REVIEW

Chance, genetics, and the heterogeneity of disease and pathogenesis in systemic lupus erythematosus

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Abstract Systemic lupus erythematosus (SLE) is a remarkably complex and heterogeneous systemic autoimmune disease. Disease complexity within individuals and heterogeneity among individuals, even genetically identical individuals, is driven by stochastic execution of a complex inherited program. Genome-wide association studies (GWAS) have progressively improved understanding of which genes are most critical to the potential for SLE and provided illuminating insight about the immune mechanisms that are engaged in SLE. What initiates expression of the genetic program to cause SLE within an individual and how that program is initiated remains poorly understood. If we extrapolate from all of the different experimental mouse models for SLE, we can begin to appreciate why SLE is so heterogeneous and consequently why prediction of disease outcome is so difficult. In this review, we critically evaluate extrinsic versus intrinsic cellular functions in the clearance and elimination of cellular debris and how dysfunction in that system may promote autoimmunity to nuclear antigens. We also examine several mouse models genetically prone to SLE either because of natural inheritance or inheritance of induced mutations to illustrate how different immune mechanisms may initiate autoimmunity and affect disease pathogenesis. Finally, we describe the heterogeneity of disease manifestations in SLE

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and discuss the mechanisms of disease pathogenesis with emphasis on glomerulonephritis. Particular attention is given to discussion of how anti-DNA autoantibody initiates experimental lupus nephritis (LN) in mice.

Keywords Systemic lupus erythematosus · Autoimmunity · Glomerulonephritis · Autoantibody · Pathogenesis · Immune tolerance

For most autoimmune diseases, we know more about the middle and end stages of the disease than the beginning. Lupus, systemic lupus erythematosus (SLE), is not different in that respect. SLE is the prototypic systemic autoimmune disease [1]. We are developing an understanding of how the potential for SLE is inherited and many genetic susceptibility loci that may contribute to SLE have been identified, but we are still in the very early stages of understanding how the identified susceptibility loci combine to produce disease phenotypes in SLE. More importantly, we do not know how the genetic program inherent within the inherited susceptibility genes is initiated to cause SLE nor what events or stimuli initiate the program. The heterogeneity of disease presentation in SLE further complicates understanding of how SLE is initiated. Virtually all organ systems of the body are potential targets for damage by the disease processes of SLE. Just what determines in a given individual with SLE which organs will be targeted is poorly understood and is an important area for future research. The plethora of autoantibodies that occurs in many individuals with SLE is thought to be the main drivers of organ damage or altered cellular function in the disease [2]. Established criteria for clinical diagnosis of SLE have been modified and updated to better reflect clinical presentation in patients and improvements in diagnostic tools and capabilities [3-7]. The published criteria include most, if not all, pathologic manifestations of SLE. A more recent guideline has been published specifically for diagnosis and management of glomerulonephritis

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in SLE, lupus nephritis (LN) [8]. Although there are more deaths due to cardiovascular disease in SLE patients, renal disease had the highest standardized mortality ratio (SMR) among patients in a very large, multicenter international cohort [9]. SMR was calculated as the ratio of deaths observed to deaths expected by cause for calendar-year periods and accounting for gender and age. Since patients are diagnosed with SLE after onset of clinical symptoms and because clinical symptoms can be so heterogeneous, there has been minimal opportunity to understand how SLE is initiated within individual patients or why disease phenotypes are so variable. This review will highlight current knowledge regarding the etiopathogenesis of damage to major target organs in SLE.

SLE

Autoimmunity in SLE is a consequence of the progressive innate immune stimulation of antigen-selective, adaptive immune responses to autoantigens [10-13]. The products of the autoimmune response are autoantibodies primarily, but not exclusively [2], to a variety of nuclear antigens including DNA, RNA, ribonuclear proteins, and histones [14] Pathogenic manifestations of lupus can encompass many tissues and organs and may include but are not limited to inflammation in the skin, joints, and other connective tissues; vasculitis; glomerular and interstitial nephritis; cardiopulmonary inflammation; central and peripheral nervous system inflammation; and thrombocytopenia [3, 15]. SLE is more prevalent in women than men with an estimated prevalence of 1/1,000 among American women above the age of 17 [16]. SLE also has an unequal prevalence depending upon race and ethnicity being more prevalent [17, 18] and with worse disease severity [19, 20] among African Americans, Asian, and Hispanic individuals. The frequency of lupus among female children below age 17 is estimated to be as high as 1/400 for non-Caucasian Americans [21]. The disease is generally more severe at onset in children than in adults [22, 23].

Mouse models for SLE

There are several experimental mouse models for SLE [24, 25]. All of the mouse models of spontaneous SLE share the phenotypes of antinuclear and anti-DNA autoantibody production and glomerulonephritis [1]. Similar to SLE in humans, multiple susceptibility loci may contribute to SLE in mice [26]. The first identified autoimmune mouse model was NZB and its F₁ hybrid with NZW, NZY, or NZC [27]. Autoimmunity in (NZB × NZW)F₁ (B/W) mice most closely resembles SLE in humans [26, 28] with female gender bias, complex genetic associations including major histocompatibility complex (MHC)-linked and non-linked loci [29–33], antinuclear and anti-DNA autoantibody [24], and lupus-like glomerulonephritis [28]. NZM, derived by inbreeding progeny of unintended backcross of B/W with NZW, have similar complex inheritance of SLE as B/W but are homozygous [25, 34]. Genetic susceptibility to SLE in MRL^{lpr/lpr} and BXSB^{Yaa} is primarily the result of a single mutation *lpr* that affects Fas expression in MRL and an X chromosome translocation *Yaa* that duplicates a region that includes the *tlr7* gene in BXSB [35]. B/W and other lupus-susceptible mice have been invaluable as experimental models to test hypotheses related to disease pathogenesis in SLE.

Genetics and stochasticity in SLE

At the Fourth International Congress of Immunology (Toronto, 1986), Dr. C. Garrison Fathman opened his presentation on autoimmunity in type I diabetes with the statement that "Autoimmunity is a combination of genetics and bad luck." The statement was and continues to be astute and accurate. Most autoimmune diseases have significant linkages to one or more genetic loci. Immune dysregulation, polyendocrinopathy, enteropathy, X-linked syndrome (IPEX), and autoimmune polyendocrinopathy-candidiasis-ectodermal dystrophy (APECED) are exceptions in which autoimmune disease is linked to mutations in single genes, foxp3 for IPEX [36, 37] and aire for APECED [38-40]. SLE has a strong heritable component, estimated to be approximately 66 % [41, 42], with rates of concordance between 20 and 40 % in monozygotic twins and from 2 to 5 % in dizygotic twins or siblings [41, 43, 44]. The sibling recurrence risk ratio in SLE patients is 29-fold higher than in the general population [41], and the higher concordance among monozygotic than dizygotic twins [44] indicates the importance of susceptibility inheritance. Genome-wide association (GWA) and gene mapping studies have identified approximately 30 susceptibility loci for SLE [42, 45, 46]. Individually, each locus has relatively modest risk association, odds ratio (OR)<2.5, and together account for only 15 % or less of the estimated genetic heritability of SLE [47, 48]. What accounts for the "missing heritability" for SLE is unknown or at least unresolved but may include epigenetic factors, other risk factors, or the likely possibility that the "SLE phenotype" is a collection of several distinct and rare subtypes [48, 49]. Penetrance for most identified risk loci is low, and as noted above, concordance is relatively low for monozygotic twins. Monozygotic twins receive the same genetic "hand," but "luck" clearly influences outcome as the genetic hand is played. Similarly, MRL lpr/lpr mice are genetically homogeneous. All develop SLE, but only 25 % produce the anti-Sm autoantibody [50]. No C57 BL/6^{lpr/lpr} mice produce anti-Sm. Anti-Sm in MRL^{lpr/lpr} is independent of gender, age, parentage, and environment. The potential to produce anti-Sm autoantibody is genetically determined, but anti-Sm production in the 25 % of MRL hpr/lpr that produce the autoantibody is determined by chance. Epistatic interactions among susceptibility loci have been identified [51–55], most notably between HLA and *CTLA4*, although again with relatively modest risk, OR<2. Low concordance and penetrance among susceptibility loci for SLE are consistent with stochastic expression of multiple susceptibility genes [1] and epigenetic effects on susceptibility gene expression [56, 57]. Low concordance has also been cited as indication for an environmental stimulus to initiate autoimmunity in SLE, which would also be manifested as a stochastic effect on disease susceptibility [41, 44, 58].

