Genetic evidence for the role of plasmacytoid dendritic cells in systemic lupus erythematosus

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Systemic lupus erythematosus (SLE) is an autoimmune disorder characterized by the production of antibodies to self-nucleic acids, immune complex deposition, and tissue inflammation such as glomerulonephritis. Innate recognition of self-DNA and -RNA and the ensuing production of cytokines such as type I interferons (IFNs) contribute to SLE development. Plasmacytoid dendritic cells (pDCs) have been proposed as a source of pathogenic IFN in SLE; however, their net contribution to the disease remains unclear. We addressed this question by reducing gene dosage of the pDC-specific transcription factor E2-2 (Tcf4), which causes a specific impairment of pDC function in otherwise normal animals. We report that global or DC-specific *Tcf4* haplodeficiency ameliorated SLE-like disease caused by the overexpression of the endosomal RNA sensor Tlr7. Furthermore, *Tcf4* haplodeficiency in the B6.*Sle1*.*Sle3* multigenic model of SLE nearly abolished key disease manifestations including anti-DNA antibody production and glomerulonephritis. *Tcf4*-haplodeficient SLE-prone animals showed a reduction of the spontaneous germinal center reaction and its associated gene expression signature. These results provide genetic evidence that pDCs are critically involved in SLE pathogenesis and autoantibody production, confirming their potential utility as therapeutic targets in the disease.

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Abbreviations used: cDC, classical DC; CKO, conditional KO; dsDNA, double-stranded DNA; GC, germinal center; IFNAR, IFN-α receptor; PCA, principal component analysis; pDC, plasmacytoid DC; SLE, systemic lupus erythematosus.

Systemic lupus erythematosus (SLE) is an autoimmune disorder in which the production of autoantibodies leads to the formation and deposition of immune complexes, resulting in tissue damage. The hallmark of SLE is the presence of pathogenic autoantibodies specific for nuclear antigens such as double-stranded DNA (dsDNA), chromatin, and RNA-containing antigens (Fairhurst et al., 2006). Aberrant recognition of self-nucleic acids through innate immunoreceptors, including endosomal Toll-like receptors TLR7 and TLR9 (specific for single-stranded RNA and unmethylated CpG DNA, respectively), is thought to be at the crux of autoantibody production and SLE pathogenesis (Marshak-Rothstein and Rifkin, 2007; Shlomchik, 2009). For example, a duplication of mouse *Tlr7* gene (the spontaneous *Yaa* mutation) accelerates SLE development, whereas multiple copies of *Tlr7* (as a transgene) are sufficient to cause SLE-like disease (Pisitkun et al., 2006; Deane et al., 2007; Fairhurst et al., 2008).

One of the main consequences of innate recognition of DNA/RNA is the secretion of type I IFN (IFN-α/β), a key antiviral cytokine typically produced during viral infections. Notably, leukocytes from many SLE patients manifest an IFN signature, i.e., the expression of IFN-induced genes (Baechler et al., 2003; Bennett et al., 2003). Because of the powerful adjuvant activity of IFN, increased IFN levels are thought to promote immune hyperactivation and tissue damage in the disease (Elkon and Wiedeman, 2012). Genetic ablation of

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IFN-α receptor (IFNAR) ameliorates experimental SLE in the Tlr7-overexpressing model (Buechler et al., 2013) as well as in NZB/NZW-derived strains (Santiago-Raber et al., 2003; Agrawal et al., 2009). Conversely, IFN overexpression strongly exacerbates experimental SLE (Liu and Davidson, 2013). Hence, the blockade of IFN signaling (for example, using antibodies to IFN or IFNAR) represents a potential therapeutic approach to SLE (Bronson et al., 2012).

Plasmacytoid DCs (pDCs) are a distinct lineage of DCs specialized in IFN production in response to viral nucleic acids sensed through TLR7 and TLR9 (Gilliet et al., 2008; Reizis et al., 2011). In addition to virus-derived DNA and RNA, pDCs can be activated by self-nucleic acids complexed with antibodies (Båve et al., 2003) or DNA/RNA-binding proteins such as HMGB1 (Tian et al., 2007). In particular, DNA complexes released from activated neutrophils induce pDCs to secrete IFN, which fuels the "vicious circle" of myeloid cell activation in SLE patients (Garcia-Romo et al., 2011; Lande et al., 2011). TLR-activated pDCs become resistant to glucocorticoids, underlying the limited efficacy of these drugs in SLE (Guiducci et al., 2010a). Therefore, pDCs have been proposed as a key source of aberrant IFN production and a major driver of SLE progression (Rönnblom and Alm, 2001). In experimental SLE, minor signs of pDC activation have been described in the *Tlr7* transgenic model (Buechler et al., 2013), and antibody-mediated pDC ablation prevented trauma-induced skin inflammation in the (NZBxNZW)F1 model (Guiducci et al., 2010b). However, the precise role and significance of pDC function in SLE remains moot, largely because models for specific, long-term pDC ablation have not been available.

