-8.0)	6.1 (4.2-8.0) $3.2 (2.1-4.3)$ $2.9 (2.0-3.8)$	2.9 (2.0–3.8)
			TCZ (4 mg/kg) + MTX	81***	0.34***	0.21*	0.13*
LITHE	Genant-modified Sharp score	52 W	TCZ (8 mg/kg) + MTX	84***	0.29***	0.17***	0.12^{**}
			MTX	29	1.13	0.71	0.42

 $^*P < 0.05, ^{**}P < 0.01, ^{***}P < 0.001, ^{***}P < 0.0001.$ TSS: total Sharp score; CI: confidence interval; TCZ: tocilizumab; DMARDs: disease-modifying antirheumatic drugs; JSN: joint space narrowing; MTX: methotrexate.

nonprogression and functional remission were achieved in 62.8% and 26.4% of 232 patients, respectively [72]. Interestingly, progression of joint destruction was found to be similar with or without concomitant MTX, glucocorticoids, or previous use of TNF inhibitors. The ACT-RAY trial was performed to compare TCZ plus MTX with TCZ plus a placebo in a setting that closely resembled real-life clinical practice [73]. After 24 weeks, ACR20, 50, and ACR70 response rates were 71.5%, 45.5%, and 24.5%, respectively, for the TCZ plus MTX group and corresponding rate of 70.3%, 40.2%, and 25.4% for the TCZ monotherapy group. This study demonstrated that TCZ plus MTX combination therapy and TCZ monotherapy could both be expected to be effective in real-life clinical practice, and importantly, that TCZ plus MTX combination was not significantly superior to TCZ monotherapy (Table 2). These and other studies showed that TCZ treatment improved disease activity, joint destruction, and quality of life. Moreover, a recent trial comparing TCZ (8 mg/kg intravenously every 4 weeks) monotherapy with adalimumab (40 mg subcutaneously every 2 weeks) monotherapy (ADACTA trial) proved the clinical superiority of TCZ [74] (Table 2). TCZ as monotherapy can thus be considered to be more beneficial than other biologics [75]. However, a meta-analysis of systematic reviews of clinical trial data indicates that TCZ, TNF inhibitors, and abatacept have similar efficacy in combination with MTX [76].

5.5. Efficacy of Subcutaneous Injection of TCZ in Phase III Trials. Intravenous injection every 4 weeks of TCZ (4 or 8 mg/kg) is currently used for the treatment of moderateto-severe active RA, but recent clinical trials (MUSASHI and SUMMACTA) demonstrated that subcutaneous administration of TCZ (162 mg) weekly or every 2 weeks showed efficacy and safety comparable to those of intravenous injection of TCZ (8 mg/kg every 4 weeks) [77, 78] (Table 2). The MUSASHI study was a double-blind, double-dummy, parallel-group, comparative phase III study to evaluate the efficacy and safety of subcutaneous (SC) versus intravenous (IV) TCZ monotherapy for patients with RA and an inadequate response to synthetic DMARDs and/or biologics. A total of 346 patients were randomized to receive TCZ-SC 162 mg every 2 weeks or TCZ-IV 8 mg/kg every 4 weeks. At week 24, ACR20 response was achieved in 79.2% of the TCZ-SC group and in 88.5% of the TCZ-IV group, showing that TCZ-SC was not inferior to TCZ-IV [77]. The incidences of all adverse events (AEs) and serious AEs were 89.0% and 7.5% for the TCZ-SC group and 90.8% and 16.4% for the TCZ-IV group, respectively, while serum trough TCZ concentrations were similar for the two groups during the test period. The SUMMACTA trial was a randomized, double-blind, parallelgroup study to evaluate the safety and efficacy of TCZ-SC in comparison with TCZ-IV combined with DMARD for patients with moderate-to-severe RA. A total of 1,262 patients were randomly assigned to receive TCZ-SC 162 mg weekly or TCZ-IV 8 mg/kg every 4 weeks in combination with DMARD [78]. At week 24, 69.4% of the TCZ-SC-treated patients versus 73.4% of the TCZ-IV-treated patients attained

an ACR20 response. Moreover, ACR50/70 responses, DAS28 improvement and the safety profiles were similar for the two groups.

