Interferon-induced mechanosensing defects impede apoptotic cell clearance in lupus

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Systemic lupus erythematosus (SLE) is a severe autoimmune disease that is associated with increased circulating apoptotic cell autoantigens (AC-Ags) as well as increased type I IFN signaling. Here, we describe a pathogenic mechanism in which follicular translocation of marginal zone (MZ) B cells in the spleens of BXD2 lupus mice disrupts marginal zone macrophages (MZMs), which normally clear AC debris and prevent follicular entry of AC-Ags. Phagocytosis of ACs by splenic MZMs required the megakaryoblastic leukemia 1 (MKL1) transcriptional coactivator–mediated mechanosensing pathway, which was maintained by MZ B cells through expression of membrane lymphotixin-αβ(T)2 (mLT). Specifically, type I IFN–induced follicular shuttling of mLT-expressing MZ B cells disengaged interactions between these MZ B cells and LTβ receptor–expressing MZMs, thereby downregulating MKL1 in MZMs. Loss of MKL1 expression in MZMs led to defective F-actin polymerization, inability to clear ACs, and, eventually, MZM dissipation. Aggregation of plasmacytoid DCs in the splenic perifollicular region, follicular translocation of MZ B cells, and loss of MKL1 and MZMs were also observed in an additional murine lupus model and in the spleens of patients with SLE. Collectively, the results suggest that lupus might be interrupted by strategies that maintain or enhance mechanosensing signaling in the MZM barrier to prevent follicular entry of AC-Ags.

Introduction

Systemic lupus erythematosus (SLE) and mouse models of lupus both exhibit a central feature of increased circulating apoptotic cell autoantigens (AC-Ags) and, in most cases, elevated type I IFN signaling produced by plasmacytoid DCs (pDCs) (1–3). The most accepted model is that the presence of uncleared ACs or AC-autoantibody immune complexes with DNA- or RNA-containing immune components can signal production of type I IFNs (4–8). Although it is known that ACs might be cleared by plasmacytoid DCs (pDCs), this process requires recognition of AC debris by scavenger receptors including macrophage receptor with collagenous structure (MARCO) and SIGN-R1, which send signals to the cytoskeletal apparatus of macrophages to promote proper engulfment and vesicular trafficking to phagolysosomes as well as induction of tolerogenic signals (23, 24). Defective serum-dependent, Rho-mediated mechanosensing cytoskeletal reorganization has been identified in macrophages obtained from 6 strains of lupus mice prior to disease onset (25). However, the molecular mechanism for the defects in mechanosensing signaling in lupus is not known.

Here, we describe how the maintenance of proper numbers and function of MZMs requires signaling through the lymphotixin β receptor (LTβR) on MZMs by mLT-expressing MZ B cells. Importantly, type I IFNAR signaling on the MZ B cells results in mislocalization of MZ B cells into the follicle and disrupts crosstalk between MZMs and B cells. Signaling through LTβR on decrease in the apoptotic debris clearance function and, later, with a loss in the number of MZMs surrounding the splenic follicles (2). Such a defect is associated with follicular translocation of AC-Ags bearing B cells to induce an AC-Ag-reactive T cell response (16–21). Interestingly, follicular translocation of marginal zone (MZ) B cells and marginal zone precursor (MZ-P) B cells can be promoted by type I IFN–induced upregulation of CD69, which prevents normal MZ localization of B cells by downregulating the chemotactic responses for sphingosine-1-phosphate (SIP) (20, 22).

Efficient and tolerogenic clearance of ACs by MZMs is a complex process requiring recognition of AC debris by scavenger receptors including macrophage receptor with collagenous structure (MARCO) and SIGN-R1, which sends signals to the cytoskeletal apparatus of macrophages to promote proper engulfment and vesicular trafficking to phagolysosomes as well as induction of tolerogenic signals (23, 24). Defective serum-dependent, Rho-mediated mechanosensing cytoskeletal reorganization has been identified in macrophages obtained from 6 strains of lupus mice prior to disease onset (25). However, the molecular mechanism for the defects in mechanosensing signaling in lupus is not known.

Here, we describe how the maintenance of proper numbers and function of MZMs requires signaling through the lymphotixin β receptor (LTβR) on MZMs by mLT-expressing MZ B cells. Importantly, type I IFNAR signaling on the MZ B cells results in mislocalization of MZ B cells into the follicle and disrupts crosstalk between MZMs and B cells. Signaling through LTβR on...
MZMs is shown to regulate megakaryoblastic leukemia 1 (MKL1), a mechanosensing transcriptional coactivator maintaining MZM homeostasis in the MZ as well as AC phagocytosis and clearance by these MZMs (23, 24, 26–31). Dissociation between MZMs and mLT+ B cells was shown in 2 strains of lupus-prone mice, BXD2 (17, 32–37) and B6.Sle1.Sle2.Sle3 (B6.TC) (38). Diminished expression of MKL1 as well as loss of MARCO+ cells associated with follicular translocation of CD1c+ MZ B cells were similarly identified in the spleens of SLE patients. The results reported herein may therefore be more generally applicable, as they identify an important defect associated with lupus.