We have previously identified the transcription factor E2-2 (official symbol Tcf4) as a specific regulator of pDC development in mice and in humans (Cisse et al., 2008). Tcf4 is expressed in pDCs but not in classical DCs (cDCs), and its deletion abolishes the development of pDCs but not of cDCs or other immune cell types. Importantly, even monoallelic loss of *Tcf4* causes specific impairment of pDC function in mice and human patients. For example, $Tcf4^{+/-}$ mice fail to produce IFN in response to the TLR9 ligand CpG but show normal IFN induction by the TLR3/RIG-I ligand poly-I:C and normal T cell–dependent antibody responses (Cisse et al., 2008). Thus, *Tcf4* haplodeficiency represents a specific tool for constitutive functional blockade of pDCs. In this study, we applied this tool to determine the role of pDCs in two distinct genetic models of SLE.

RESULTS AND DISCUSSION

Tcf4 haplodeficiency ameliorates SLE caused by Tlr7 overexpression

To validate *Tcf4* haplodeficiency as a pDC-specific tool, we first used a model of SLE induced by the administration of saturated hydrocarbon tetramethylpentadecane (pristane). This model is characterized by autoreactivity to small ribonucleoproteins (anti-Smith antigen, anti-Sm), which is dependent on TLR7-induced IFN production by inflammatory monocytes rather than by pDCs (Lee et al., 2008). We found that the expression of IFN-inducible genes and anti-Sm antibody production were similar in pristane-treated WT and $Tcf4^{+/-}$ animals (unpublished data). Thus, *Tcf4* haplodeficiency does not generally affect autoantibody production that is not dependent on pDCs.

Next, we used a monogenic SLE model based on multiple transgenic copies of the *Tlr7* locus. These *Tlr7*.Tg animals develop an SLE-like disease characterized by anti-RNA antibody production, expansion of monocyte-like myeloid cells in the blood, massive immune activation, and glomerulonephritis (Deane et al., 2007). We have used a line of *Tlr7*.Tg animals with moderate Tlr7 mRNA overexpression (4–8-fold) and the transgene integrated on the Y-chromosome. On the hybrid B6129F1 background, nearly all *Tlr7*.Tg males became