6. Safety Profile of Tocilizumab

The comparison of AEs between the control population (4,199) and the TCZ-treated population (4,009) was reported in 2011 [79]. Overall AE and serious AE rates were 278.2/100 patient-year (PY) and 14.4/100 PY, respectively. These events included serious infections (4.7/100 PY), opportunistic infections (0.23/100 PY), gastrointestinal perforations (0.28/100 PY), malignancy (1.1/100 PY), myocardial infarction (0.25/100 PY), and stroke (0.19/100 PY). Shortterm (28 weeks) safety of TCZ for 7,901 patients was monitored in a postmarketing surveillance in Japan [80]. The incidence of total AEs and serious AEs was 43.9% and 9.6%, respectively. Infection and infestation were the most frequent AEs (11.1%) and serious AEs (0.5%). Analysis of long-term safety showed that rates of serious AEs, serious infections, and cardiovascular events remained stable during continued exposure to TCZ in long-term clinical trials. Infection was identified as the most frequent serious AE. The most commonly reported infections in RCTs were pneumonia (0.9/100 PY) and skin or soft tissue infections (0.9/100 PY). These results lead to the conclusion that infections were the most frequent AEs but a meta-analysis comparing the safety profile of TCZ with that of other biologics including TNF inhibitors, anakinra (IL-1R antagonist), abatacept, and rituximab showed similar rates of infection [81]. In contrast to the finding for infections, no increase in the incidence of malignancy or reactivation of tuberculosis was seen in TCZ-treated RA patients [82]. Gastrointestinal perforation appeared to be an AE specific for TCZ with an incidence rate of 1.9/1,000 PY [83]. This rate fell between those of 3.9/1,000 PY for corticosteroids and 1.3/1,000 PY for TNF inhibitors listed in the United Health Care database. While it is not clear at present why IL-6 blockade induced perforation, most cases were complications of diverticulitis. IL-6 also affects metabolism. Increases in mean fasting levels of plasma lipids such as total cholesterol, low-density lipoprotein, triglycerides, and high-density lipoprotein were detected in 20-30% of patients treated with TCZ. These higher lipid levels resulting from TCZ treatment are perhaps mediated by the influence of TCZ on lipoprotein receptor expression, since it has been recently shown that overproduction of IL-6 lowers blood lipid levels via upregulation of the very-low-density lipoprotein (VLDL) receptor [84]. In spite of this elevation of lipids, an analysis combining the data of various clinical trials showed no apparent increase in cardiac events in a followup of up to 5 years [82].

7. Other IL-6 Inhibitors in Development

The success of the indication of TCZ for the treatment of RA clarified that IL-6 blockade was a therapeutic strategy for RA, so that other IL-6 inhibitors are now being

TABLE 2: Pivotal clinical trials of tocilizumab.

				TIVOCAL CITILICAL	LABEL 2: 1 170tm Cinical dilais of Contemina.					
Study	Population	Week at evaluation	Treatment arms F	Patient number	Patient number HAQ (% ≥MCID)	Response ra ACR20	ites (%), OF ACR50	(95% CI) ACR70	Response rates (%), OR (95% CI) DAS28 remission rate ACR20 ACR50 ACR70 (%), OR (95% CI)	Conclusion
			TCZ (8 mg/kg) + PBO	276	$\Delta - 0.5$	70	40	25	35	No difference of
ACT-RAY	MTX-IR	24 W	TCZ (8 mg/kg) + MTX	277	$\Delta - 0.5$	72	46	25	40, 5.6 (-2.4-13.7)	efficacy between TCZ and TCZ + MTX
							47***	33**	40****	
ATACTA	MTV ID	74.147	TCZ-IV (8 mg/kg/4 weeks)	163	$\Delta - 0.7$		2.4	2.3	5.7	TCZ is superior to
ADACIA		74 AV	,			(1.2-3.1)	(1.5-3.9)	(1.3-3.8)	(3.1-10.3)	ADA as monotherapy
			ADA-SC (40 mg/2 weeks)	162	$\Delta - 0.5$		28	18	11	
di VTM ILLA SUITA	MTV ID	24 147	TCZ-IV (8 mg/kg/4 weeks)	173	89	68	29	41	62	Noninferiority of
MOSASIII	MI-VIII	V #-7	TCZ-SC (162 mg/2 weeks)	173	57	79	63	37	50	TCZ-SC to TCZ-IV
STIMMACTA	SIMMACTA DMAPDEID 24 W	7.4 1.67	TCZ-IV (8 mg/kg/4 weeks) + DMARD	631	29	73	48	27	36	Noninferiority of
SOMMAN	MI-SCHWING I	V 1-7	TCZ-SC (162 mg/week) + DMARD	631	92	69	47	24	38	TCZ-SC to TCZ-IV