Results

**Decreased MARCO+ macrophages and increased pDCs are common features of lupus in both humans and mice.** A common feature of SLE in both human and mouse models of SLE is decreased clearance of ACs and increased production of type 1 IFNs by pDCs (1–3, 6, 9–11, 13, 14, 39). We and others have previously shown that physical deletion or spontaneous loss of MARCO+ MZMs resulted in defective AC clearance (2, 12–15, 40, 41) and that such a defect is associated with the development of lupus in susceptible mouse models (2, 42). We analyzed the distribution of MARCO+ cells in the spleens of non-SLE controls (n = 6) and in the spleens of patients with SLE (n = 5) and found a dense layer of MARCO+ cells in the perifollicular regions in all non-lupus control spleens; however, this layer of MARCO+ cells was significantly reduced in all SLE spleens (Figure 1A). In contrast, we observed a dense layer of PDCA1+ pDCs in the splenic perifollicular region in SLE patients, and this dense pDC layer was significantly diminished in the same region in control spleens (Figure 1B).

A similar reciprocal distribution of low numbers of MARCO+ MZMs (Figure 1C) and dense aggregation of PDCA1+ pDCs (Figure 1D) were identified in the splenic MZ in 2 different strains of lupus-prone mice, BXD2 and B6.TC. Production of type 1 IFNs by pDCs could be stimulated by mammalian nucleic acids derived from apoptotic debris as a result of AC clearance defects (43). pDCs accumulated in the splenic MZ in 3-month-old BXD2 and B6.TC mice, but MZM loss became prominent in 11-month-old mice (Figure 1, C and D), suggesting that type 1 IFNs may play an important role in orchestrating the loss of MZMs. Indeed, a deficiency of IFNAR in BXD2 (BXD2-Ifnar−/−) mice rescued the age-related loss of MZMs (Figure 1C), prevented the aggregation of pDCs in the splenic MZ (Figure 1D), and also diminished spontaneous germinal centers (GCs) in the spleen and autoantibody sera titers of BXD2 mice (Supplemental Figure 1, A and B; supplemental material available online with this article; doi:10.1172/JCI81059DS1). Together, these findings suggest that loss of MZMs and accumulation of pDCs exhibit a reciprocal association in both human and mouse spleens and that enhanced IFNAR signaling may dissipate critical AC phagocytic MZMs in the splenic MZ to promote lupus in BXD2 mice.

**Type 1 IFN induces loss of MZMs via follicular translocation of mLT+ B cells from the MZ.** To determine whether increased IFNs acted directly on MZMs to result in their reduction, BXD2-Rag1−/− mice were reconstituted with BM from either GFP+ BXD2-Ifnar−/− or GFP− BXD2-Ifnar−/− mice. The number of pDCs and expression levels of type 1 Ifn genes in BXD2-Rag1−/− mice and WT BXD2 mice were comparable (Supplemental Figure 2), making it possible to assess the effects of pDCs and type 1 IFNs in these recipients. MZMs were quantitated by F4/80 CD11b+SIGN-R1hi and I-A^+ macrophages. Four months after the transfer, there was no difference in the percentage of MZMs, whether they were derived from IFNAR− or IFNAR− donors (Figure 2A). However, confocal image analysis revealed that IgM^+ B cells derived from IFNAR− mice had predominately translocated into the follicle, whereas IgM^+ B cells from IFNAR− mice were predominately localized in the MZ (Figure 2, B and C), suggesting that defective retention of MZ B cells in the MZ can be an important factor leading to the loss of MZMs in IFNAR-intact BXD2 mice.

The importance of MZ B cells in maintaining MZMs was verified using an antibody directed against the NOTCH2 ligand delta-like 1 (anti-DLL1) to block NOTCH2-DLL1 interaction (44), a signal needed for MZ B cell development. We showed that normal MZM numbers (Supplemental Figure 3, A and B) in both B6 and BXD2 mice were significantly reduced by specifically depleting CD11c+CD23+ and CD21+CD23+ MZ B cells (Supplemental Figure 3, C and D) in anti-DLL1–treated mice (44). As NOTCH2 is mainly expressed by MZ B cells, but not MZMs (Supplemental Figure 3, E and F), these results suggest that, as in B6 mice, maintenance of MZMs in the splenic MZ of BXD2 mice requires MZ B cells.