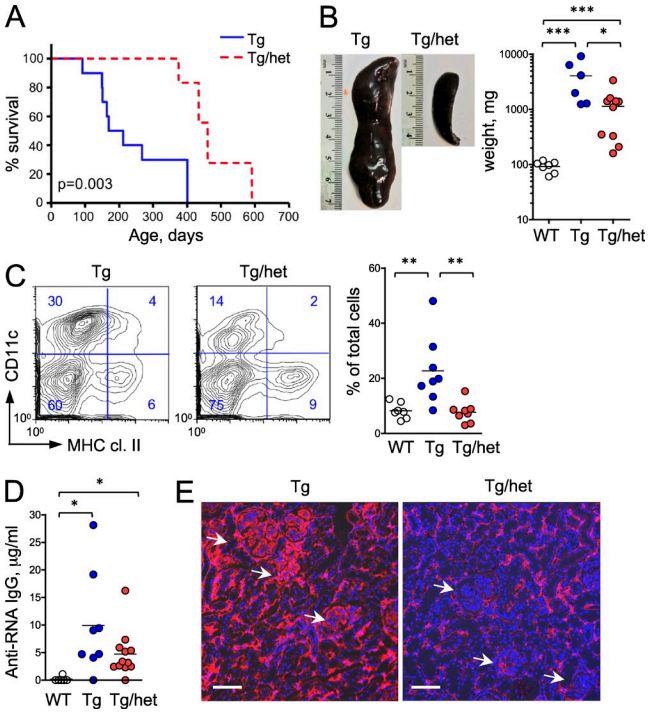

Figure 1. *Tcf4* haplodeficiency ameliorates SLE-like disease in Tlr7 transgenic mice. *Tlr7*.Tg males, haplodeficient for *Tcf4* (Tg/het) or their *Tcf4*-sufficient littermates (Tg), were analyzed. (A) Kaplan-Meier survival plot (n = 7–10). Significance was determined by log-rank test. (B) Splenic size (left) and splenic weights were determined for individual 50-wk-old transgenic animals and WT controls (right). (C) Peripheral blood cells from the indicated mice were analyzed by flow cytometry (left); thresholds of positive staining and percentages of cells within the resulting quadrants are indicated. The frequencies of the $CD11c^+$ MHC cl. II^- population (top left quadrant) in individual 30-wk-old animals were determined (right). Data were pooled from 3 independent experiments. (D) Anti-RNA IgG levels in the sera of 30–40-wk-old animals were determined by ELISA. Data were pooled from 3 independent experiments. (E) Kidney cryosections of 50–60-wk-old animals were stained for IgG (red) and DNA (blue) and analyzed by fluorescence microscopy (bars, 100 µm). Arrows show kidney glomeruli. Shown is a representative of 5 animals in each group from 2 independent experiments. Horizontal bars indicate mean. *, $P \le 0.05$; **, $P \le 0.01$; ***, $P \le 0.001$.

moribund and succumbed to the disease within 1 yr (Fig. 1 A). The presence of a single null allele of *Tcf4* did not reduce the level of *Tlr7* overexpression in pDCs and B cells from *Tcf4*$^{+/-}$ *Tlr7*.Tg animals (unpublished data). Nevertheless, all *Tcf4*$^{+/-}$ *Tlr7*.Tg males survived beyond 1 yr (Fig. 1 A) and showed a significantly lower (albeit still elevated) spleen weight at 50 wk (Fig. 1 B). Moreover, the increased population of CD11c^{+} MHC cl. II^{-} myeloid cells in the peripheral blood at 30 wk of age was reduced to normal levels (Fig. 1 C). No consistent changes in other blood cell types were detected in *Tlr7*.Tg animals (unpublished data). A trend toward lower levels of anti-RNA antibodies was observed in older *Tcf4*$^{+/-}$ animals at the same age, although the difference was not significant due to high variability (Fig. 1 D). No anti-DNA antibodies were detected in the majority of control or *Tcf4*$^{+/-}$ animals (unpublished data). The kidneys of *Tlr7*.Tg males at 50–60 wk showed abundant IgG deposition in both glomeruli and tubular interstitium, with the latter suggesting interstitial nephritis. In contrast, *Tcf4*$^{+/-}$ *Tlr7*.Tg males showed reduced IgG deposition in the kidneys (Fig. 1 E). Thus, global haplodeficiency of *Tcf4* improved survival and reduced immune activation in the *Tlr7*.Tg model of SLE.

Tcf4 haplodeficiency in DCs ameliorates Tlr7-induced SLE

Although Tcf4 deficiency primarily affects pDCs, Tcf4 is also expressed at low levels in B cells, as well as in nonimmune tissues including the brain. To confirm that the effect of *Tcf4* haplodeficiency in *Tlr7*.Tg mice originates in pDCs, we combined a single conditional (floxed) allele of *Tcf4* with the *Itgax*-Cre deleter strain. This strain (also known as *CD11c*-Cre) mediates Cre recombination specifically in the DC lineage including cDCs and pDCs (Caton et al., 2007). However, Tcf4 is not expressed in cDCs; therefore, any consequences of *Itgax*-Cre–mediated deletion of Tcf4 would reflect its function in pDCs only. We therefore analyzed conditional KO (CKO) *Tlr7*.Tg *Tcf4*$^{+/flox}$ *Itgax*-Cre^{+} males and their *Tlr7*.Tg *Tcf4*$^{+/flox}$ *Itgax*-Cre^{-} littermate controls for SLE manifestations.

Because *Tlr7*.Tg animals on pure B6 background survive for >1 yr, differential survival could not be assessed in this experiment. Nevertheless, similar to the germline *Tcf4* haplodeficiency, DC-specific *Tcf4* haplodeficiency significantly reduced splenomegaly (Fig. 2 A) and completely abolished myeloid cell expansion (Fig. 2 B). It also significantly reduced the fraction of activated T cells, although the latter was still increased relative to WT (Fig. 2 C). Control *Tlr7*. Tg animals at 30–40 wk showed increased levels of total serum IgG and IgM (Fig. 2 D), the presence of anti-RNA IgG (Fig. 2 E), and the associated autoreactivity to cytoplasmic antigens (Fig. 2 F). In contrast, *Tlr7*.Tg CKO animals had normal Ig levels and no significant anti-RNA autoreactivity (Fig. 2, D–F). This was accompanied by reduced IgG deposition in the kidneys of CKO mice (Fig. 2 G). Thus, *Tcf4* haplodeficiency in the DC lineage reduces autoreactivity and immune activation in *Tlr7*. Tg animals, similar to the germline *Tcf4* haplodeficiency. These data confirm that the effect is intrinsic to Tcf4-expressing cells within the DC lineage, which correspond to pDCs.