Exceptions to low penetrance for susceptibility loci in SLE are genes that encode early complement components [42], particularly C1q [59, 60], and TREX1, a gene that encodes a nuclease important in the degradation of cytosolic DNA [61]. Mutations in C1q [59] and TREX1 [62] are rare, but both are strong risk factors for lupus (OR=10 and 25, respectively). Mutations that inhibit function of those genes initiate autoimmunity and SLE without a requirement for "bad luck" other than inheriting a bad C1q or TREX1 gene. Although there have been fewer genetic studies in pediatric lupus patients with concomitantly much less data, the risk and confirmed loci are similar to those in adults [63]. Inherited deficiencies in early complement components present the highest risk and, when present, account for the earlier disease manifestation in children [59].

MHC

Genetic risk for SLE is associated with inheritance of MHC class II and class III loci [49]. Within MHC class II, HLA-DRB1 haplotypes DBR1*1501 and DBR1*0301 confer the strongest MHC class II association with SLE [64, 65]. The MHC class III locus contains genes encoding complement components and other proteins, single nucleotide polymorphisms (SNP) for which GWA has established linkage to SLE. These include the early complement components C1q, C4, C1r/s, C2, and C3 [66-68], the MutS homolog 5 (MSH5), super viralicidic activity 2-like (SKIV2L), integrin alpha m (ITGAM, CD11b), integrin beta chain beta 2 (ITGB2, CD18), and Fcy receptor (FcyR) genes [69–75]. The phenotypic contributions of complement, ITGAM, and $Fc\gamma R$ are discussed in more detail below. MSH5 is important in immunoglobulin (Ig) class switch recombination [76], meiosis, and DNA mismatch repair [76]. The phenotypic contribution of SKIV2L is less understood.

Type I IFN

As found in other autoimmune diseases such as systemic sclerosis, type 1 diabetes, rheumatoid arthritis, psoriasis, Sjogren's syndrome, and dermatomyositis, over half of patients with SLE exhibit a type I interferon (IFN)-inducible gene signature in their peripheral blood leukocytes [77–82].

As it turns out, close to half of the genetic susceptibility loci found to be associated with SLE are involved in type I IFN production or downstream signaling [83]. Type I IFNs that consist of 13 IFN- α isotypes, IFN- β , IFN- ϵ , IFN- κ , and IFN- ω , are major mediators of inflammation and the innate immune response. Plasmacytoid dendritic cells (pDCs) produce IFN in response to cell membrane or endosomal signaling when innate immune receptors, including toll like receptors (TLR) 3, 7, 8, and 9, are engaged by pathogen-associated molecular patterns (PAMPs) or damage-associated molecular patterns (DAMPs) or when specialized receptors, such as RIG-I or IFIH1, are engaged by intracellular RNA and DNA [84]. The IFNAR1/2 receptor when engaged by type I IFN initiates a signaling cascade through the Janusactivated protein kinases (JAK), JAK1 and TYK2, which regulate a myriad of downstream genes [83, 85, 86]. Many of these downstream genes are likely involved in SLE pathogenesis by affecting expression of chemokines, facilitating monocyte and DC maturation, activating autoreactive T and B cells, promoting autoantibody secretion from differentiated, autoreactive plasma cells, and by facilitating apoptosis of immune cells [86]. The importance of the type I IFN signature in SLE pathogenesis is supported by the observation that those patients with endogenous anti-IFN α autoantibodies tend to have lower serum type I IFN levels, reduced activation of type I IFN pathways, and lower SLE disease activity scores [87].

Other cytokines and cytokine signaling

Although members of the tumor necrosis α (TNF- α) family have been associated with SLE, the role of TNF α specifically is still to be determined. TNF ligand superfamily 4 (TNFSF4) polymorphism confers susceptibility to SLE [88]. The TNFSF4 receptor is expressed mainly on activated antigen-presenting cells (APCs) and activated CD4⁺ T cells, and increased expression of TNFSF4 may enhance interactions with APCs or by modulating T cell activation [88–90]. B/W mice inherit a dominant TNF- α allele from NZW H-2^z that results in reduced TNF- α [91]. Recombinant TNF- α replacement therapy induces a significant delay in LN in B/W mice. Associations between interleukin (IL)-10 [92–94], IL-1 signaling [95], IL-21 [96], and inducible T cell co-stimulator (ICOS) [97] and susceptibility to SLE have also been identified.

Genetic risk and intrinsic versus extrinsic problems in disposal of cellular debris

The highest risk associations for SLE are in genes that control disposal and degradation of apoptotic cells and cellular debris, C1q [59, 60] and TREX1 [62, 98]. TREX1 is a negative

regulator of the type I interferon-stimulatory DNA (ISD) response [99]. TREX1 deletion in mice results in the accumulation of endogenous retroelement DNA, ISD-dependent IFN production, inflammation, and autoimmunity. C1q binds apoptotic cells and particles and facilitates their degradation and removal [60, 100, 101]. C1q is a complex of three polypeptides, A, B, and C, encoded by genes within chromosomal region 1p34.1 to 1p36.3 [102]. C1q deficiency may be caused by nonsense or missense mutations in A, B, or C with no identified preference [59]. Mice made genetically deficient in either C1q [60] or DNaseI [103] accumulate apoptotic cells and nuclear debris and develop SLElike autoimmunity including LN. Similarly, mutant mice that lack functional Tyro 3 family member Mer also have defective phagocytosis and clearance of apoptotic cells and also develop SLE-like autoimmunity [104].