The expression of mLT by B cells has been implicated in the maintenance of MZMs (45–51). As type 1 IFNs exhibit an important property for the promotion of follicular translocation of MZ B cells (Figure 2, B and C, and refs. 20, 21, 42), we analyzed whether there was mislocation of mLT+ B cells in the spleens of BXD2 mice. FACS analysis confirmed that in B6, WT BXD2, and BXD2-Ifnar−/− mice, mLT was highly expressed on MZ and MZ-P B cells (Figure 2D). Confocal image analysis showed that in B6 and BXD2-Ifnar−/− mice, the majority of the MZCD1+ B cells were located in the MZ (Figure 2, E and F). However, in the spleens of WT BXD2 mice, the majority of mLT+CD1+ B cells were located in the follicle (Figure 2, E and F). The essential role of mLT+ B cells in the maintenance of MZMs was verified by analysis of MARCO+ MZMs in 11.2bCd19-Cre B6 mice, which lack mLT specifically on the surface of B cells (51). 11.2bCd19-Cre B6 mice exhibited a significant decrease in MARCO+ MZMs (Figure 2G), which was further confirmed using FACS analysis by gating on the F4/80+ CD11b+I-A^+SIGN-R1hi subpopulation (Figure 2H). These results suggest that lack of mLT+ B cells or lack of mLT+ B cell retention in the MZ as a result of IFNAR-dependent follicular translocation leads to loss of MZMs.

**Loss of LTβR leads to loss of MZMs and enables development of GCs.** LTβR signaling in endothelial cells (ECs) has been suggested to play an important role in high endothelial venule formation (50), which may then affect MZ organization. Further, signaling provided by mLT+ B cells has been shown to play an important role in the formation of a GC response through interactions between B cells and follicular DCs (FDCs) (48). Our results thus far, however, suggest a concept in which mLT+ B cells support both the MZ and GC structures, depending on their anatomic location. We generated 11.2bLys-Cre B6 mice to determine whether loss of LTβR signaling on macrophages, but not ECs or FDCs, perturbs MZMs without affecting GC formation. We found that splenic MZMs in 1-month-old 11.2bLys-Cre B6 mice were fully developed (Figure...
Figure 1. Decreased spleen MZMs and increases pDCs as a common feature of lupus. (A and B) IHC staining and intensity quantitation of MARCO+ cells (A) or PDCA1+ pDCs (B) in the spleens of normal (n = 6) versus SLE (n = 5) individuals. Representative images of spleen follicles. Original magnification, ×20. Boxed areas in the left panels were digitally magnified and are shown in the right 2 panels. Bar graphs show ImageJ intensity quantitation of 10 randomly selected splenic perifollicular regions per section. (C and D) Spleens obtained from B6, BXD2, B6.TC, and BXD2-Ifnar−/− mice at 3 and 11 months of age were analyzed. Representative confocal microscopic images of (C) PNA (blue), IgM (red), and MARCO (green), and (D) MADCAM1 (white) and PDCA1 (green) for representative splenic follicles. Original magnification, ×20. Bar graphs show ImageJ intensity quantitation of 10 randomly selected spleen MZ regions per section. Data represent the mean ± SEM. All images are representative splenic regions or splenic follicles (∗P < 0.01, †P < 0.005 vs. control or B6, Student’s t test; n = 2–3 mice per group for 2 independent experiments).

3A). However, the percentage of MZMs was reduced in 4-month-old Ltbbr+/+ Lys-Cre B6 mice compared with the percentage detected in B6-Ltbbr−/− mice (Figure 3, A and B). The essential role of LTβR− expression on MZMs in preventing autoimmunity was confirmed by the observation that Ltbbr−/− Lys-Cre B6 mice gradually developed features of autoimmunity, including the accumulation of uncleared TUNEL+ ACs in the MZ (Figure 3C), elevated levels of serum malondialdehyde (MDA), a lipid antigen derived from ACs (ref. 1 and Figure 3D), spontaneous formation of GCs (Figure 3, A, C, and E), and a relatively small, yet statistically significant, elevation of IgG autoantibody serum titers (Figure 3F).

LTβR signaling maintains MKL1 expression in MZMs. The above results suggest that elevated IFNAR signaling and the lack of LTβR signaling in the splenic MZ exhibited a similar deleterious effect on MZMs. To determine the molecular mechanism by which LTβR signaling maintains MZMs, BXD2 mice were treated with either control PBS or LTβR-Fc to block LTβR signaling. GeneChip analysis of MZMs indicated that a predominant signaling modification...
analyses indicated normalization of these pathways in BXD2-Ifnar–/– MZMs (Supplemental Table 1 and Supplemental Figure 4), which exhibited sustained interactions with mLT+ MZ B cells as compared with BXD2 MZMs.

We showed that in 2-month-old B6 mouse spleens, MKL1 expression was mainly localized in the MZ in a region where was the downregulation of mechanosensing MKL1 (MRTF-A)/MKL2 (MRTF-B)/serum response factor (SRF) pathways in LTβR-Fc–treated MZMs (Supplemental Table 1 and Supplemental Figure 4A). Changes in the expression of genes in this pathway were further confirmed by quantitative RT-PCR (qRT-PCR) analysis (Supplemental Figure 4B). In contrast, GeneChip and qRT-PCR analyses indicated normalization of these pathways in BXD2-Ifnar–/– MZMs (Supplemental Table 1 and Supplemental Figure 4), which exhibited sustained interactions with mLT+ MZ B cells as compared with BXD2 MZMs.