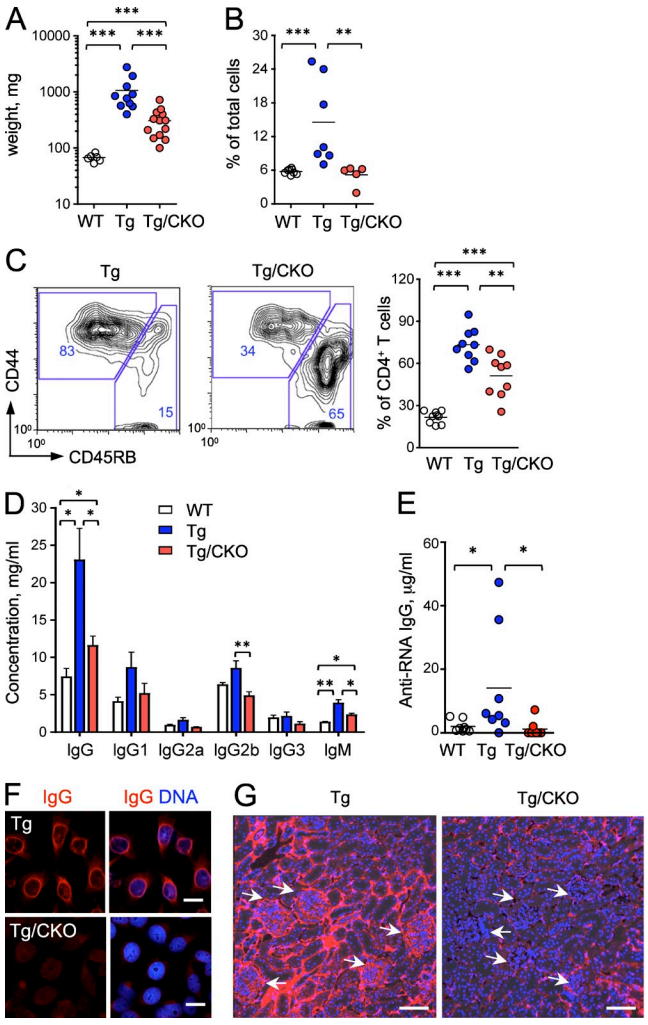

Figure 2. DC-specific *Tcf4* haplodeficiency ameliorates disease in Tlr7 transgenic mice. *Tlr7*.Tg *Tcf4*$^{flox/+}$ *Itgax*-Cre^{-} males (Tg) or their *Itgax*-Cre^{+} littermates with DC-specific *Tcf4* CKO (Tg/CKO) were analyzed along with WT controls. (A) Splenic weights were determined in individual 60-wk-old animals. (B) Frequencies of CD11c^{+} MHC cl. II^{-} myeloid cells in the peripheral blood of 30–40-wk-old animals were determined by flow cytometry. Data were pooled from 3 independent experiments. (C) Peripheral blood cells from the indicated 30–40-wk-old mice were analyzed by flow cytometry, gated on CD4^{+} T cells, and the frequencies of activated CD44^{+} CD45RB^{-} cells among CD4^{+} T cells were determined. Data were pooled from 4 independent experiments. (D) Levels of total IgM, IgG, and IgG subclasses in the sera of 30–40-wk-old animals were determined by ELISA (mean ± SD of 5 animals per group pooled from 2 independent experiments). (E) Anti-RNA IgG levels in the sera of 30–40-wk-old animals were determined by ELISA. Data were pooled from 3 independent experiments. (F) Fixed HEp-2 cells were incubated with sera from Tg mice, stained for IgG (red) alone or with DNA (blue), and analyzed by fluorescence microscopy (bars, 20 µm). Images are representative of 2 independent staining experiments. (G) Kidney cryosections of 60-wk-old animals were stained for IgG (red) and DNA (blue) and analyzed by fluorescence microscopy (bars, 100 µm). Arrows show kidney glomeruli. Images are representative of 6 animals in each group from 2 independent experiments. Horizontal bars indicate mean. *, P ≤ 0.05; **, P ≤ 0.01; ***, P ≤ 0.001.