Circulating monocytes and macrophages from SLE patients exhibit a reduced capacity for eliminating apoptotic cells [105, 106]. What is not clear is whether that observed phagocytic defect is intrinsic to phagocytic cells or extrinsic from the effects of chronic inflammation on phagocytic cells in SLE patients. Peritoneal macrophages but not bone marrowderived macrophages in B/W mice have phagocytic defects similar to those in phagocytes from SLE patients [107, 108]. Those results indicated that the phagocytic defect in circulating or peripheral tissue macrophages in B/W mice is extrinsic and related to autoimmunity in the mice and not intrinsic to the macrophages. The latter is relevant to understand whether phagocytic defects and poor elimination of apoptotic cells contribute to initiation of SLE early in disease pathogenesis, "cause," or simply reflect the cumulative effects of autoimmunity and ongoing chronic inflammation, "effect." Whether cause or effect, reduced phagocytosis and elimination of apoptotic, necroptotic, NETotic, or necrotic debris would exacerbate autoantibody production and disease progression.

Izui et al. were the first to realize that inflammatory stimuli such as lipopolysaccharide (LPS) could induce release of circulating DNA, formation of circulating DNA-anti-DNA complexes, and glomerulonephritis [109-111]. Immune complexes of antinuclear autoantibodies and remnants of secondary necrosis from poorly phagocytosed apoptotic cells augment inflammatory cytokine release ex vivo in phagocytic cells from SLE patients [112] likely as a result of increased signaling from FcyR and TLR. That enhanced ability to phagocytose cellular debris from secondary necrosis contrasts with the inherited susceptibility locus in ITGAM, CD11b. An inherited polymorphism in ITGAM is a susceptibility locus for SLE although with modest individual risk [74, 75]. Monocytes/macrophages and neutrophils from individuals homozygous [113] or heterozygous [114] for the susceptibility allele have reduced iC3b-dependent phagocytosis by complement receptor 3 (CR3). The reduced phagocytic function of CR3 encoded by the susceptible allele is consistent with the association of susceptibility in SLE with reduced potential to eliminate apoptotic cells and cellular debris. The modest single risk for SLE associated with ITGAM implies that other intrinsic and/or extrinsic factors must operate with ITGAM to affect disease.

As noted above, the rather low penetrance and low concordance for most inherited susceptibility loci have been interpreted as indication for the necessary contribution of environmental factors for autoimmunity and disease in SLE [41, 44, 58]. At least in B/W and other mice genetically predisposed to SLE, initiation of spontaneous autoimmunity is independent of an identified external innate or adaptive immune stimulus [1]. Mice not genetically prone to autoimmunity and homozygous for an induced null mutation in the inhibitory FcyRIIb develop SLE-like autoimmunity including glomerulonephritis [115]. The elimination of a critical regulatory pathway for inhibiting B cell activation results in SLE-like autoimmunity in an otherwise normal background. Sanroque mice produce anti-DNA autoantibody and develop LN [116]. Sanroque mice are homozygous for an induced mutation in the roquin ubiquitin ligase gene Rc3h1 [117]. Sanroque mice have spontaneous T follicular helper cell (T_{FH}) expansion and germinal center (GC) formation. $Lyn^{-/-}$ mice have defective B cell signaling and development with reduced B cell numbers, more rapid turnover, and abnormal response to T-independent (TI) and T-dependent (TD) antigens [118–120]. As $Lyn^{-/-}$ mice age, they develop autoantibodies and lupus-like autoimmune disease. Lyn function is not required to initiate B cell receptor-dependent activation but is essential for tolerance and negative regulation including FcyRIIb [121]. $Cd22^{-/-}$ mice have a similar B cell phenotype to $Lyn^{-/-}$ [122]. Chronic graft-versus-host (GVH) disease in mice produces SLElike autoimmunity including selective production of antinuclear autoantibodies, including anti-DNA autoantibody, and glomerulonephritis [123–125]. The intensive, chronic T cell stimulation in GVH stimulates normally tolerant autoreactive B cells to produce autoantibodies. Intraperitoneal pristane injection of mice not genetically predisposed to autoimmunity induces chronic inflammation, autoantibody production, including anti-DNA, and lupus-like disease [126]. The mechanism for autoantibody production in that experimental system is not understood but is likely due to chronic stimulation of mononuclear cells, particularly Ly6C-positive monocytes, and type I interferon production [127]. Mice from strains not genetically predisposed to autoimmunity produce IgG anti-DNA antibody with glomerular immune deposits and proteinuria when immunized with DNApeptide complexes, but the induced autoantibody production is not sustained [128, 129].

Eilat and Wabl [130] have introduced a new and interesting hypothesis for the role of endogenous retroviral elements in the induction of autoimmunity in B/W and other autoimmune mice. Their hypothesis derives from the experimental effects of an antiretroviral drug on disease progression in B/W mice [131]. The hypothesis predicts that intracellular replication and accumulation of retroviral DNA and RNA stimulate IFN production and the creation of neo-epitopes to which T cells are not tolerant. The hypothesis is consistent with SLE susceptibility associated with TREX1 deficiency discussed above and the function of nucleic acid sensing TLR7 and 9 in B cell activation [11, 132].

Tolerance and self-reactivity

Whether good versus bad luck in SLE reveals itself as random environmental influence, inherited [133] or stochastic epigenetic regulation, or other stochastic genetic events remains largely unknown. The immune system has evolved recognition and sensing capabilities to maximize pathogen detection at the risk of self-reactivity [134]. For example, a surprising percentage of Ig heavy and light chain variable regions genes in the mouse primary B cell repertoire encode anti-DNA antibodies [13, 135]. That potential for self-reactivity must be and normally is restrained [134]. Any genetic [115, 116], innate immune [126, 136], or adaptive immune [123, 124, 128, 129] disruption of the regulatory balance and control of self-reactivity can initiate autoimmunity. If the activation is sustained or progressive, the acute autoimmunity can become chronic and produce autoimmune disease.

Autoantibodies and autoimmune B cell activation

Disease phenotypes in SLE are highly pleomorphic [3, 4, 15, 15]137] due to the heterogeneity of molecular and cellular dysregulation of immune function [138]. The most frequent immune aberration, common to human and mouse SLE, is antinuclear autoantibody production. Antinuclear autoantibodies in human and mouse SLE may include antibodies reactive to DNA; chromatin; nucleosomes; histones; nonhistone DNA-binding proteins; and ribonuclear proteins (RNP), Sm, U1-RNP, Ro/SSA, and La/SSB [14] with reactivity or cross-reactivity to phospholipids [139, 140]. Reactivity to double-stranded DNA (dsDNA) and the Sm ribonuclear protein antigen are generally specific for SLE [3]. Immune pathogenesis in human [141–143] and mouse [24] SLE is most correlated with autoantibody production to native DNA (dsDNA), although most anti-dsDNA monoclonal antibodies (mAbs) also bind chromatin and nucleosomes [135, 144].

How autoreactive B cell activation and anti-DNA autoantibody production are initiated and what initiates the activation is still basically unknown. What is known is that autoreactive B cells undergo clonally selective specificity maturation and class switching to IgG driven by specificity for DNA or other nuclear antigens within GC [12, 13, 145]. Initiation of the autoimmune response depends upon innate immune signaling primarily through TLR7 and 9 on B cells and APCs [11, 132]. IFN production by APCs, particularly pDC, is a consistent and critical mechanism in the innate immune-dependent initiation of inflammation and T and B cell activation [146–148]. The IgG autoimmune antibody response, including IgG anti-DNA, is CD4 T cell-dependent [149], although determination of which CD4 T cell subsets are necessary for autoantibody production is somewhat confusing and seems mostly to depend upon the experimental system or autoimmune mouse model. T_{FH} seem to be the most critical T cell subset because of their critical role in the GC response [116, 150].