We showed that in 2-month-old B6 mouse spleens, MKL1 expression was mainly localized in the MZ in a region where
within the actin-binding domain of MKL1 (52). This enables nuclear transport of MKL1 and activation of its downstream target SRF to induce genes related to proper function and survival (26, 29, 53). MZMs isolated from B6, B6-\textit{Ltbr}^{fl/fl}, and BXD2-\textit{Ifnar}^{–/–} mice exhibited intense, predominantly nuclear expression of MKL1 and F-actin polymerization (Figure 5A). In contrast, both nuclear expression of MKL1 and F-actin polymerization were significantly reduced in MZMs isolated from B6-\textit{Ltbr}^{fl/fl} \textit{Cd19-Cre}, B6-\textit{Ltbr}^{fl/fl} \textit{Lys-Cre}, and BXD2 mice (Figure 5A and Supplemental Figure 6).

To determine whether the absence of LTβR signaling only in hematopoietic cells, especially myeloid lineage cells, could affect MZM repopulation and maintenance, MKL1 expression, and F-actin polymerization, a mixed BM transfer experiment was carried out, in which BM from WT CD45.1 mice was transferred with BM from either WT CD45.2 mice or \textit{Ltbr}^{fl/fl} \textit{Lys-Cre} CD45.2 mice into B6-\textit{Rag1}^{–/–} mice (Supplemental Figure 7A). Four months after BM reconstitution, there was an age-related loss of \textit{Ltbr}^{fl/fl} \textit{Lys-Cre} BM–derived MZMs in the spleens of recipient mice, although the MARCO+ MZMs were also identified (Figure 4A). Interestingly, MKL1 expression was significantly reduced in the splenic MZ of \textit{Ltbr}^{fl/fl} \textit{Cd19-Cre} B6 and BXD2 mice (Figure 4A and Supplemental Figure 5). In contrast, IFNAR deficiency in BXD2 mice restored MKL1 expression levels in the splenic MZ (Figure 4A and Supplemental Figure 5). Consistent with these findings, acute induction of type I IFNs via in vivo administration of CpG or blockade of mLT-LTβR interaction via LTβR-Fc both resulted in a significant reduction in MKL1 expression in MZMs (Figure 4B) and in the percentage of MZMs in B6 mice (Figure 4C), suggesting that either strong IFNAR signaling or reduced mLT signaling abrogated MKL1 expression in MZMs.

\textit{LTβR} signaling is required for normal cytoskeletal organization in MZMs. MKL1 is localized in the cytoplasm of unstimulated cells by binding to cytoplasmic G-actin (30). Nuclear translocation of MKL1 occurs during mitogenic or mechanical stimulation, which triggers RhoA-mediated actin polymerization, liberating MKL1 from G-actin and exposing a nuclear localization sequence (NLS) within the actin-binding domain of MKL1 (52). This enables nuclear transport of MKL1 and activation of its downstream target SRF to induce genes related to proper function and survival (26, 29, 53). MZMs isolated from B6, B6-\textit{Ltbr}^{fl/fl}, and BXD2-\textit{Ifnar}^{–/–} mice exhibited intense, predominantly nuclear expression of MKL1 and F-actin polymerization (Figure 5A). In contrast, both nuclear expression of MKL1 and F-actin polymerization were significantly reduced in MZMs isolated from B6-\textit{Ltbr}^{fl/fl} \textit{Cd19-Cre}, B6-\textit{Ltbr}^{fl/fl} \textit{Lys-Cre}, and BXD2 mice (Figure 5A and Supplemental Figure 6).

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repopulation of WT and Ltbrfl/fl Lys-Cre MZMs 1 month after the chimeric transfer was comparable (Supplemental Figure 7B). Despite the small number of events that could be collected, ImageStream cytometric analysis further showed lower expression of MKL1 and defective F-actin polymerization in B6-Ltbr fl/fl Lys-Cre BM–derived MZMs in the spleens of recipient mice 4 months after BM transfer (Figure 5B and Supplemental Figure 7C). The results suggest that LTβR signaling in MZMs may act through MKL1 for maintenance, but not recruitment or early development, of MZMs in the MZ.

MKL1 deficiency leads to gradual loss of MZMs. It was shown previously that macrophage phagocytic function is impaired when SRF expression is suppressed (54). B cell–specific deletion of SRF also leads to complete deficiency of MZ, but not follicular, B cells, suggesting that MKL1-SRF–mediated cell elasticity is essential for the maintenance of MZ integrity (55). We analyzed B6-Mkl1–/– mice to directly show that an MKL1 deficiency affects MZM numbers and function. Consistent with the results obtained in older Ltbrfl/fl Lys-Cre mice, there was a dramatic reduction in the percentage of MZMs derived from CD45.2 B6-Mkl1–/– mice compared with the percentage of CD45.1 B6-MKL1 + MZMs in the same splenic microenvironment (Supplemental Figure 8B), as well as defective F-actin polymerization in the cytoplasmic rim of MKL1-deficient MZMs (Figure 6E and Supplemental Figure 8C). The results suggest that an intrinsic MKL1 deficiency can gradually promote mechano-sensing defects in MZMs.