Tcf4 haplodeficiency ameliorates SLE in B6.Sle1.Sle3 animals

Although *Tlr7*.Tg animals develop robust SLE-like disease, this monogenic model contrasts with the complex polygenic nature of human SLE. Furthermore, Tlr7-driven SLE does not recapitulate several important features of the human disease, including the production of antibodies against dsDNA (anti-dsDNA) and prominent glomerulonephritis. We therefore turned to a polygenic model that harbors large genomic intervals from the NZW strain (*Sle1*, *Sle2*, and *Sle3*) on B6 background (Morel et al., 2000). Notably, the homozygosity for only two intervals, *Sle1* and *Sle3*, is sufficient to cause full-blown SLE with nearly complete penetrance (Morel et al., 2000). We therefore analyzed animals on B6 background that were homozygous for *Sle1* and *Sle3*, heterozygous for *Sle2*, and either haplosufficient or haplodeficient for *Tcf4*.

The spleens of B6.*Sle1.Sle3* $Tcf4^{+/-}$ animals at 30 wk were significantly smaller than in $Tcf4^{+/+}$ littermates, although still enlarged relative to WT (Fig. 3 A). Peripheral blood leukocytes of B6.*Sle1.Sle3* mice showed no myeloid cell expansion or other major changes except for a slight decrease of B cell fraction (unpublished data). In contrast, the observed increase in the fraction of activated T cells was abolished in $Tcf4^{+/-}$ animals (Fig. 4 B). Peripheral blood leukocytes in B6.*Sle1.Sle3* animals showed increased expression of Sca-1, an IFN-inducible gene whose induction on B and T cells is associated with persistent IFN signaling (Lee et al., 2008). In $Tcf4^{+/-}$ animals, the levels of Sca-1 on B and T cells were significantly reduced to normal or near-normal levels, respectively (Fig. 3 C). Similar changes in T cell activation and Sca-1 expression were observed in the spleens of experimental animals (unpublished data).

B6.*Sle1.Sle3* mice showed increased levels of total serum IgG (particularly IgG1) and IgM, which were reduced to normal levels by *Tcf4* haplodeficiency (Fig. 3 D). The majority (9 out of 11) of control B6.*Sle1.Sle3* mice showed high titers of anti-dsDNA IgG and 5 out of 9 showed anti-RNA IgG (Fig. 3 E). Both the frequency and titers of these autoantibodies were significantly reduced in $Tcf4^{+/-}$ animals (Fig. 3 E), accompanied by the loss of anti-nuclear IgG reactivity (Fig. 3 F) and reduced IgG deposition in the kidneys (Fig. 3 G). We conclude that *Tcf4* haplodeficiency greatly reduced autoantibody production and immune activation in the B6.*Sle1.Sle3* model of SLE.

Tcf4 haplodeficiency ameliorates kidney inflammation in SLE models

Because glomerulonephritis is a key inflammatory manifestation and morbidity cause in SLE, we analyzed the effect of *Tcf4* haplodeficiency on kidney pathology in both experimental models. Control *Tlr7*.Tg animals at 50 wk manifested a relatively mild kidney inflammation with minimal glomerular deposits (Fig. 4 A and not depicted). Nevertheless, *Tlr7*.Tg CKO animals showed significant reductions in mean glomerular size (Fig. 4 B), extent of endocapillary proliferation and leukocyte infiltration, and median cumulative score of the disease (Fig. 4 C). Control B6.*Sle1.Sle3* animals at 30 wk manifested prominent glomerulonephritis with interstitial inflammation, leukocyte infiltration, and glomerular deposits. In contrast, $Tcf4^{+/-}$ B6.*Sle1.Sle3* littermates

