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## Pathogenic mechanisms in systemic lupus erythematosus

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### Abstract

Systemic lupus erythematosus (SLE) is a chronic inflammatory disease characterized by the dysfunction of T cells, B cells, and dendritic cells and by the production of antinuclear autoantibodies. This editorial provides a synopsis of newly discovered genetic factors and signaling pathways in lupus pathogenesis that are documented in 11 state-of-the-art reviews and original articles. Mitochondrial hyperpolarization underlies mitochondrial dysfunction, depletion of ATP, oxidative stress, abnormal activation, and death signal processing in lupus T cells. The mammalian target of rapamycin, which is a sensor of the mitochondrial transmembrane potential, has been successfully targeted for treatment of SLE with rapamycin or sirolimus in both patients and animal models. Inhibition of oxidative stress, nitric oxide production, expression of endogenous retroviral and repetitive elements such as HRES-1, the long interspersed nuclear elements 1, Trex1, interferon alpha (IFN- $\alpha$ ), toll-like receptors 7 and 9 (TLR-7/9), high-mobility group B1 protein, extracellular signal-regulated kinase, DNA methyl transferase 1, histone deacetylase, spleen tyrosine kinase, proteasome function, lysosome function, endosome recycling, actin cytoskeleton formation, the nuclear factor kappa B pathway, and activation of cytotoxic T cells showed efficacy in animal models of lupus. Although B cell depletion and blockade of anti-DNA antibodies and T–B cell interaction have shown success in animal models, human studies are currently ongoing to establish the value of several target molecules for treatment of patients with lupus. Ongoing oxidative stress and inflammation lead to accelerated atherosclerosis that emerged as a significant cause of mortality in SLE.

### Keywords

lupus; genetics; mitochondria; nitric oxide; endosome traffic

### Introduction

Systemic lupus erythematosus (SLE) is an auto-immune inflammatory diseases attributed to genetic and environmental factors causing the dysfunction of T cells, B cells, and dendritic

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cells and the production of antinuclear autoantibodies [1–3]. The pathogenesis of SLE is incompletely understood and current therapies largely relying on the use of corticosteroids and cytotoxic anti-proliferative drugs have limited efficacy and carry significant risks of toxicity. A rational approach for therapeutic design requires a detailed understanding of disease pathogenesis. Independent lines of evidence have implicated environmental factors and genetic determinants of the host in the causation of the disease [4].

Genome-wide association studies (GWAS) have identified numerous chromosomal loci that may harbor susceptibility genes [5]; however, the functional significance of these GWAS-derived polymorphisms is presently unknown. Therefore, a systematic characterization of the molecular and cellular basis of signaling abnormalities within the immune system that leads to autoreactivity and inflammation and their relationship to regulation of gene expression remain critical for understanding of disease pathogenesis [6]. This issue of *Autoimmunity* is dedicated to the state-of-the-art reviews and original articles providing novel insights into the pathogenesis of SLE.

## Genetic and epigenetic factors contributing to the pathogenesis of SLE

Endogenous retroviruses (ERV) have long been implicated in triggering autoimmunity through structural and functional molecular mimicry with viral proteins [7–10]. The notion that ERV contribute to the pathogenesis of autoimmunity provides genetic linkages between the host genome and the environment. A polymorphic single nucleotide polymorphism of HRES-1 endogenous retrovirus was earlier associated with the development of SLE [11,12]. Recently, polymorphic haplotypes of the HRES-1 long-terminal repeat (LTR) have been associated with SLE in case-control and family studies [13]. The HRES-1 LTR harbors an enhancer that upregulates the expression of the HRES-1/Rab4 gene product, encoding a small GTPase that regulates receptor recycling through endosome traffic [14]. GST pull-down studies revealed a direct interaction of HRES-1/Rab4 with CD4, CD2AP, and the T cell receptor (TCR) chain [15].