As mechanosensing signaling has been implicated in the normal phagocytic function of macrophages (23, 24, 28), we tested the possibility that the MKL1 pathway affects the AC clearance function of MZMs. For this experiment, CFSE-labeled apoptotic...
thymocytes from B6 mice were administered to 1.5-month-old B6 and B6-Mkl1 –/– mice, prior to the loss of MZMs in B6-Mkl1 –/– mice. Residual uncleared ACs in the splenic MZ were visualized by confocal imaging analysis. Although B6 MZMs rapidly internalized ACs within 15 minutes, there was a markedly lower uptake of ACs in MZMs from B6-Mkl1 –/– mice at both the 15- and 30-minute time points (Figure 6F). Consistent with these observations, the AC phagocytic function of BM-derived macrophages from B6-Mkl1 –/– mice was considerably impaired compared with that observed in BM-derived macrophages derived from normal B6 mice (Figure 6G). In vitro treatment of BM-derived macrophages from B6 mice with CCG-100602, an SRF inhibitor, resulted in a significant decrease in AC uptake, suggesting that a transient impairment in this pathway is sufficient to interfere with the AC clearance function of macrophages (Figure 6H).

Decreased MKL1 in B6.TC mice and in patients with SLE. We have analyzed the spleens of lupus-prone B6.TC mice and of patients with SLE, which also exhibited aggregation of pDCs and loss of MARCO+ MZMs in the MZ (Figure 1 and ref. 42). Consistent with the findings in BXD2 mouse spleens, we observed an age-related follicular migration of mLT+ cells (Figure 7A) and a significant loss of MKL1 expression in MARCO+ MZMs (Figure 7B) in spleens from older B6.TC mice. Importantly, consistent with findings in both lupus mouse strains, a significantly reduced number of perifollicular CD1c+ MZ B cells was associated with visible follicular translocation of CD1c+ MZ B cells (ref. 56 and Figure 7C) and loss of MKL1 expression in the perifollicular region (Figure 7D) in the spleens of patients with SLE. These results suggest that the combined features described above can be identified in the spleens of patients with SLE.

MKL1/SRF defects enhance autoimmunity. A key question is whether a deficiency of MKL1 by itself is sufficient to promote autoimmunity in otherwise normal mice. There was a 2-fold increase in the percentage of PNA Fas+ GC B cells in the spleens of 4-month-old B6-Mkl1 –/– mice compared with that observed in B6 mouse spleens (Figure 8A). Circulating levels of autoantibodies were significantly elevated in 4-month-old B6-Mkl1 –/– mice compared with those detected in age-matched B6 mice. Interestingly, these autoantibodies were less prominent compared with those that developed in age-matched BXD2 mice (Figure 8B), which exhibit additional immune dysregulation in the GCs (17, 34). However, at 8 months of age, B6-Mkl1 –/– mice developed severe IgG glomerulonephritis, as shown by significantly elevated IgG deposition in glomeruli (Figure 8C).

The SRF pathway may be regulated via signaling of MKL1 and MKL2 (26, 54, 57), and MKL1 signaling may be important to maintain other hematopoietic cells (27). We thus administered CCG-100602 (58) using a liposome-based delivery system to induce selective uptake by MZMs (2) in both B6 and BXD2 mice. MZM numbers were decreased in both B6 and BXD2 mice 4 weeks after CCG-100602-liposome treatment compared with those detected in control PBS-liposome–treated groups (Figure 8, D and E). In association with the reduction of MZMs in CCG-100602-liposome–treated mice, there was significantly enhanced GC formation (Figure 8F) in the spleen, elevated autoantibody serum titers (Figure 8G), and statistically significantly increased IgG deposition — especially in BXD2 mice — in the glomeruli (Supplemental Figure 9) compared with PBS-liposome–treated mice, suggesting that MZM-targeted disruption of the SRF pathway initiated and further exacerbated MZM loss and autoantibody development in both normal and autoimmune mice.