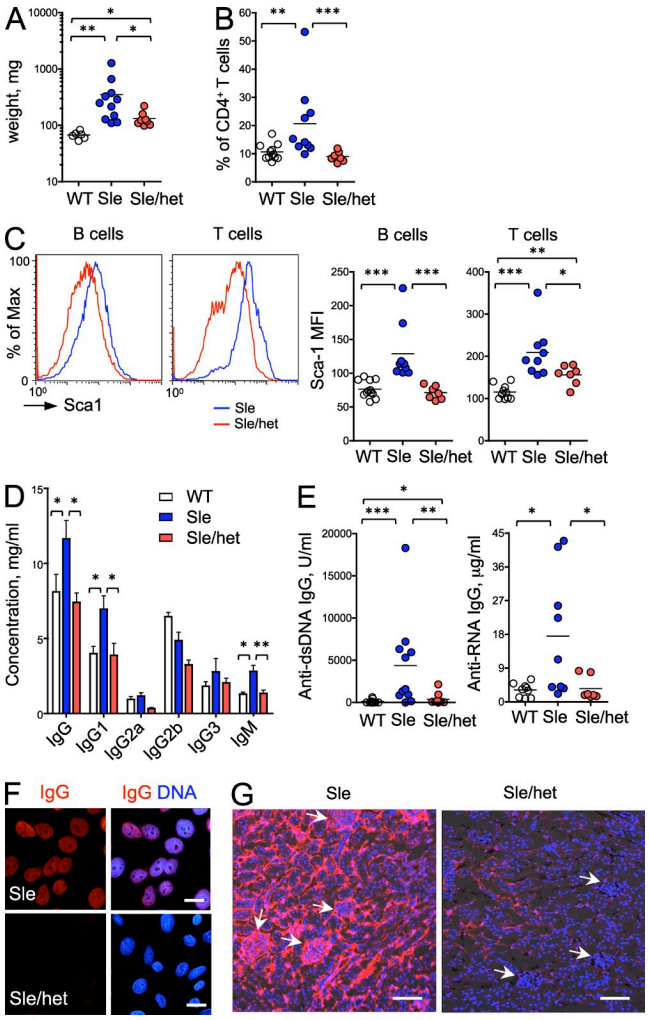

Figure 3. *Tcf4* haplodeficiency ameliorates immune activation in B6.*Sle1.Sle3* mice. 30-wk-old B6.*Sle1.Sle3* mice (Sle) or their *Tcf4* haplodeficient littermates (Sle/het) were analyzed along with WT controls. (A) Splenic weights were determined in individual indicated animals. (B) Peripheral blood cells from the indicated mice were analyzed by flow cytometry, gated on $CD4^+$ T cells, and the frequencies of activated $CD44^+$ $CD45RB^-$ cells among $CD4^+$ T cells were determined. Data were pooled from 3 independent experiments. (C) Sca-1 expression on gated B and T cells (left) and mean fluorescent intensities (MFIs) of Sca-1 on these cells from individual mice was determined by flow cytometry. Data were pooled from 3 independent experiments (right). (D and E) Levels of total IgM, IgG, and IgG subclasses (mean ± SD; D), anti-dsDNA, and anti-RNA IgG (E) in the sera of indicated experimental groups were measured by ELISA. Data were pooled from 2 independent experiments. (F) Fixed Hep2 cells were incubated with sera from Sle mice, stained for IgG (red) alone or with DNA (blue), and analyzed by fluorescence microscopy (bars, 20 µm). Images are representative of 2 independent staining experiments. (G) Kidney cryosections were stained for IgG (red) and DNA (blue) and analyzed by florescence microscopy (bars, 100 µm). Arrows show kidney glomeruli. Images are representative of 9 animals in each group from 3 independent experiments. Horizontal bars indicate mean. *, $P \le 0.05$; **, $P \le 0.01$; ***, $P \le 0.001$.