Both the knockdown of HRES-1/Rab4 expression by siRNA and the inhibition of lysosomal function increased TCR- $\zeta$  levels in lupus T cells. These observations identified HRES-1/Rab4-dependent lysosomal degradation as a novel mechanism contributing to the critical loss of TCR in lupus T cells [16]. Thus, HRES-1/Rab4 may constitute the susceptibility gene at the 1q42 chromosomal locus previously linked to SLE by multiple laboratories [17–21]. The expression of full-length RNA encoded by a modified polytropic ERV in the Sgp3 (serum gp70 production 3) locus has been implicated in the pathogenesis of murine lupus [22].

GWAS studies provided strong new evidence for the genetic linkage of SLE with STAT4 [23] and IRF-5 [24], which are involved in cytokine signaling. The associations with these novel genetic loci remain less robust than the impact of the HLA locus [25]. Another interesting polymorphism that has been linked to lupus results in a non-conserved R77H substitution of the ITGAM gene that encodes the  $\alpha$  chain of CD11b [5], which is expressed on macrophages and may contribute to the dysfunction of these cells in SLE. Additionally, a polymorphism of interleukin-1 receptor-associated kinase-1 (IRAK1) has been identified as

an X chromosome-encoded risk factor for SLESLE [26]. Importantly, deficiency of IRAK1 protects against the development of auto-reactivity and nephritis in lupus-prone mice, suggesting that the increased activity of this gene may also be relevant for disease pathogenesis in patients with SLE (Table I).

Induction of type I interferons (IFNs) by viral DNA is a principal element of antiviral defense but can cause autoimmunity if misregulated. Cytosolic DNA detection activates a potent, cell-intrinsic antiviral response through a poorly defined pathway. A screen for proteins relevant to this IFN-stimulatory DNA response identified the 3'–5' repair exonuclease 1 (Trex1). Mutations in the human Trex1 gene are associated with Aicardi–Goutieres syndrome and chilblain lupus [27]. Trex1 metabolizes single-stranded DNA reverse transcribed from endogenous retroelements. Single-stranded DNA accumulates and stimulates IFN- $\alpha$  production in Trex1-deficient cells. Thus, Trex1 deficiency is identified as a novel cell-intrinsic mechanism for initiation of autoimmunity by endogenous retroviral elements [28]. Lupus-linked polymorphisms of PTPN22 [29] lead to sustained signaling through the TCR and B cell receptor [30]. STAT4 and IRF5 polymorphisms facilitate IFN signaling in lupus [31]. In addition to linkages with nuclear genes, polymorphisms of the mitochondrial DNA (mtDNA) have also been associated with SLE [32].

Crow provides a highly innovative concept that a unique class endogenous retroelements, the long interspersed nuclear elements (LINE-1, L1), contribute to autoimmunity via stimulating the production of IFNs [33]. She proposes that increased expression of L1 transcripts or decreased degradation of L1 DNA or RNA could provide potent stimuli for an innate immune response, priming of the immune system, and inducing autoimmunity and inflammation in SLE. Genomic and genetic variations among individuals, sex-related differences in L1 regulation, and environmental triggers are among the potential mechanisms that might account for increased L1 expression. Induction of type I IFN by L1-enriched nucleic acids through Toll-like receptor-independent pathways could represent a first step in the complex series of events leading to systemic autoimmune disease.

Alternatively, epigenetic mechanisms may contribute to T and B cell hyperreactivity in SLE. In particular, drug-induced lupus has been associated with inhibition of DNA methyltransferase 1 (Dnmt1) and demethylation and activation of T cell genes, such as leukocyte function-associated antigen 1 and CD70 [34]. Procainamide and hydralazine inhibit phosphorylation and activity of extracellular signal-regulated kinase, which is proposed by Gorelik and Richardson to be a key mechanism causing the downregulation of the Dnmt1 gene [34]. Earlier studies suggest that increased activity of histone deacetylases is involved in T cell hyperreactivity in murine lupus [35]. Epigenetic mechanisms may directly contribute to the production of pathogenic anti-dsDNA immunoglobulin G (IgG) autoantibodies by B cells [36]. These autoantibodies are mutated and class switched, mainly to IgG, indicating that Ig gene somatic hypermutation (SHM) and class-switched DNA recombination (CSR) are important in their generation. The significant upregulation of SHM and CSR is associated with increased expression of activation-induced cytidine deaminase [36].