Sanroque mice (roquin^{san/san}) are a mutant strain with spontaneously expanded T_{FH} and GC [117]. Sanroque mice develop lupus-like autoimmunity including anti-DNA autoantibody production and glomerulonephritis. The roquinsan/san mutation disrupts an ICOS repressor resulting in excessive costimulation of T_{FH} and IL-21 production. GC formation and autoantibody production were independent of T_H1, T_H2, and T_H17 [116]. Interestingly, T_{FH} and GC expansion requires T cell signaling but is independent of IL-21. The results with sanroque mice contrast with other results implicating a necessity for IL-17 and/or T_H17 in immune and autoimmune GC formation [151, 152]. Spontaneous GC formation and pathogenic autoantibody production in BXD2 mice were dependent upon IL-17 signaling through the IL-17 receptor [152]. The effect of IL-17 may be to promote B cell retention in GC to promote autoreactive B cell activation [150]. GWA has identified genetic associations between IL-21 [96] and ICOS [97] with susceptibility to SLE in humans.

Disease pathogenesis

Disease pathogenesis in SLE is manifested as systemic acute and chronic inflammation that affects many organ systems. although to varying degrees within individual SLE patients [3, 4, 15, 137]. The major cause of mortality in adult SLE is myocardial infarction consequent to premature atherosclerosis and coronary heart disease [15], although renal end-stage disease has the highest SMR in SLE [9]. Interestingly, even though the most recognized pathology related to SLE in B/W mice is glomerulonephritis [28], atherosclerotic lesions and myocardial infarction were described in early reports of pathology in those and other hybrids with NZB [27]. LN is also a severe life-threatening disease manifestation of SLE in both adults [153, 154] and children [155], generally being more severe at disease onset in children [22, 23]. The following sections will discuss the mechanisms of tissue damage for different manifestations of disease pathogenesis.

Lupus nephritis

Glomerulonephritis in human [142, 156–158] and mouse [24, 159] SLE has long been associated with glomerular immune

deposits of IgG autoantibody to DNA. Glomerular lesions in affected kidneys contain both subendothelial and subepithelial complexes of chromatin, IgG anti-DNA antibody, and complement [160-162]. The glomerular immune complexes induce leukocyte infiltration and accumulation and initiate a tissue destructive chronic inflammation. The role for B cells that secrete anti-DNA autoantibodies is obvious, and the antibodies in LN are discussed in detail below. T cells, monocytes and macrophages, dendritic cells, and neutrophils also contribute to glomerular inflammation, but their function is more heterogeneous and varies within different experimental systems and mouse models of SLE. Common to all of the experimental systems and mouse models for LN is antibody that binds DNA and/or chromatin except one. mIgM.MRL/ MpJ-Fas^{lpr} mice have surface Ig receptor-positive B cells, but the B cells cannot secrete Ig [163]. Those mice are autoimmune and develop a B cell-dependent interstitial nephritis. The most prominent immunohistology of the interstitial nephritis in mIgM.MRL/MpJ-Fas^{lpr} mice was T cell infiltration. Although different from the diffuse proliferative nephritis in wild-type (wt) MRL-Fas^{lpr} and other mice that develop spontaneous LN, the phenotype of mIgM.MRL/MpJ-Fas^{lpr} mice provides insight about kidney pathogenesis in LN unrelated to anti-DNA autoantibody. In contrast to the mIgM.MRL/MpJ- Fas^{lpr} mice, F2 mice homozygous for Fas^{lpr} and a J_H deletion (JhD) with ~50 % genetic contribution from MRL/MpJ had no kidney pathology [164]. JhD homozygous mutant mice lacked B cells from birth. The JhD mutant mice indicated the requirement for B cells for kidney pathology in mIgM.MRL/MpJ-Fas^{lpr} mice.

FcγR

Mice with homozygous null mutation of the FcyR chain have reduced cell surface expression of FcyRI, III, and IV, no signaling capability through the receptors, and consequently defective FcyR-dependent activation and phagocytic function among cells that normally express activating cell surface Fc γ R [165, 166]. When the $\gamma^{-/-}$ mutation was backcrossed into NZB and NZW to create NZB. $\gamma^{-/-}$ and NZW. $\gamma^{+/-}$ that were mated to create F_1 , the B/W $\gamma^{-/-}$ were autoimmune with similar anti-DNA autoantibody titers as wt B/W [167]. In contrast to wt B/W, however, $\gamma^{-\!/\!-}$ B/W had attenuated LN including reduced glomerulonephritis, reduced proteinuria, and prolonged survival. These results were profound in their implication that FcyR-dependent rather than complementdependent activation of inflammatory effector cells is more important for glomerular inflammation in LN. On the other hand, mice with a homozygous null mutation of the inhibitory FcyRIIB developed spontaneous autoimmunity including anti-DNA autoantibody production and glomerulonephritis depending upon genetic background. All of the results with Fc γ R mutations in mice are consistent with genetic linkages between SLE susceptibility and Fc γ R loci [46]. Complement activation may be important for glomerular recruitment of leukocytes [168] that initiate and accelerate glomerulonephritis [169]. Activated complement components also induce increased Fc γ R expression on neutrophils and monocytes making them more susceptible to activation by immune complexes via Fc γ R [168, 170, 171]. Early complement components and activating Fc γ R are both important in SLE susceptibility for their roles in removing and eliminating necrotic and apoptotic cells and cellular debris [46, 172].

Mesangial cells

In vitro experiments have implicated mesangial cells for promoting inflammation in LN through Fc γ R or innate immune, TLR stimulation [173–176], or direct binding by nephritogenic anti-DNA autoantibody [177]. The results are controversial if not contradictory and difficult to reconcile with in vivo genetic results. Until activated by IFN γ to express activating Fc γ RI, IIA, and IIIA, mesangial cells only expressed inhibitory Fc γ RIIB [173, 178]. This result would imply that IgG immune complexes should inhibit not promote proinflammatory cytokine expression by normal mesangial cells. Mesangial cells also do not express TLR 7, 8, and 9 but do express TLR 1–6 [179]. In the absence of TLR9 [132, 180], it is unclear how DNA or nucleosomes would activate mesangial cells in the absence of mononuclear or myeloid cells [176].

The most insightful results about the role for mesangial cells in LN were obtained with B/W bone marrow chimeric mice [181]. Only mice chimeric for B/W $\gamma^{+/+}$ bone marrow cells but not B/W $\gamma^{-/-}$ bone marrow cells developed glomerulonephritis, even though both had equivalent glomerular IgG deposits. B/W $\gamma^{-/-}$ bone marrow chimeric mice had no myeloid or mononuclear cellular infiltrates that would have been expected if Fc γ R⁺ mesangial cells produced chemokines and cytokines in response to the glomerular immune complexes. Together, the above results indicate that signaling through activating Fc γ R on resident myeloid and mononuclear cells initiate glomerulonephritis in SLE. Complement's role in LN is in recruiting leukocytes and accelerating their response to glomerular IgG deposits [168, 169].