** P < 0.01, *** P < 0.001, **** P < 0.0001.

HAQ: health assessment questionnaire disability index; MCID: minimal clinical important difference; OR: odds ratio; CI: confidence interval; MTX: methotrexate; IR: inadequate response; TCZ: tocilizumab; PBO: placebo; IV: intravenous injection; ADA: adalimumab; SC: subcutaneous injection; DMARDs: disease-modifying antirheumatic drugs.

developed. These include fully human anti-IL-6R Ab (sar-ilumab/REGN88/SAR153191), anti-IL-6R nanobody (ALX-0061), anti-IL-6 Abs such as sirukumab (CNTO 136), BMS-945429 (ALD518), olokizumab (CDP6038), and MEDI5117, and soluble gp130-Fc fusion protein (FE301), which selectively inhibits trans-signaling but not classic signaling [5].

The favorable results of phase II, randomized, doubleblind, placebo-controlled trials of sarilumab [85] and sirukumab [86] confirmed the effectiveness of IL-6 blockade strategy in RA. The phase II MOBILITY study evaluated efficacy and safety of subcutaneous injection of sarilumab, in which 306 RA patients were randomized to receive a 12-week administration of sarilumab 100 mg or 150 mg every week, 100 mg, 150 mg, or 200 mg every 2 weeks, or placebo added to stable MTX [85]. An ACR20 response was seen in 49.0% of the patients receiving the lowest sarilumab dose regime and in 72.0% of the patients receiving the highest dose regime, compared to 42.0% of those treated with placebo plus MTX. The types and incidence of AEs were consistent with those previously reported for TCZ. Sirukumab is a fully human monoclonal Ab to IL-6, and 151 RA patients were enrolled into a phase II trial [86]. The patients were randomized equally to receive subcutaneous injections of placebo every 2 weeks for weeks 0-10 and sirukumab 100 mg every 2 weeks for weeks 12-24, or sirukumab 25, 50, or 100 mg every 4 weeks, or 100 mg every 2 weeks for weeks 0-24. At week 12, more patients receiving sirukumab were in remission than those given the placebo according to Boolean- and simplified disease activity index (SDAI)-based ACR/EULAR criteria (2% versus 0% and 6% versus 3%). At week 24, high remission rates were attained with sirukumab at dose regimens ranging from 25 to 100 mg every 2-4 weeks, determined with ACR/EULAR or DAS28 (CRP) criteria. The types and incidence of AEs were consistent with those observed for TCZ.

8. Perspectives

In view of the outstanding clinical efficacy and tolerable safety of TCZ, TCZ is now recommended as one of first-line biologics for the treatment of active RA. However, several issues need to be clarified for realization of the optimal use of TCZ. First, an important issue is to clarify the mechanisms, which render IL-6 blockade efficacious for RA. Although it is clear that TCZ treatment led to improvements in markers related to systemic inflammation and bone and cartilage metabolisms [87–89], it remains to be determined whether the treatment can correct fundamental immunological abnormalities in RA [90]. As mentioned before, IL-6 has the capability of promoting autoantibody production and of causing imbalance between Th17 and Treg [31, 32]. Recent preliminary studies showed that TCZ treatment could rectify the imbalance in the peripheral blood CD4+ T cell population [91, 92]. Moreover, a 6-month treatment with TCZ led to a selective decrease in IL-21 production by memory/activated T cells in eight patients with RA [93]. Elevation of IL-21 has been detected in patients with RA [94] and is known to induce plasma cell differentiation and induce IgG4 production but the TCZ

treatment resulted in a reduction in IgG4 subclass ACPA titer [35, 94]. These findings suggest that IL-6 blockade strategy may indeed correct immunological abnormalities in RA, but the findings of these studies have limited robustness due to the small sample size, so that further analyses will be required.