## New insights into signaling abnormalities in SLE

Defective activation of T cells, B cells, DCs, and macrophages has been observed in both human and animal models of SLE [2]. Diminished IL-2 production [37] and impaired T cell-mediated cytotoxic (CTL) activity have long been recognized as biomarkers of T cell dysfunction in SLE [38,39]. Diminished IL-2 production has been attributed to defective expression of the TCR/CD3 chain [37]. Via and Shearer offer new evidence that lupus-associated defects in IL-2 synthesis and CTL responses mediate T cell-driven B cell hyperactivity [40]. Using the parent-into-F1 (P\_F1) model of graft-versus-host disease-induced lupus, they have demonstrated the early appearance of diminished IL-2 production and defective CTL activity which in turn account for the subsequent B cell activation and autoantibody production. They propose that *in vitro* assessment of IL-2 production may serve as a sensitive measure of lupus disease severity [40].

Perl et al. reviewed the mechanism and consequences of the activation of the mammalian target of rapamycin (mTOR) that plays a central role in T cell dysfunction, including the diminished production of the TCR/CD3 chain, in patients with SLE [41]. mTOR serves as a sensor of the mitochondrial transmembrane potential ( $\psi_m$ ) [42] and it is activated by NO in human T cells [15]. mTOR promotes the endosomal recycling of TCR $\alpha$  and targets this protein for lysosomal degradation via activation of HRES-1/Rab4 [15]. Beyond its effect on endosomal traffic, the role of mTOR is likely to be more complex and cell-type dependent. Indeed, mTOR also controls the expression of Foxp3 and development of regulatory T cells [43,44] that are deficient in patients with SLE [45,46].

The activation of B cells [47] and DCs is also dependent on mTOR [48]. Therefore, the inhibition of T, B, and DC activation and expansion of Tregs may all contribute to the therapeutic efficacy of rapamycin in murine [49] and human SLE [50]. Activation of spleen tyrosine kinase (Syk) is mapped downstream of mTOR in lupus T cells [15]. R788, an orally bioavailable Syk inhibitor, was recently found to prevent the development of renal disease and to treat established nephritis in NZB/W mice [51]. R788 minimally affected autoantibody titers, while its dose dependence reduced the numbers of CD4 + activated T cells, suggesting that T cells might be the effective targets of Syk inhibition [51]. Syk is also involved in B cell dysfunction in SLE [52]. As reviewed by Ghosh and Tsokos, preclinical and early clinical studies have urged Syk inhibition for the treatment of patients with rheumatoid arthritis, whereas *ex vivo* experiments and preclinical studies point to a therapeutic potential of Syk inhibition in patients with crystal-induced arthritides [52].

Mitochondrial dysfunction, characterized by the elevation of the  $\psi_m$  or mitochondrial hyperpolarization (MHP), increased mitochondrial biogenesis, increased production of reactive oxygen intermediates (ROI) or oxidative stress, and the depletion of ATP predispose T cells to death by necrosis [53]. Increased production of nitric oxide plays key roles in MHP [54] and activation of mTOR in lupus T cells [15]. Oates emphasized the importance of ROI in modulating the effect of NO on cellular processes, the activation of innate immune responses, autoimmunity and organ damage in SLE [55]. The release of necrotic materials, DNA, RNA, and, in particular, high-mobility group B1 (HMGB1) protein stimulates DCs and B cells [56]. HMGB1, an abundant DNA-binding protein,

remains immobilized on chromatin of apoptotic bodies; however, it is released from necrotic cells [56]. Necrotic but not apoptotic cells also release heat shock proteins (HSPs), HSPgp96, hsp90, hsp70, and calreticulin [57]. pDCs are important sources of increased IL-10 [58] and promote plasma cell differentiation through production of IL-6 [59]. IFN-matured mDCs activate autoreactive T cells [60].