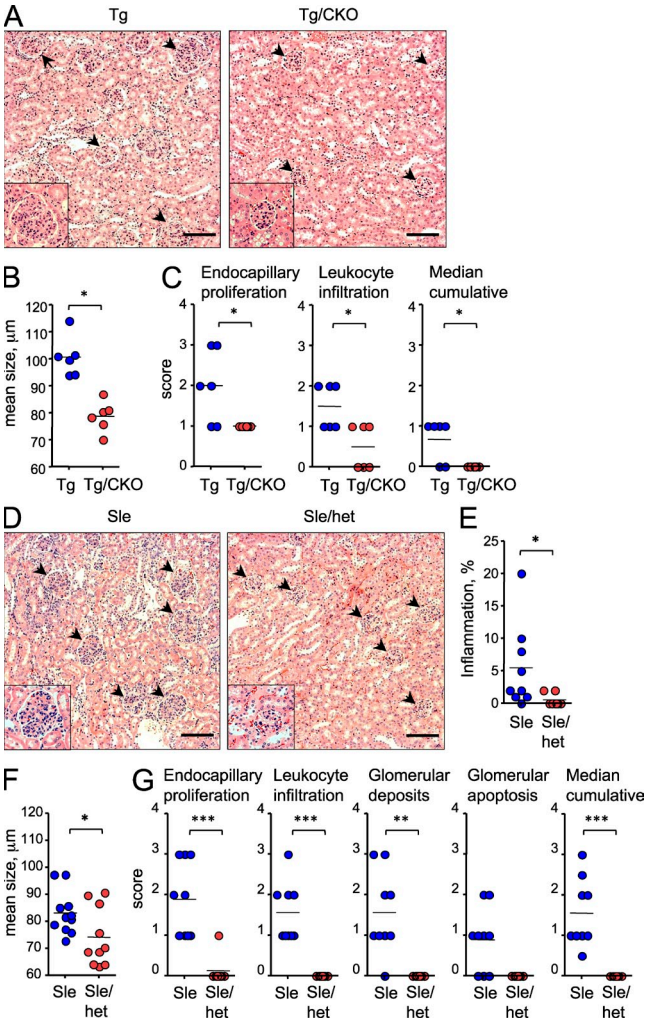

Figure 4. *Tcf4* haplodeficiency ameliorates kidney disease in SLE-prone mice. (A) Kidney paraffin sections from *Tlr7*.Tg animals with or without DC-specific *Tcf4* CKO (Tg/CKO) were stained with H&E and analyzed by microscopy (bars, 100 µm). Arrows show kidney glomeruli, with a representative glomerulus on the inset. Images are representative of 6 animals in each group from 2 independent experiments. (B) Mean diameter of kidney glomeruli was determined in individual 60-wk-old *Tlr7*.Tg animals. (C) Histopathological score of indicated disease parameters in the kidneys from individual *Tlr7*.Tg animals were determined using microscopy. (D) Kidney paraffin sections from B6.*Sle1.Sle3* mice with (Sle/het) or without (Sle) *Tcf4* haplodeficiency were stained with H&E and analyzed by microscopy (bars, 100 µm). Arrows show kidney glomeruli, with a representative glomerulus on the inset. Images are representative of 9 animals in each group from 2 independent experiments. (E–G) Percentage of parenchyma with interstitial inflammation in the kidneys (E), mean diameter of kidney glomeruli (F), and histopathological scores of indicated disease parameters (G) were determined in individual B6.*Sle1.Sle3* animals. Horizontal bars indicate mean. *, $P \leq 0.05$; **, $P \leq 0.01$; ***, $P \leq 0.001$.

showed a lower degree of interstitial inflammation, smaller glomeruli, and a nearly complete absence of glomerulonephritis (Fig. 4, D–G). We conclude that *Tcf4* haplodeficiency ameliorates autoreactivity-driven kidney inflammation in both *Tlr7*.Tg and B6.*Sle1.Sle3* models of SLE.

Tcf4 haplodeficiency reduces the germinal center (GC) signature of SLE

To explore the molecular correlates of SLE amelioration by *Tcf4* haplodeficiency, we performed microarray expression analysis of total splenocytes from WT, B6.*Sle1.Sle3* (Sle), and B6.*Sle1.Sle3 Tcf4*$^{+/-}$ (Sle/het) animals. Hierarchical clustering showed that Sle and Sle/het samples were highly similar yet distinct from the WT (Fig. 5 A). Indeed, principal component analysis (PCA) identified two major clusters of genes that were coordinately up- or down-regulated in both Sle samples compared with WT (Fig. 5 B and Dataset S1). Genes that were up-regulated in both Sle and Sle/het splenocytes (Fig. 5 B, cluster 1b) included proliferation-associated genes and granulocyte-specific genes, as well as genes associated with immune activation such as high mobility group proteins and defensins (Dataset S1). Consistent with previous observations in the B6.*Sle1.Sle2.Sle3* mice (Sriram et al., 2012), IFN-inducible genes were not significantly up-regulated in either Sle sample. Notably, PCA identified a distinct cluster of 49 genes that were up-regulated in Sle but not in Sle/het splenocytes (Fig. 5 B, cluster 2a). This cluster included several genes that are highly specific for GC B cells, including the *Aicda* gene encoding activation-induced cytidine deaminase (AID) (Dataset S1). Also present were several genes expressed in plasma cells (e.g., *Xbp1*) and in follicular helper T cells (*Il21* and *Pdcd1*). The reduction of *Aicda* overexpression in splenocytes from *Tcf4*-haplodeficient animals was confirmed by qRT-PCR for both B6.*Sle1.Sle3* and Tlr7.Tg models (Fig. 5 C). Furthermore, immunofluorescent staining revealed massive GC reaction in the spleens of B6.*Sle1.Sle3* mice that was virtually abolished in *Tcf4*-haplodeficient littermates (Fig. 5 D). We conclude that *Tcf4* haplodeficiency does not generally affect the SLE-associated gene expression profile, but specifically reduces the GC reaction and the associated expression signature.