Discussion
Expression of type I IFN signature genes is a well-established characteristic of SLE. The pathogenic role of type I IFNs has been
Figure 6. Deficiency of MKL1 is associated with defective F-actin polymerization and reduced AC clearance of MZMs. (A) Representative fluorescence photomicrographs (top) and ImageJ 3D intensity plots (bottom) of splenic MARCO+ MZMs in 8-month-old mice (original magnification, ×4). Maximal and minimal intensity scales set for the plots are shown on the left. (B–D) Splenics of B6 and B6-Mkl1<sup>−/−</sup> mice were analyzed for (B) MKL1 and F-actin polymerization (phalloidin<sup>+/-</sup>) in FACS-sorted MZMs, (C) frequency of F4/80<sup>−</sup>CD11b<sup>+/-</sup>SIGN-R1<sup>R1+</sup>I-Ab<sup>+</sup> MZMs (red boxed areas), and (D) quantitation of total MZM cells. (E) Representative ImageStream photomicrographs of MKL1 expression and F-actin polymerization in splenic MZMs (CD11b<sup>+</sup>SIGN-R1<sup>R1+</sup>F4/80<sup>+</sup>) from recipient B6-Rag1<sup>−/−</sup> mice. (F) Confocal microscopic images of AC clearance in the indicated mouse spleens following transfer of CFSE-labeled ACs (green) at the indicated times. Original magnification, ×20; digitally magnified views of the boxed areas are shown on the right. (G) FACS analysis of in vitro CFSE<sup>+</sup> AC uptake by BM-derived macrophages 30 minutes after incubation with ACs. (H) FACS analysis of the effects of CCG-100602 on uptake of CFSE<sup>+</sup> ACs by BM-derived macrophages from B6 mice. Bar graph shows the percentage of macrophages that were positive for CFSE<sup>+</sup> ACs by BM-derived macrophages from B6 mice. Data represent the mean ± SEM. Results are from 3 to 5 randomly chosen follicles (A) or 20 randomly chosen cells (B) (n = 4–6; *P < 0.05, **P < 0.01, and ***P < 0.005, compared with results from age-matched B6 mice, PBS-treated controls, or between the indicated groups, Student’s t test).
mainly implicated in directly stimulating adaptive autoimmune responses (43), and the increased expression of type I IFNs was considered a downstream consequence of AC clearance defects (1). The new findings presented here suggest an alternative pathogenic role of type I IFNs in lupus, whereby type I IFNs perpetuate AC clearance defects and promote the loss of immune tolerance to AC-Ags in SLE by promoting a defective LTβR/MKL1 axis in MZMs. Our results suggest that although type I IFNs do not directly act on MZMs, they dissipate MZMs via disruption of the interactions between MZ B cells and MZMs. This interferes with the mLT/LTβR signaling that is associated with this cellular interaction. Our results therefore provide what we believe to be a new model of lupus based on the concept that type I IFNs interfere with key MZ B cell-MZM crosstalk in the perifollicular structure by promoting follicular migration of mLT+ MZ B cells (Supplemental Figure 10). In this model, the definition of an autoimmune pathogenic cell is based on the cell’s anatomic location, in that type I IFNs shift the innate-like mLT+ MZ B cells from their tolerogenic site in the MZ, where they are essential for maintenance of MZMs to clear ACs, to an immunogenic site near the FDC network, where they can stimulate a GC response (48).

At the structural and molecular levels, we have identified that pDCs are increased in the splenic MZ of both lupus-prone BXD2 (20, 21) and B6.TC mice (42) and that both strains exhibit follicular...
suggest that under conditions of chronically elevated type I IFN levels, as seen in BXD2 mice and other lupus-prone mice, the clearance of AC-Ags is gradually compromised as a result of MZM defects. The present studies also underscore the significance of cellular elasticity in controlling immune activation and tolerogenic responses (59, 60). Mechanical receptor activity and actin cytoskeletal dynamics are regulated through key molecules such as MKL1 to activate the signaling cascades that are necessary to control the migration of mLT+ cells and decreased MKL1 expression in MZMs. A strikingly similar finding was identified in the spleens of patients with SLE. In mice, we found that IFNAR deficiency corrected MZM cytoskeletal defects and rescued MZMs in BXD2 mice. In contrast, local deficiency of LTβR or MKL1 promoted such defects. Consistent with our findings, it was reported that in BXSB mice, abnormally elevated TLR7 is associated with loss of MZ B cells and that elimination of pDCs also reversed this phenotype (3). Collectively, these results suggest that under conditions of chronically elevated type I IFN levels, as seen in BXD2 mice and other lupus-prone mice, the clearance of AC-Ags is gradually compromised as a result of MZM defects.

The present studies also underscore the significance of cellular elasticity in controlling immune activation and tolerogenic responses (59, 60). Mechanical receptor activity and actin cytoskeletal dynamics are regulated through key molecules such as MKL1 to activate the signaling cascades that are necessary to control the
movement and protrusion of extracellular membrane and thus exhibit an important function to integrate immune responses (53). Alterations in the MKL1/SRF axis can lead to defects in nuclear translocation and function of stress fiber actin cytoskeleton, leading to changes in cell morphology, function, and, eventually, cell fate (59). This is consistent with previous findings that members of the Rho family GTPases are important mediators of macrophage recruitment and function in both humans and mice (61). Thus, in different mouse models of lupus and potentially in patients with SLE, aberrant mechanosensing signaling in phagocytic macrophages might occur by the effects of type I IFN or by an intrinsic genetic defect. In either case, we believe this constitutes an important central defect underlying the gradual changes in MZMs, whereby they lose their phagocytic function and survival in the important niche in the spleen, thus leading to defective clearance of ACs in lupus (Supplemental Figure 10).

Potential limitations of the immunohistological studies of the spleen from lupus and unaffected subjects are that the depletion of MZMs and MZ B cells may result from other factors associated with the disease, such as elevated anti-MARCO and class A scavenger receptor (SR-A) antibodies, which has been reported in patients with SLE (62). Additionally, the depletion of MZMs and B cells in patients with SLE could be due to treatment with cytotoxic therapies that may deplete these cells or MZMs. Therefore, additional studies of human SLE spleens would be required to confirm the present results. Studies using ImageStream analysis are limited by the small number of cells that can be analyzed and the small percentage of MZMs in BM chimeric mice.