Second, the reason or reasons why IL-6 synthesis is continuously induced in RA remain to be clarified. One genetic polymorphism (-174) in the IL-6 gene promoter, which was found to affect IL-6 levels [95], did not appear to universally increase susceptibility to RA, but a recent metaanalysis showed that the -174 polymorphism might confer susceptibility to RA, at least in Europeans [96]. IL-6 can be produced by immune competent cells, fibroblasts, synoviocytes, endothelial cells, and many other cells in response to various stimuli [13]. The synthesis of IL-6 is strictly regulated by transcriptional and posttranscriptional mechanisms and a number of transcriptional factors, RNA binding proteins, and microRNAs have been shown to control IL-6 synthesis [97]. Moreover, it has been recently reported that newly found molecules such as Regnase-1 and Arid5a affect posttranscriptional regulation of IL-6 mRNA degradation [98-100]. Regnase-1 binds to the 3' untranslated region of IL-6 mRNA and splits up IL-6 mRNA, whereas Arid5a binds to a similar region and stabilizes IL-6 mRNA. Moreover, some viral proteins or microRNAs reportedly activate the IL-6 gene and/or inhibit mRNA degradation [97]. It can therefore be anticipated that clarification of mechanisms by which dysregulated, persistent production of IL-6 is induced in RA will lead to an enhanced understanding of the pathogenesis of RA.

Conflict of Interests

The authors declare that there is no conflict of interests regarding the publication of this paper.

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Research Article

Serum Levels of Three Angiogenic Factors in Systemic Lupus Erythematosus and Their Clinical Significance

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Our research investigates the serum levels of three angiogenic factors in the AF family, namely, placenta growth factor (PIGF), basic fibroblast growth factor (bFGF), and vascular endothelial growth factor (VEGF), in 54 patients with SLE (SLE group) and 28 healthy controls (normal control) through ELISA measurement. And their interrelationships were also systematically analyzed. The SLE patients were then divided into active SLE group and inactive SLE group according to the SLEDAI score. The results show that serum levels of PIGF, bFGF, and VEGF in all SLE group and active SLE group were higher than those in normal controls. Serum levels of PIGF and bFGF in inactive SLE group were higher than those in normal controls. The level of PIGF was positively correlated with VEGF in SLE patients and positive correlation is also shown in bFGF with VEGF. The levels of PIGF and VEGF in SLE patients were positively correlated with both ESR and SLEDAI score. Thus a tentative conclusion can be drawn that the serum levels of the angiogenic factors, for example, PIGF, bFGF, and VEGF, may be relevant in the pathogenesis of SLE, and the concentrations of PIGF and VEGF seem to be the markers of SLE activity.

1. Introduction

Systemic lupus erythematosus (SLE) is a typical autoimmune disease that involves quite a few organs, with vasculitis and angiopathy as some of its typical clinical expressions [1]. The damage and activation of vascular endothelial cells are the initiation factors in the pathogenesis of SLE. Angiogenic factor (AF) is a superfamily comprising of more than 20 factors, of which the placenta growth factor (PIGF), the basic fibroblast growth factor (bFGF), and the Vascular endothelial growth factor (VEGF) are our subject of study. Previous research shows that angiogenic factors increase substantially once the damage and activation of vascular endothelial cells happen and play a significant role in vascular permeability, vascular growth, and inflammatory response. For instance, angiopoietin-2 (Angpt-2), a marker of endothelial cell activation, has been proposed as a mediator of angiogenesis, which might play an important role in the regulation of endothelial integrity and inflammation and thus is related to severity and cardiovascular disease in patients with rheumatoid arthritis [2]. And antitumour

necrosis factor-α therapy modulates angiopoietin-2 serum levels in nondiabetic ankylosing spondylitis patients [3]. Angiogenesis may play a role in vasculitides by providing a compensatory response to ischemia and to the increased metabolic activity and may be also a further inflammatory stimulus because endothelial cells of newly-formed vessels express adhesion molecules and produce colony-stimulating factors and chemokines for leukocytes [4]. In addition, vascular endothelial growth factor (VEGF) as one of the most important proangiogenic mediators may play a role in the development of severe ischemic manifestations of giant cell arteritis [5]. Controversially, research by Rodríguez-Rodríguez et al. suggests that VEGFA polymorphisms do not seem to exert a significant influence on the risk of cardiovascular disease in patients with rheumatoid arthritis [6]. Whilst well investigated in the tumor research, the role of angiogenic factors in systemic lupus erythematosus has far been from fully understood [7]. Our clinical research aims at studying the angiogenic factors, in particular, the PIGF, bFGF, and VEGF—their expressions in the SLE patients, their interrelationships, and their correlations with other clinical

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indicators, by which investigating the role of AF in the pathogenesis of SLE.