T cells

The role for T cells in glomerular pathogenesis in SLE is complicated. Part of the difficulty is in distinguishing whether the accumulation of activated T cells in inflamed glomeruli or tubular interstitium is cause or effect. Interstitial T cell infiltration in MRL/MpJ-*Fas^{lpr}* mice is discussed above. In human SLE patients [182] and B/W

[183] and NZM2328 mice [184], LN has been correlated with glomerular IL-18 and IFN γ indicative of T_H1 infiltration. In both cases, T_H1 were likely more important for progression than initiation of glomerular pathogenesis. The discovery of IL-17 and T_H17 and their role in inflammation and autoimmune disease [185] has yielded a new perspective for disease development in SLE [186]. The requirement for IL-17 signaling for autoimmunity in BXD2 [152] described above is an excellent example.

 $Fc\gamma r2b^{-/-}.Traf3ip2^{-/-}$ mice also present an insightful if not intriguing example for the role of IL-17 in LN. $Fc\gamma r2b^{-/-}.Traf3ip2^{-/-}$ mice lack the inhibitory FcγRIIB but also lack the CIKS/ACT1 adaptor required for signaling by all IL-17 cytokines through the IL-17 receptor [187]. These mice produce IgG anti-DNA with glomerular IgG deposits like $Fc\gamma r2b^{-/-}$ mice but have attenuated glomerular disease and increased survival. $Fc\gamma r2b^{-/-}.il17a^{-/-}$ mice had a similar phenotype to $Fc\gamma r2b^{-/-}.Traf3ip2^{-/-}$ mice. Unlike the BXD2 mice, loss of IL-17a or IL-17 receptor signaling did not diminish autoantibody production or GC formation in $Fc\gamma r2b^{-/-}.Traf3ip2^{-/-}$ mice. Recruitment of inflammatory cells, particularly neutrophils, was reduced in both $Fc\gamma r2b^{-/-}.Traf3ip2^{-/-}$ and $Fc\gamma r2b^{-/-}.il17a^{-/-}$ mice.

Anti-DNA antibody specificity and lupus nephritis

The strongest immunological and serological correlate for glomerulonephritis in SLE is IgG autoantibody to dsDNA [141, 143]. Glomerular lesions consist of fibrinoid, electron dense subendothelial and subepithelial deposits of complexes of IgG anti-DNA, chromatin, and complement [142, 160-162, 188]. Nevertheless, a subset of SLE patients [154, 189–192] and anti-DNA antibody VH and VL transgenic B/W mice [193–195] produce anti-dsDNA similarly to patients with LN or wt B/W, respectively, but do not develop LN. Serum IgG anti-dsDNA may precede LN by several years in serologically positive clinically quiescent patients (SPCQ), and the transgenic B/W live well beyond a year with no signs of LN. As such, the transgenic B/W are reasonable models for SPCQ in SLE patients. Ebling and Hahn had observed that eluted IgG anti-DNA were limited to a subset of total serum IgG anti-DNA [188]. The restricted subset was limited to anti-DNA IgG with relatively high pI. Krishnan et al. [144] passively induced LN in non-autoimmune mice by injecting anti-DNA mAbs or mAb-producing hybridomas. Only mAbs that also bound cross-reactively to basement membrane matrix antigens in vitro bound to glomerular basement membrane (GBM) or mesangial matrix (MM) in vivo and induced proteinuria. Binding in glomeruli by the mAbs was independent of DNA, chromatin, or nucleosomes. Non-GBM-binding mAbs had similar or even higher relative affinity for dsDNA and chromatin as the GBM-binding mAbs [144].

The 3H9 mAb, from which the 3H9, VH, and VL transgenic B/W [193] were derived, does not bind basement membrane matrix antigens or GBM and does not induce passive LN [144, 196]. The subset of anti-DNA IgG in glomerular eluates isolated by Ebling and Hahn [188] likely included antibodies that bound directly to GBM or MM. The pioneering work of Madaio and colleagues [197–199] and Eilat and colleagues [200] had already demonstrated that anti-DNA mAbs may bind directly to glomerular antigens independently of DNA and initiate LN. The experiments of Krishnan et al. [144] demonstrated that only GBM-binding anti-dsDNA bound in glomeruli when co-injected with non-GBM-binding anti-dsDNA. The conclusion from these results is that binding to DNA, chromatin, or nucleosomes alone is neither necessary nor sufficient for anti-DNA IgG to initiate glomerular binding and LN. The stochastic processes of somatic recombination and somatic hypermutation determine antibody specificity, and at least for B/W mice, only about 20 % of individual anti-DNA antibodies could be expected to initiate glomerular binding and LN [144]. These stochastic processes may contribute to SPCQ in SLE patients and the variation in onset of LN in B/W and other autoimmune mice.

An alternative conclusion to the above suggests that anti-DNA autoantibody may only bind to chromatin on GBM or in MM and is based upon morphologic data from nephritic kidneys [201, 202] or kidneys perfused with nucleosomeanti-DNA complexes [203]. Essentially, the proposed mechanism requires histone-dependent binding of nucleosomes to GBM or MM. Izui et al. [204] had earlier demonstrated that both ssDNA and dsDNA bound GBM in vitro. In those experiments, ssDNA bound more efficiently. Although intuitively appealing, the proposed mechanism is inconsistent with the known structure of nucleosomes [205] and chromatin [206] and their physical chemical properties [207]. The highly negatively charged nucleosomes are unlikely to promote interaction with the negatively charged GBM [208, 209]. Nucleosomes may bind to individual GBM components on a laboratory sensor chip [210], but nucleosomes do not bind to GB or other areas of the kidney in vivo in either humans [211] or mice [212]. In the aforementioned experiments above, nucleosomes were only bound to GBM in the presence of anti-DNA antibody [201] or when the perfused immune complexes were prepared with high antibody excess. Under such conditions, excess antibody in the complexes may be able to bind directly to GBM [144]. The morphologic data [201, 202] are also consistent with direct GBM and MMbinding of anti-dsDNA antibody. GBM or MM-bound antibody may bind to extracellular chromatin and increase the size of glomerular immune complexes [144, 213, 214]. The morphologic data may reflect the middle to end stages of glomerular IgG deposition [142, 160-162] but not the initiating event.

Accumulating results in mice and humans indicate at least an indirect role for neutrophil extracellular traps (NETs) and NETosis in SLE. Since Radic and Marion recently reviewed that topic in this series [213], no further discussion will be included here. It is important to note, however, that recent experiments in MRL^{*lpr/lpr*} *nox2^{-/-}* mice that are defective for NETosis and NET release from neutrophils have even worse SLE disease symptoms than MRL^{*lpr/lpr*} Nox2 sufficient mice [215]. NETosis by neutrophils is at least not required for SLE in MRL^{*lpr/lpr*} mice. Important to note, however, DNA extracellular traps can be formed without NADPH oxidase and by innate immune cells other than neutrophils [216].