In summary, the present work suggests a novel pathogenic role for type I IFN–mediated follicular shuttling of innate-like mLT+ B cells in systemic autoimmunity. Furthermore, alterations in the mechanosensing properties of MZMs responsible for phagocytosis of apoptotic debris represent a risk factor for loss of immune tolerance to AC-Ags which, combined with other risk factors, can ultimately lead to development of autoreactive GCs (2, 17, 21, 36). Suppression of type I IFNs or their signals may act through restoration of MZMs and MZ B cells in vivo and in vitro and in vivo AC clearance assay. For the generation of ACs, thymocytes collected from 8-week-old female B6 mice were cultured with 1 μM dexamethasone (D4902-100MG; Sigma-Aldrich) for 6 hours at 37°C in RPMI 1640 media plus 1% FBS (MT-17-105-CV; Fisher Scientific). BM-derived macrophages were polarized by culturing BM cells in RPMI medium with M-CSF (10 ng/ml) for 7 days. For in vitro AC clearance assays, 5 × 106 BM-derived macrophages were cultured with 1 × 105 Vybrant CFDA SE Cell Tracer–labeled ACs (V12883; Life Technologies) for 30 minutes. For in vivo administration of ACs, each mouse was injected i.v. with 2 × 107 apoptotic thymocytes and sacrificed at 5-, 15-, and 30-minute time points.

Type I IFN induction in vivo. For in vivo induction of type I IFNs, 5 μg CpG-A (HC4037; Hycult Biotech) was mixed with 50 μl PBS, while in another reaction tube, 30 μl DOTAP (118117001; Roche) was mixed with 70 μl PBS. The CpG solution was then mixed with the DOTAP solution, incubated at room temperature for 15 minutes prior to i.v. administration in the tail.

Type I IFN RNA quantitation. Expression levels of the type I IFN isoforms Ifna1, Ifna4, Ifna7, Ifna9, Ifna11, and Ifnb in peripheral blood were determined using a previously described qRT-PCR method (21). The qRT-PCR mixtures contained SYBR Green PCR Master Mix (Bio-Rad) with the following primers: Ifna1, forward: 5′-AGTTAAGCTGACC-CAGCAGAT-3′; reverse: 5′-GGTGGAGGTCATTGCGAAG-3′; Ifna4, forward: 5′-TCTGCAAATGACCTTCTCATTGAC-3′; reverse: 5′-TATGTCTCACGACCCAGCAG-3′; Ifna7, forward: 5′-ATGGATCCCTCCTCTGACTCATT-3′; reverse: 5′-CAACATTTGGCTGAGGAACCA-3′; Ifna9, forward: 5′-TGATGGTCCTGTGTTGTGTAAG-3′; reverse: 5′-GTGAGCGAGGTGTCATTGAGATGT-3′; Ifna11, forward: 5′-CCACGACAGTTCATTTGAACCTC-3′; reverse: 5′-GGTGGAGGTCATTGCGAAGA-3′; Ifnb, forward: 5′-CTTCCACCACCCCTTCTC-3′; reverse: 5′-GAAGGAGACCCCTTCTCTCGA-3′.