2. Materials and Methods

2.1. Participants. We identified 54 SLE in-patients within the Department of Nephrology, the Department of Rheumatology, and the Department of Dermatology in the First Affiliated Hospital of Soochow University during January 2010 and November 2010, among which 4 are males and 50 are females with mean age of 36.81 ± 12.52 years. All patients satisfied at least four items of the established American Rheumatism Association diagnostic criteria (1982) for the classification of SLE, and those patients with primary vasculitis, cerebrovascular accident, primary renal disease, tumor, and any recent infections were excluded. Among those 54 patients, 9 were newly diagnosed cases. The disease activity score of SLE was evaluated by the systemic lupus erythematosus disease activity index (SLEDAI) score, and according to it, a patient was diagnosed as active if SLEDAI score was higher than or equals to 10. Of those 54 patients in our study, 36 cases were in active SLE group and 18 cases were in inactive SLE group. In the control group there were 28 participants, all of those were healthy routine medical examinees in the First Affiliated Hospital of Soochow University during November 2010 to December 2010. Among them 6 were males and 22 were females, with mean age of 37.82 ± 12.86 years. After inquiry of medical history, medical examination, and laboratory analysis, the possibilities of other diseases or diseases of genetic inheritance were excluded. This study has been reviewed and approved by the ethics committee of the First Affiliated Hospital of Soochow University, and informed consent has been signed by all participants.

2.2. Lab Measurements. Venous blood of 5 mL was collected for each participant with an empty stomach, and then anticoagulated with EDTA-K2. Within 30 minutes immediately after the collection, each sample was centrifuged for 10 minutes at the speed of 3,000 r/min, so that serum samples could be extracted and then frozen and stored at -80°C for further test. The serum levels of PIGF, bFGF, and VEGF were tested through the double antibody sandwich ABC-ELISA method, with the testing kit ordered from Shanghai Westang Bio-tech Co., Ltd.. The intra and interassay coefficients of variation of all ELISA kits are less than 10%. All practical details were operated strictly in accordance with the instructions on the manual of the kit. Specimens were tested once and for all after all the collection tasks were finished. Complete blood count, blood biochemistries, humoral immunity, erythrocyte sedimentation rate (ESR), and 24-hour urine protein were routinely tested by the department of clinical laboratories of our hospital.

2.3. Statistical Analyses. All the quantitative data are represented as mean \pm standard deviation. Independent-samples t test and Levene's analysis of variance are used in the comparison between groups. Pearson method is used with correlation analysis. All data are processed with statistical software SPSS 17.0.

3. Results

3.1. Clinical Data among Groups. The diastolic blood pressure (DBP) of the disease group, including the all SLE group in general and those in active SLE group and those in inactive SLE group in particular, is higher than that of the control group. Levels of hemoglobin (Hb), plasma albumin (Alb), and fasting blood glucose (FBG) in all SLE group in general and those in active SLE group and in inactive SLE group in particular are lower than those in the control group. Platelet counts (Plt) of the SLE group are lower than those of the control group. Levels of plasma triglyceride (TC) and serum creatinines (Cr-s) in the active SLE group are higher than those in the control group. Levels of blood uric acid (UA) in the inactive SLE group are lower than those of the control group. There are statistical significances in all the above differences (P < 0.05). There are differences on the levels of hemoglobin, plasma triglyceride, diastolic blood pressure, plasma albumin, and serum creatinine between the active SLE group and the inactive SLE group (P < 0.05). (Table 1).

3.2. Comparisons of the Levels of PIGF, bFGF, and VEGF among Groups. The levels of PIGF, bFGF, and VEGF in all SLE group and in the active SLE group are significantly higher than those in the control group (P < 0.01, P < 0.01, and P < 0.05). The levels of PIGF and bFGF in the inactive SLE group are significantly higher than those in the control group, and the differences have statistical significances (P < 0.05, P < 0.01). The levels of PIGF, bFGF, and VEGF in the active SLE group are higher than those in the inactive SLE group, but there is no statistical significance in the differences (P > 0.05). (Table 2).