The mechanistic pattern for lupus nephritis that emerges from the above mouse models is likely as follows (Fig. 1):

- The stochastic generation, activation, and antigen selection of DNA-reactive B cells will eventually yield an IgG anti-DNA that cross-reacts with relatively high affinity to GBM and/or MM antigens.
- 2. IgG anti-DNA binds directly to cross-reactive GBM or MM antigens [144] and activates complement and resident hematopoietic cells expressing activating $Fc\gamma R$ [167, 181].
- Chromatin [202], apoptotic bodies [217], and/or microparticles [218] released by necrosis or inflammationinduced NETosis, necroptosis, or apoptosis may bind to GBM-bound IgG anti-DNA to produce progressively larger immune complexes [219]. Cytokines and chemokines produced by activated leukocytes [220], including IL-17 [187] and IL-12 [182], recruit more cellular infiltration by myeloid cells, monocytes, and T cells.

The initial binding of IgG anti-DNA and small immune complexes to GBM will likely be reversible and represents the rate-limiting step for initiation of LN [144]. The above process will establish a feed-forward, progressive accumulation of IgG and immune complexes, inflammatory cells, and mediators that eventually destroy glomerular and tubular structure and function.

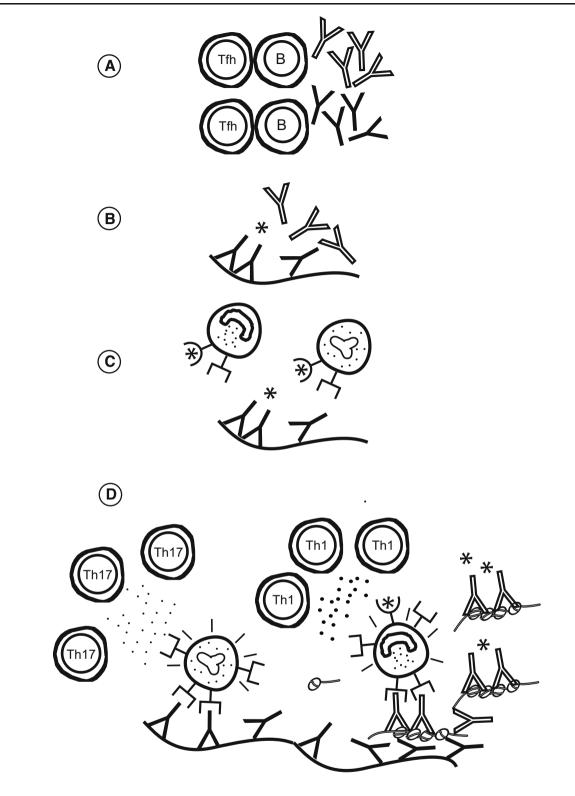
Skin

The skin is a target of tissue damage in several different forms of lupus erythematosus (LE). Ultraviolet radiation (UVR) from sun exposure has been implicated in triggering onset and/or exacerbation of the cutaneous lesions of LE by several possible mechanisms. The term "cutaneous lupus erythematosus" (CLE) encompasses several conditions that share histologic features of hyperkeratosis, follicular plugging, and inflammation of adnexal structures [221]. Major groups include acute cutaneous lupus erythematosus (ACLE), subacute cutaneous lupus erythematosus (SCLE), chronic cutaneous Fig. 1 GBM/MM-binding anti-dsDNA initiates glomerulonephritis in SLE. a Activated T_{FH} activate DNA-reactive and stimulated B cells to produce IgG anti-dsDNA autoantibody. b IgG anti-dsDNA binds directly to GBM or MM cross-reactive antigen(s). c Resident neutrophils and monocytes/macrophages are activated by FcyR and complement. d GBM/MM-bound anti-dsDNA can bind to extracellular chromatin, apoptotic bodies, microparticles, or DNA extracellular traps. The large GBM/MM-bound immune complexes activate more complement and activating FcyR-expressing neutrophils and monocyte/macrophages. Chemokines and cytokines released by activated leukocytes attract and activate T_H1 and T_H17 CD4 T cells. This process establishes a progressive, feed-forward mechanism to sustain chronic inflammation that eventually destroys glomerular structure and function. , GBM/MM; 🔎 , chromatin; 💥, activated complement;)-, complement receptor;]-, activating $Fc\gamma R$; >-, GBM/MM cross-reactive anti-DNA IgG; ≫, non-cross-reactive anti-DNA IgG; (\Im), neutrophil; $\xrightarrow{2} \mathfrak{D}_{\mathfrak{L}}$, activated neutrophil; (\mathfrak{H}) monocyte/macrophage; $\mathcal{H}_{H^{1}}^{V}$, activated macrophage; \bigcirc , $T_{H^{1}}$, $T_{\rm H}17$, or $T_{\rm FH}$ T cell; \bigcirc , B cell

lupus erythematosus, and intermittent cutaneous lupus erythematosus (ICLE) [222]. Chronic CLE is further subdivided into discoid lupus erythematosus (DLE) and chilblain LE with the former being triggered by UVR with cold and humidity acting as a trigger for the latter [222]. The patient with CLE may follow a classical course in which LE remains confined to the skin or can develop other organ involvement to become SLE. The reverse can also occur in which initially there is no skin involvement in SLE with one form of CLE appearing later in the course of the disease.

The cellular infiltrates in CLE include CD8⁺ cytotoxic and CD4⁺ T effector cells, CD68⁺ macrophages, pDCs, and V α 24⁺ V β 11⁺ invariant natural killer T cells (iNKT) [223–225]. Inflammation-promoting cytokines, including IL-1 β , IL-17, IL-18, TNF α , IFN γ , and high-mobility group box 1 (HMGB1) protein, are present in CLE lesional skin and can stimulate production of chemokines and expression of adhesion molecules (intracellular adhesion molecule-1 (ICAM-1) and E-selectin) to promote leukocyte influx [226–232]. IL-17A is positively correlated with expression of IFN- α and antiviral myxovirus A protein (MxA) in all subtypes of CLE [233].

Exposure to UVR-A and UVR-B can induce apoptosis of keratinocytes and is associated with c-Jun N-terminal kinase (JNK) that facilitates induced nitric acid synthase (iNOS) production [234–237]. Increased iNOS leads to increased production of nitric oxide (NO) that may counter UVR-A-induced apoptosis by increasing Bcl-2 expression and reducing Bax protein in endothelial cells [238]. Compared to skin of normal individuals in which iNOS expression is upregulated within 2 days after UVR, iNOS in CLE patients appears 72 h after UVR exposure that would allow apoptosis of keratinocytes to proceed unopposed within the first 72 h after UVR exposure [238–240]. Apoptotic keratinocytes in turn



may become a source for innate and subsequent adaptive immune cell activation [112, 136]. Recent experiments in mice demonstrated that repeated epicutaneous stimulation with the TLR-7 agonist imiquimod not only induced a lupus-like systemic autoimmune disease but also increased skin photosensitivity to UVR-B light [241]. In those experiments, systemic autoimmunity and photosensitivity were dependent upon pDC. These results are important because they implicate the skin as a potential primary organ for TLR-7 dependent initiation of SLE.