qRT-PCR analysis for GeneChip analysis validation. Expression levels of Prq2, Prq3, Prtn5, Cldn15, Slip1, Epx, Cpa3, and Ets1 in isolated MZMs from the indicated mouse strains as shown in Supplemental Figure 4B were determined using the qRT-PCR method described above with the following primers: Ets1, forward: 5′-TCTTCGAGAAAGAGC-3′; Ets1, reverse: 5′-GGTACGACTACTGAGAAGA-3′; Cpa3, forward: 5′-TCCTGCAGAAAGAGACTGAG-3′; Cpa3, reverse: 5′-CCGATCTCTCTCTGAGAAG-3′; Slip1, forward: 5′-TCTTCGAGAAAGAGACTGAG-3′; Slip1, reverse: 5′-AAAGAGACCCCTTCTCTCGA-3′; Epx, forward: 5′-TCTCACCACCCCTTCTC-3′; Epx, reverse: 5′-GAAGGAGACCCCTTCTCTCGA-3′; Cldn15, forward: 5′-GTTGGAGGTCATTGCGAAGA-3′; Cldn15, reverse: 5′-CCACGACAGTTCATTTGAACCTC-3′; Prtn5, forward: 5′-GTGAGCGAGGTGTCATTGAGATGT-3′; Prtn5, reverse: 5′-GGTGGAGGTCATTGCGAAGA-3′; Prq2, forward: 5′-AGTTAAGCTGACC-CAGCAGAT-3′; Prq2, reverse: 5′-GGTGGAGGTCATTGCGAAG-3′; Prq3, forward: 5′-TCTGCAAATGACCTTCTCATTGAC-3′; Prq3, reverse: 5′-TATGTCTCACGACCCAGCAG-3′;
bated overnight with the purified rabbit anti-human MARCO (cata-
tutes to reduce nonspecific staining. The sections were then incu-
EDTA, and 0.15 mM NaN3, pH 7.6) with 1% goat serum for 20 min-
tions were incubated in PBE buffer (PBS containing 1% BSA, 1 mM
without the primary antibody, were included in the analyses. In situ
was prepared immediately before use and applied for 7 minutes. The
rinulate antibody cocktails and biotinylated PNA (B-1075; Vector
from the UAB Tissue Procurement Shared Facility. Following
cadaver paraffin-embedded splenic tissue sections were obtained
immersion objective lens (numerical aperture 1.45) and processed
staining (Life Technologies). 
Further antibodies were from either eBioscience or BioLegend, except biotiny-
anti-F4/80 (clone BM8); and anti–SIGN-R1 (clone 22D1). All anti-
against CD45.2+ cells were further plotted. A total of 10,000 splenic
Autoantibody detection. Assays for serum autoantibodies were car-
ried out as described previously (17). Multiple antigenic targets were analyzed due to the development of polyreactive pathogenic autoan-
tibodies in BxD2 mice (34). Immulon II plates (Dynatech) precoated
μg/ml recombinant mouse SR-AI/MSR1 (Sigma-Aldrich), 25 μg/ml MDA (Cell Biolabs), 25 μg/ml calf thymus DNA
μg/ml with BSA were coated individually with 50 μg/ml recombinant mouse MARCO, or 25 μg/ml recombinant mouse SR-AI/MSR1 (R&D Systems). The serum was diluted and assayed for autoantigen
-reactivity against the plates described above by incubation for 2 hours at room temperature. Bound IgG was detected with a goat polyclonal
HRP–anti-mouse IgG detection antibody (catalog 1030-50; SouthernBiotech) and visualized at 450 nm using a tetracyanobenzidine (TMB) substrate (Sigma-Aldrich).
Detection of MDA. Immulon II plates precoated with BSA were coated with 50 μg/ml goat polyclonal anti-MDA antibody (catalog
Secondary rabbit polyclonal anti-MDA antibody (catalog ab6463; Abcam) was applied for 1 hour at room temperature. Bound antigens or cytokines were detected with goat anti-rabbit IgG–HRP (catalog 4030-05; SouthernBiotech) and visualized at 450 nm using a TMB substrate (Sigma-Aldrich).
GeneChip analysis. Gene expression analysis was performed using the mouse WG-6 BeadChip and iScan system (Illumina). Total RNA
FACS sorted from MZMs, gated as F4/80+CD11b+SIGN-R1+Ab+, was converted to cDNA by reverse transcription, followed by second-
strand synthesis to generate double-stranded cDNA. After purification, the cDNA was converted to biotin-labeled cRNA, hybridized to a mouse WG-6 BeadChip, and stained with streptavidin-Cy3 for
The mouse WG-6 BeadChips contain sequences representing approximately 45,200 curated and putative genes and expressed sequence tags (ESTs). Quality standards for hybridization, labeling, staining, background signal, and basal level of housekeeping
gene expression for each chip were verified. After scanning the probe array, the resulting image was analyzed using GenomeStudio software, version 2011.1 (Illumina). Gene lists were further analyzed using GeneSpring software, version 12.1 (Agilent Technologies). Data
were analyzed using Ingenuity Pathways Analysis (IPA) (Ingenuity Systems, www.ingenuity.com). Upstream Regulator Analysis from IPA was used to identify the upstream regulators that were responsible for the gene expression changes observed in the data. The activation Z-score (an algorithm designed to reduce the chance that random data will generate significant predictions) identifies upstream regulators that can explain observed gene expression changes in the data and predicts the activation state of the upstream regulators. An absolute Z-score greater than or equal to 2 was considered significant. Predictions in which both the Z-score is significant (absolute value ≥2) and the P value is significant (<10^-6) are the most reliable predictions. Microarray data were deposited in the NCBI’s Gene Expression Omnibus (GEO) database (GEO GSE66687). Samples were derived from splenic MZMs (F4/80*CD11b*SIGN-R1*I-A*) of BXD2 mice administered PBS (GSM1627971 and GSM1627972), BXD2-Iftar-/– mice administered PBS (GSM1627973), and BXD2 mice administered sLTβR-Fc (GSM1627974). Each chip is the result of 2 spleens.

**Statistics.** All results are shown as the mean ± SEM. A 2-tailed, unpaired Student’s t test was used when 2 groups were compared for statistical differences. The distribution differences of mLT+ B cells in the anatomical MZ area versus those in the anatomical follicular area between different strains of mice were tested using a χ^2 test. P values of less than 0.05 were considered significant.

**Study approval.** All human studies were designated by the IRB of the University of Alabama at Birmingham as “Not Human Subject Research” (NSHR), since all tissues were deidentified cadaveric autopsy specimens. All animal studies were approved by the IACUC of the University of Alabama at Birmingham.

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