3.3. Correlations among PIGF, bFGF, and VEGF. There are positive correlations in the level of PIGF with VEGF and in the level of bFGF with VEGF in the SLE group (r = 0.310, P < 0.05; r = 0.257, P < 0.05), while there is no correlation between the levels of PIGF and bFGF (r = 0.121, P > 0.05).

3.4. Correlations of PIGF, bFGF, and VEGF with Clinical Indicators. There are positive correlations in the level of PIGF with serum creatinine, erythrocyte sedimentation rate (ESR), SLEDAI score, and 24-hour urine protein (UP) and negative correlations in the level of PIGF with hemoglobin and plasma albumin. There is positive correlation between the level of bFGF and erythrocyte sedimentation rate and negative correlation between the level of bFGF and complement component C3. There are positive correlations in the level of VEGF with erythrocyte sedimentation rate, SLEDAI score, and 24-hour urine protein and negative correlation between the level of VEGF and plasma albumin. (Table 3).

4. Discussion

Systemic lupus erythematosus (SLE) is a rather common autoimmune disease, whose etiology or pathogenesis has not been fully understood. Deposits of the circulating immunocomplex (CIC) adhere to the inner lining of the arterial walls

Table 1: Clinical data among groups (mean \pm standard deviation).

	Control group	All SLE group	Active SLE group	Inactive SLE group
Number of cases	28	54	36	18
Age	37.82 ± 12.86	36.81 ± 12.52	34.50 ± 11.84	41.44 ± 12.91
Gender (F/M)	22/6	50/4	34/2	16/2
SBP (mmHg)	120.11 ± 14.27	126.39 ± 27.28	130.28 ± 28.79	118.61 ± 22.81
DBP (mmHg)	72.54 ± 8.39	80.69 ± 18.867^{a}	84.36 ± 19.97^{b}	73.33 ± 14.25^{d}
Hb (g/L)	145.89 ± 13.192	113.96 ± 20.84^{a}	$108.22 \pm 21.71^{\rm b}$	125.44 ± 13.19^{cd}
Plt (109/L)	196.29 ± 39.93	167.31 ± 83.35^{a}	165.36 ± 95.04	171.22 ± 55.11
TC (mmol/L)	4.89 ± 1.19	5.56 ± 2.41	5.78 ± 2.58	5.12 ± 12.03
TG (mmol/L)	1.63 ± 1.00	2.20 ± 1.43	2.42 ± 1.62^{b}	1.74 ± 0.79^{d}
Alb (g/L)	45.20 ± 2.42	33.42 ± 8.18^{a}	31.80 ± 7.88^{b}	36.68 ± 8.00^{cd}
Cr-s (µmol/L)	60.25 ± 13.36	86.66 ± 68.23	97.03 ± 81.57^{b}	65.92 ± 11.50^{d}
UA (mmol/L)	339.29 ± 91.91	314.24 ± 134.31	330.93 ± 155.32	$280.85 \pm 69.29^{\circ}$
FBG (mmol/L)	5.84 ± 0.97	5.10 ± 0.89^{a}	5.17 ± 0.09^{b}	4.95 ± 0.91^{c}

Note: When compared with the control group, ${}^{a}P < 0.05$, ${}^{b}P < 0.05$, and ${}^{c}P < 0.05$; When compared with the active SLE group, ${}^{d}P < 0.05$.

TABLE 2: Serum Levels of PIGF, bFGF, and VEGF among groups (mean ± standard deviation).

Groups	PlGF (pg/mL)	bFGF (pg/mL)	VEGF (pg/mL)
Control group	41.53 ± 3.40	23.87 ± 24.53	47.29 ± 52.62
All SLE group	$51.51 \pm 20.75^{\mathrm{b}}$	$69.75 \pm 88.88^{\mathrm{b}}$	91.47 ± 108.67^{a}
Active SLE group	54.40 ± 24.35^{b}	73.49 ± 103.26^{b}	100.87 ± 129.89^{a}
Inactive SLE group	45.71 ± 8.20^{a}	$62.28 \pm 50.87^{\mathrm{b}}$	72.70 ± 39.05

Note: When compared with the control group, ${}^{a}P < 0.05$, ${}^{b}P < 0.01$.

within the body of the patient and activate the complement pathway that generates anaphylatoxins and chemotactic factors, stimulating the white blood cells to damage the vascular endothelium, thus causing the further damages to the blood vessels and organs [8]. Under the stimulation of various pathological factors, vascular endothelial cells will release more cytokines and inflammatory mediators, causing the activation and damage of vascular endothelium, which may play a key role in the angiopathy of SLE [9].