Wickramarachchi et al. provide insight into the modulation of T cell activation through remodeling of cytoskeletal actin filaments by coronins, which control the disassembly of actin filaments [61]. In particular, coronin-1A deficiency is associated with diminished antigen receptor-mediated T cell activation and  $Ca^{2+}$  flux, loss of mitochondrial membrane potential, and spontaneous apoptosis, primarily in the single-positive thymocyte and naïve T cell subsets [62]. A function-impairing mutation of coronin-1A has also been recently identified as the genetic alteration responsible for the lupus-associated *Lmb3* locus in mice [85]. This *Coro1a* allele was unexpectedly derived from the non-autoimmune strain, and therefore, it was a lupus-suppressing variant. This finding raised the possibility that allelic variants of other actin regulatory genes may also influence immune responses and susceptibility to SLE [61].

Avalos et al. provide new evidence that HMGB1, which is released from necrotic T cells, can also directly activate B cells [63]. IgG2a-reactive BCR transgenic AM14 B cells proliferate in response to endogenous chromatin immune complexes (ICs), in the form of the anti-nucleosome antibody PL2-3 and cell debris, in a TLR9-dependent manner, and that these ICs contain HMGB1. Activation of AM14 B cells by these chromatin ICs was inhibited by a soluble form of the HMGB1 receptor, RAGE-Fc, suggesting HMGB1–RAGE interaction was important for this response. Avalos et al. found that HMGB1 bound both CG-rich and CG-poor DNA. However, HMGB1/DNA complexes could not activate AM14 B cells unless HMGB1 was bound by IgG2a and thereby able to engage the BCR. Using RAGE-deficient mice, DNA ICs were found to activate RAGE<sup>+</sup> and RAGE<sup>-</sup> AM14 B cells to a comparable extent.

These results suggest that HMGB1 promotes B cell responses to endogenous TLR9 ligands through a RAGE-independent mechanism. Avalos et al. also reviewed the role of TLR9 and TLR-7 in B cell responses to DNA- and RNA-associated autoantigens [64]. Recent evidence suggests that B cell activation by BCR/TLR pathways depends on the balance of stimulatory and inhibitory signals. Either IFN- $\alpha$  engagement of the type I IFN receptor or loss of IgG ligation of the inhibitory Fc(RIIB) receptor promotes B cell activation by weakly stimulatory DNA and RNA TLR ligands. These mechanisms have important implications for the role of B cells *in vivo* in the pathology of SLE [64].

Jacob and Stohl illuminate the newly appreciated role of B cells in antigen presentation and T cell activation through the expression of co-stimulatory molecules and the production of cytokines. With these points in mind, they focus on the exploitation of autoantibody-dependent and autoantibody-independent roles of B cells for the treatment of SLE [65]. Sherer et al. reviewed the pathogenesis of accelerated atherosclerosis in SLE, its role in morbidity and mortality, as well as the importance of early detection and treatment [66]. Oxidized low-density lipoprotein (oxLDL) is prone to undergo uptake by macrophages,

which turns them into the foam cells detectable in atherosclerotic lesions. Although anti-oxLDL antibodies are associated with the extent of atherosclerosis in patients, induction of anti-oxLDL antibodies with malondialdehyde-oxLDL inhibited the development of atherogenesis in animal models [67]. These results support the notion that oxidative stress also contributes to atherogenesis, and certain anti-oxLDL antibodies may protect against atherosclerosis in SLE.

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**Table I**

New genetic factors associated with SLE.

<b>Gene</b>	<b>Pathway</b>	<b>Reference</b>
ITGAM/CD11b	Macrophage activation	[5]
IRAK1	NF-kappaB activation	[26]
TREX1	IFN- $\alpha$ production	[27,28]
STAT4	Cytokine signaling	[23]
IRF-5	Cytokine signaling	[24]
PTPN22	Sustained TCR/BCR signaling	[29,30]
BANK1	Sustained BCR signaling	[68]
B-lymphocyte kinase	B cell activation	[69]
HRES-1/Rab4	Receptor recycling	[13,15]
Coronin-1A	Actin depolymerization	[62]
MtDNA	Electron transport	[32]