Lungs

Some form of pulmonary inflammation occurs in 50-70 % of patients with SLE [242–244]. Pleuritis is the most common and occurs with or without pleural effusions [245]. Etiology and pathogenesis of pleuritis and pleural effusions in SLE patients is unknown. Other less common pulmonary involvement includes bronchiolitis obliterans, interstitial lung disease, shrinking lung syndrome, pulmonary arterial hypertension, diffuse alveolar hemorrhage, vasculitis, pulmonary nodules, and diaphragmatic weakness [242, 245, 246]. Although the cause of diffuse alveolar hemorrhage (DAH) in SLE has not been completely elucidated, immune-mediated damage of small blood vessels and alveolar space is suspected. There are three different histologic patterns of tissue damage that include pulmonary capillaritis, diffuse alveolar damage, and bland pulmonary hemorrhage [242, 246-255]. Patients with DAH often have lupus nephritis, high titers of anti-DNA antibody, hypocomplementemia, and anemia [242, 248, 256]. Pulmonary embolism, often associated with antiphospholipid syndrome, is increased in patients with SLE [247]. Pulmonary arterial hypertension not secondary to pulmonary emboli or cardiac disease is uncommon, and its cause and pathogenesis are unknown.

Interstitial lung disease (ILD) most commonly has the nonspecific interstitial pneumonia (NSIP) pattern and can occur with desquamative interstitial pneumonitis but only rarely in non-smoking SLE patients [257]. The cause of ILD in SLE, as in other conditions, is unknown. In SLE patients, ILD can develop with no previous lung disease or after lupus pneumonitis, in which there are deposits of IgG and C3 within alveolar septa, diffuse alveolar inflammation associated with hyaline membranes, and alveolar hemorrhage [258, 259].

Cardiovascular system

The pericardium may be involved in up to 100 % of SLE patients with involvement consisting of an acute pericarditis often associated with pleurisy and pleural effusions and pericardial effusion that rarely progresses to cardiac tamponade or constrictive pericarditis [260–264]. The pericardial effusion is exudative having a straw-colored appearance with a high leukocyte count that is predominantly neutrophilic [265]. In rare cases, the pericardial effusion may be hemorrhagic [266]. Antinuclear and anti-DNA antibodies, low complement, and immune complexes are commonly found in the pericardial fluid [267].

The myocardium is involved with myocarditis in up to 40– 50 % of patients with SLE, based on autopsy reports [268], but clinically significant myocarditis is less common (from 10 to 14 %) [269–271]. Histologic examination reveals widespread deposition of Ig and complement in myocardial blood vessel

walls and within muscle bundles that may or may not be associated with inflammatory plasma cell and lymphocyte infiltrates [268]. Fibrinoid deposits and hematoxylin bodies occur, and patchy myocardial fibrosis is seen in SLE patients with myocarditis who have been treated with corticosteroids [272]. Several different antibody specificities have been associated with lupus myocarditis including anti-RNP occurring with coexistence of skeletal myositis, anti-Ro antibodies, and antimyocardial antibodies, although their involvement in pathogenesis of the myocarditis is not yet proven. The association between neonatal and newborn congenital heart block and maternal SLE is well established [273]. Congenital heart block is strongly correlated with the presence of autoantibodies to SSA/Ro and SSB/La in both mothers' and infants' sera [274-277]. Infants acquire the autoantibodies transplacentally. The association between anti-SSA/Ro52 autoantibody and congenital heart block may be related to cross-reactivity of the autoantibody with the 5-HT4 serotoninergic receptor [278].

Valvular abnormalities detected by transesophageal echocardiography have been reported in up to 61 % of patients with SLE [279]. In that study, 43 % of patients had valvular vegetations, and 50 % had thickening of mitral and aortic valves. Libman-Sacks endocarditis, atypical verrucous endocarditis, is the term used to describe the atypical sterile vertucous lesions of the valves and mural endocardium originally described in the SLE patients. Such lesions were later also found in patients without SLE but with antiphospholipid antibodies [280, 281]. The active Libman-Sacks lesions have accumulations of fibrin clumps, lymphocytes, and plasma cells that upon healing are converted to dense vascularized fibrous tissue with an absence of calcification [272]. Ig and complement are found deposited often throughout the valve leaflet inside and outside of the verrucae [282]. In patients with antiphospholipid syndrome, anti-\beta2-glycoprotein antibodies are deposited in the vertucae [283].

Patients with SLE are at increased risk for accelerated atherosclerosis that cannot be explained entirely by traditional atherosclerosis risk factors [284]. While it is still undetermined what the cause(s) of the accelerated atherosclerosis in SLE are, attention has focused on the autoimmune and inflammatory state typical of SLE. Monocytes and T cells are recruited to nascent plaques in arterial walls where monocytes secrete monocyte chemotactic protein-1 (MCP-1), IL-6, and TNF α , while the Th1 CD4⁺ cells produce IFN γ , known to be proinflammatory and atherogenic [284]. Macrophages phagocytose oxidized low-density lipoprotein (oxLDL) to become foam cells. The foam cells contribute to plaque accumulation that is then followed by fibrosis from the extracellular matrix produced by arterial smooth muscle cells [284]. Contributions to accelerated atherosclerosis in SLE might include the presence of IgG anti-oxLDL antibodies and anti-apoA-I antibodies, the latter negating the atheroprotective properties of apoA-I and high-density lipoprotein (HDL) [285, 286].

Vasculitis

Vasculitis is reported to occur in as many as 40 % of patients with SLE [287–289]. Although typically small vessels are involved, medium- and large-sized vessels can also be involved in the vasculitis of SLE [288, 290, 291]. Small vessel involvement is typically that of leukocytoclastic vasculitis while medium-sized involvement shows a necrotizing or polyarteritis nodosum pathology [291, 292]. The spectrum of organs exhibiting vasculitis in SLE includes, most commonly, the skin, but also kidneys, coronary, brain, mesentery, gallbladder, and urinary bladder blood vessels [287, 288, 292–296].

The pathophysiologic mechanism of lupus vasculitis is thought to be secondary to immune complex deposition. Studies using human umbilical cord endothelial cells exposed to IgG immune complexes from lupus sera showed that the immune complexes upregulated endothelial cell expression of the receptor for advanced glycation end products (RAGE) and upregulated expression of ICAM1, vascular cell adhesion molecule-1 (VCAM-1), IL-8, IL-6, TNF α , and MCP-1 [297]. That study also implicated endothelial cell signaling via the HMGB1-RAGE axis to be critical for the lupus immune complex effect in activation of NF- κ B p65, ICAM-1, VCAM-1, chemokines, and cytokines [297].

Nervous system

Nervous system involvement has long been recognized as a major feature of SLE and includes a wide spectrum of presentations with varying clinical severity and to different degrees among different patients. There can be involvement of the central nervous system (CNS) and/or the peripheral nervous system (PNS). The term "neuropsychiatric lupus" is used to encompass both neurologic, e.g., stroke, headaches, seizures, myasthenia gravis, demyelinating syndrome, myelopathy, Guillain-Barre syndrome, polyneuropathy, cranial neuropathy, and aseptic meningitis, and psychiatric syndromes, e.g., acute confusional state, anxiety disorders, mood disorder, severe depression, psychosis, and cognitive dysfunction [298]. The incidence of neuropsychiatric lupus reported in the literature varies widely due to the lack of standardized diagnostic criteria [299]. The current mechanistic scenario, although not proven, purposes that certain autoantibodies, with or without complement activation and proinflammatory cytokine proliferation, orchestrate nervous system damage through different processes including immune complex deposition, thrombosis, vasculopathy, and inflammation that result in neurodegeneration [300]. Cerebral atrophy is a common finding on imaging of brains of SLE patients, and significant correlations have been reported between brain atrophy and cerebral dysfunction. Severe cognitive impairment is present in SLE patients in association with reduction in white and gray

matter [301, 302]. Brain vasculature in SLE patients with neuropsychiatric involvement displays abnormalities including ischemic infarcts and hemorrhages, narrowing or occlusion of small arteries and veins, and varying degrees of cerebral hypoperfusion [303–308].