VEGF could strongly induce the angiogenesis and play an active role in maintaining the survival of vascular endothelial cells. Recent discoveries show that there are other kinds of factors that have similar functionalities with VEGF, all of which have been generally named as the vascular growth factors, such as PIGF, bFGF, and platelet-derived growth factor (PDGF). Some recent research suggests that vascular growth factors such as VEGF participate in the pathogenesis and development of connective tissue diseases, and in SLE, any vasculitis, angiemphraxis, and vessel hypertrophy could stimulate the vascular endothelial cells to discharge or secrete vascular growth factors such as VEGF [10]. Research findings by Robak et al. [11] show that serum VEGF has a substantially high level of expression in SLE patients and is positively correlated with the ESR and SLEDAI score. These are consistent with our research findings. VEGF exerts its biological effects through binding with two high affinity tyrosine kinase receptors, namely, VEGFR-1 and VEGFR-2, of which VEGFR-1 mainly participates in the activation of angiogenesis while VEGFR-2 mediates the proliferation of

epithelial cells, synthesis, and migration of DNA and the vascular permeability. Some researchers point out that the imbalance between VEGF and its two soluble receptors is one of the reasons that leads to the pathogenesis of the angiopathy of SLE [12, 13].

There are fewer investigations on the role of PIGF in the connective tissue diseases such as SLE. The amino acid sequence of PIGF is 46% homologous with VEGF. PIGF promotes human embryonic angiogenesis through binding to and activating VEGFR-1 [14] and enhances monocyte chemoattraction, vascular growth, and mobilization of bone marrow precursor cells. Research shows that besides its role on the VEGF receptors, PIGF could also participate in the angiogenesis through enabling the monocytes to secrete VEGF [15, 16]. Oura et al. [17] have observed the differences between PIGF deficient mice and wild-type mice in the cutaneous delayed-type hypersensitivity (DTH) reactions and found out that PIGF deficiency resulted in a diminished and abbreviated inflammatory response, together with a reduction of inflammatory angiogenesis and edema formation. Findings by Bottomley et al. [15] show that PIGF could strongly induce the secretion of VEGF and PPMG in patients with arthropathies. Our research finds out that the levels of PIGF in all SLE group in general and in active SLE group and in inactive SLE group in particular are all higher than those in the control group. This is in consistence with the research findings of Robak et al. [18]. Meanwhile we also find out that the level of PIGF is positively correlated with that of VEGF, ESR, and SLEDAI score in the SLE group, suggesting

Clinical data	P	GF	bF	GF	VE	EGF
Cillical data	r value	P value	r value	P value	r value	P value
Hb	-0.474	0.000	-0.125	0.358	-0.151	0.275
ALB	-0.311	0.022	-0.076	0.585	-0.280	0.040
Cr	-0.581	0.000	-0.038	0.787	-0.007	0.962
ESR	0.346	0.010	0.278	0.042	0.527	0.000
Complement C3	-0.210	0.081	-0.278	0.042	-0.108	0.438
SLEDAI score	0.269	0.049	0.006	0.965	0.385	0.042
24 h UP	0.345	0.034	0.010	0.879	0.457	0.013

TABLE 3: The correlations in the serum levels of PIGF, bFGF, and VEGF with each clinical data in the SLE group.

that PIGF is very likely to play its role in the angiopathy of SLE through enabling the secretion of VEGF and binding with it to activate VEGFR-1, and PIGF might also be relevant to the disease activities.

BFGF, as a member of the multifunctional fibroblast growth factor family, is highly active both in vivo and ex vivo in enhancing the mitosis, chemotaxis, neurotrophy, and angiogenesis. Laboratory mouse tests by Seghezzi et al. [19] find out that although there is very few expression of VEGF in resting endothelial cells, added exogenous recombinant human bFGF could stimulate the endothelial cells to synthesize VEGF and enable the cornea neovascularization, whereas VEGF antibody inhibits these. In this regard it is believed that bFGF could enhance the expression and secretion of VEGF. Previous research shows that serum bFGF has an elevated expression in connective tissue diseases such as scleroderma and dermatomyositis, whilst there are few and even controversial investigations regarding the expression of serum bFGF in SLE. Hrycek et al. [20] tested the serum level of FGF in 48 SLE patients, who were then grouped according to their status of treatment. Results showed that the level of FGF was low in patients who were newly diagnosed and only higher in those patients who had received subsequent treatment. Our research shows that serum level of FGF in all SLE group, the active SLE group, and the inactive SLE group are all significantly higher than that in the control group, and the level of bFGF is positively correlated with that of VEGF, suggesting that bFGF might, along with other factors, participate in the angiopathy of SLE by enhancing the expression and secretion of VEGF. Yet the innate mechanisms and their interrelationships of how these angiogenic factors contribute to the angiogenesis of the SLE patients still remain unclear, allowing for further investigations.

Our research findings show that the levels of PIGF, bFGF, and VEGF in active SLE group are higher than those in the inactive SLE group, but there is no statistical difference in the results. It can be explained that the angiopathy of the SLE patients in active SLE group is somewhat controlled after immunosuppression treatment and the diseases tend to ease off. But some previous findings by other researchers show that the levels of the angiogenic factors in active SLE group were significantly higher than those in the inactive SLE group [11, 20], which is inconsistent with our findings. This may be due to the fact that there are differences in the selection of individual patients and the size of the sample. This discrepancy has to be further investigated. In addition,

simple correlation analysis shows that VEGF is negatively correlated with plasma albumin, and PlGF is also negatively correlated with hemoglobin and plasma albumin, suggesting that with the activity and development of the disease, the nutritional conditions of the patients gradually deteriorate, resulting in a continued increase in the serum levels of PlGF and VEGF. Our research also shows that the levels of PlGF and VEGF are positively correlated with 24-hour urine protein, and the level of PlGF is positively correlated with serum creatinines, indicating that both PlGF and VEGF might participate in the pathogenesis of lupus nephritis. Recent research by Frieri supports our view [21].

5. Conclusions

To sum up, it seems that PIGF, bFGF, and VEGF may be working in coordination in the pathogenesis of SLE. Meanwhile, both PIGF and VEGF could be the markers of SLE activity. Internationally, therapies of antiangiogenic factors for cancer and retinopathy have been put into clinical practice, for instance, thalidomide [22, 23] has been proved to be effective to SLE in which traditional trials have proven futile. With the research development in the expression and regulation mechanisms of autoimmune diseases, angiogenic factors are very promising in becoming new laboratory indicators and new therapies, playing their vital roles in the diagnosis, targeted therapy, and prognosis of diseases.

Abbreviation

(in the order of their appearance in the paper)

SLE: Systemic lupus erythematosus

AF: Angiogenic factor
PIGF: Placenta growth factor
bFGF: Basic fibroblast growth factor
VEGF: Vascular endothelial growth factor
SLEDAI: Systemic lupus erythematosus disease

activity index

ABC-ELISA: Avidin biotin complex enzyme-linked

Immunosorbent assay

ESR: Erythrocyte sedimentation rate DBP: Diastolic blood pressure

Hb: Hemoglobin

Alb: Plasma albumin FBG: Fasting blood glucose Plt: Platelet counts

TC: Plasma triglyceride Cr-s: Serum creatinines

UA: Uric acid UP: Urine protein

CIC: Circulating immunocomplex PDGF: Platelet-derived growth factor TGF: Transforming growth factor TNF: Tumor necrosis factor DTH: Delayed-type hypersensitivity SBP: Systolic blood pressure

SBP: Systolic blood pressure DBP: Diastolic blood pressure.

Conflict of Interests

The authors certify that they have no affiliations with or involvement in any organization or entity with any financial interest (such as honoraria; educational grants; participation in speakers' bureaus; membership, employment, consultancies, stock ownership, or other equity interest; and expert testimony or patent-licensing arrangements) or nonfinancial interest (such as personal or professional relationships, affiliations, knowledge or beliefs) in the subject matter or materials discussed in this paper.

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