Studies measuring neurometabolites underscore the presence of neurodegeneration in neuropsychiatric lupus [309]. Nacetylaspartate (NAA), a biomarker of axonal integrity usually present at high levels in normal axons and neurons, is reduced in normal appearing white matter (NAWM), gray matter (GM), and brain lesions in patients with neuropsychiatric lupus [304, 309, 310]. In addition, levels of glial fibrillary protein and neurofilament triplet protein are elevated in cerebrospinal fluid (CSF) of patients with neuropsychiatric lupus and brain involvement, suggesting ongoing neuronal and astrocytic damage [311]. Plasminogen inhibitor activator-1 (PAI-1) and D-dimer levels have been reported to be elevated in patients with increased CSF glial fibrillary acidic protein, neurofilament triplet protein, and tau protein [312]. This result suggests that abnormal fibrinolysis may also be contributing to neuronal and astrocyte damage.

A large array of autoantibodies has been detected in serum or CSF of patients with SLE and has been implicated to various extents in the pathogenesis of neuropsychiatric lupus. These are listed in Table 1 [309]. A subset of anti-DNA autoantibodies may cross-react with the NR2A and NR2B polypeptides of the *N*-methyl-D-aspartate (NMDA) receptor [325–327]. NMDA-binding anti-DNA antibodies caused neuronal damage only after the blood–brain barrier (BBB) was compromised by LPS-induced inflammation in mice [327]. Neuronal dysfunction caused by the combination of NMDA-binding antibody and LPS-induced BBB damage was accompanied by poor memory function in

 Table 1
 Autoantibodies potentially implicated in nervous system involvement in SLE

Antibody	Reference
NMDA cross-reactive anti-DNA	[327]
Anti-NMDA receptor	[313]
Anti-microtubule-associated protein 2	[314]
Anti-α tubulin	[315]
Anti-ganglioside(s)	[316]
Anti-glial fibrillary acidic protein	[317]
Anti-phospholipid	[318]
Anti-ribosomal P protein	[319]
Anti-endothelial cell	[320]
Anti-intermediate neurofilament α internexin	[321]
Anti-triosephosphate isomerase	[322]
Anti-Smith small nuclear ribonucleoproteins	[323]
Anti-histones	[324]

experimentally treated mice. Mice producing NMDAbinding antibody but without BBB damage showed no signs of memory loss or neuronal dysfunction. These results with NMDA cross-reacting antibodies have important implications for the role of autoantibody in CNS lupus in human SLE.

There is evidence of neuroinflammation in brains of patients with SLE, since levels of soluble VCAM-1, soluble ICAM-1, soluble L-selectin, IL-6, IL-8, IL-10, IFN γ , and TNF α are elevated in CSF of patients with neuropsychiatric lupus [311, 328–336]. The role of complement in patients with neuropsychiatric SLE is unknown, but studies in lupus prone MRL^{*lpr*} mice demonstrate evidence of complement activation contributing to neuronal apoptosis, CNS inflammation, and BBB damage [337–343]. Correlative studies show that levels of serum or CSF matrix metalloproteinase-9 are higher in SLE patients with neuropsychiatric than in SLE patients without CNS involvement [334, 344].

Hematological system

Some form of hematologic disorder is observed in most patients with active SLE. The disorder(s) take the form of anemia, neutropenia, thrombocytopenia, and/or lymphopenia. Anemia can be due to the anemia of chronic disease, arising from suppressed erythropoiesis secondary to chronic inflammation, anti-erythropoietin autoantibodies, autoimmune hemolytic anemia induced by anti-erythrocyte autoantibody and complement, pure red cell aplasia induced by antibodies to erythropoietin or bone marrow erythroblasts, or aplastic anemia secondary to antibodies to bone marrow precursor cells [345, 346]. Lymphocytes in SLE with leukopenia have reduced expression of CD55 and CD59 that renders the lymphocytes susceptible to lysis by complement [347, 348]. The cause of neutropenia is unknown but is associated with antineutrophil antibodies and increased levels of TNF-related apoptosis-inducing ligand (TRAIL) that could increase neutrophil apoptosis [349]. Thrombocytopenia is observed in up to 30 % of patients with SLE and is thought to develop as a result of platelet destruction by antiphospholipid antibodies. Anti-thrombopoietin receptor C-Mpl and anti-CD154 antibodies may also play roles in thrombocytopenia but remains to be proven [350]. In addition to immune thrombocytopenia (ITP) described above, there is also increased incidence of thrombotic thrombocytopenic purpura (TTP) in which there is increased platelet consumption from platelet aggregation and thrombosis. Severe cases of ITP are associated with ADAMTS13 (a disintegrin and metalloproteinase with a thrombospondin type 1 motif, member 13) deficiency or anti-ADAMTS13 antibody that induces platelet aggregation and thrombosis [351].

Summary and conclusions

Several major points emerge from this review. One, genetic disruption of any one of the normal mechanisms that regulate self-tolerance will cause autoimmunity to DNA and LN. This outcome is no doubt a consequence of the innate immune commitment to use nucleic acids as "pathogen danger signals" and a promiscuous, DNA-reactive B cell repertoire. Two, SLE is remarkably heterogeneous with respect to inheritance, genetic susceptibility, and disease phenotype. Clearly, genetic heterogeneity affects phenotypic heterogeneity among different individuals and racial and ethnic subpopulations. Phenotypic heterogeneity in the presence of identical genotypes, monozygotic twins and inbred mice, indicates that the genetic program for SLE is initiated and executed stochastically. Three, very little is known about what exactly initiates SLE in either mice or humans. Most of the receptors and signaling molecules and pathways have been identified, but what actually sets autoimmune activation in motion is unknown. Even in the well-defined mouse genetic models, B/W, MRL^{lpr}, BXSB, BXD2, FcγRIIB^{-/-}, and Sanroque, the initiating event leading to the well described and understood autoimmune phenotype is not understood. For example, in mice from all of those strains, DNA-reactive B cells are stimulated or activated to produce anti-DNA autoantibody. The activation is selective and Ig-receptor-dependent. The stimulus is believed to be DNA in the form of chromatin, microparticles, apoptotic bodies, or cellular debris, but the origin of the stimulus is unknown. Four, disease manifestation in SLE is heterogeneous. Both the heterogeneity of disease and the inability to know how and when autoimmunity is initiated make prognosis and therapy such a challenge for SLE. Future longitudinal studies that undertake very broad, inclusive evaluations of as many phenotypic parameters as possible will be necessary. The studies should include evaluation of the circulating proteome and RNA expression in circulating cells. If those studies can include patients prior to disease onset or at least in the very early stages of autoimmunity, the results will almost for sure produce new and useful insight for future diagnostic and therapeutic development.

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Conflict of interest The authors declare that they have no conflict of interest.

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