A recent work used germline deletion of the transcription factor Irf8 or proton-coupled oligopeptide transporter Slc15a4 to test the role of pDCs in NZB and B6.*Fas*^{lpr} models of SLE, respectively (Baccala et al., 2013). However, Irf8 deletion affects the development and/or function of multiple immune cell types (Wang and Morse, 2009), whereas Slc15a4 regulates cytokine responses to Tlr9 and NOD-like receptor ligands in both pDCs and cDCs (Sasawatari et al., 2011). Here, we used haplodeficiency for Tcf4, a specific regulator of pDC development, to target pDC function in experimental SLE. In the case of the *Tlr7*.Tg model, we confirmed that the effect was intrinsic to the DC lineage, in which only pDCs express Tcf4. Although a minor subset of noncanonical CD8$^+$ cDCs is depleted by full Tcf4 deficiency (Bar-On et al., 2010), it is unaffected by reduced gene dosage of Tcf4 (our unpublished data). Furthermore, *Tcf4* haplodeficiency did not affect autoreactivity in the pDC-independent model of pristane-induced SLE. Therefore, our approach specifically interrogates the net contribution of the pDC lineage to experimental SLE.

We found that *Tcf4* haplodeficiency significantly ameliorated SLE manifestations in both *Tlr7*.Tg transgenic model

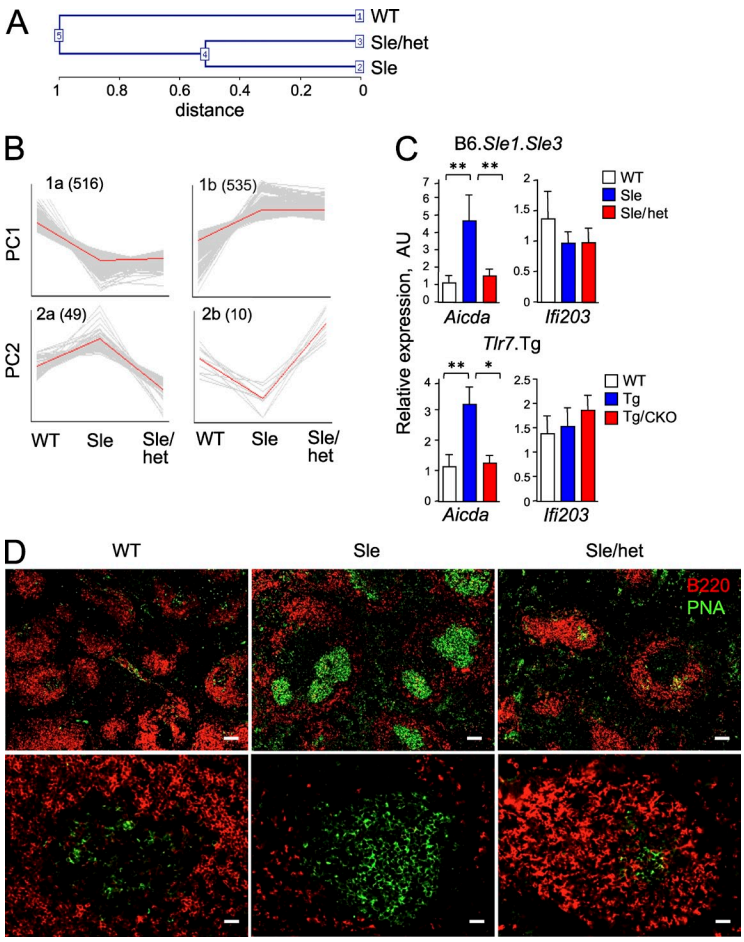

Figure 5. *Tcf4* haplodeficiency reduces GC signature in SLE-prone mice. (A and B) Total splenocytes from individual 30-wk-old WT ($n = 2$), B6.*Sle1.Sle3* (Sle, $n = 3$), or B6.*Sle1.Sle3 Tcf4*$^{+/-}$ (Sle/het, $n = 3$) mice were analyzed by expression microarrays. (A) Unsupervised hierarchical clustering of the total expression profiles of each sample group. (B) Unsupervised PCA-based clustering of genes whose expression was significantly changed between groups. Shown are clusters of genes with common pattern of differential expression according to the two principal components (PC1 and PC2). No additional clusters or principal components were identified in the PCA. Data represent expression trajectories of individual genes (gray) and a mean trajectory (red) across sample groups; the number of genes in each cluster is indicated. (C) The expression of *Aicda* was analyzed in total splenocytes from B6.*Sle1.Sle3* mice without (Sle) or with (Sle/het) *Tcf4* haplodeficiency (top), or from *Tlr7*.Tg animals without (Tg) or with (Tg/CKO) DC-specific *Tcf4* CKO (bottom). The expression of the IFN-inducible gene *Ifi203* is shown as a control. Data represent relative expression in each sample group as determined by qRT-PCR (mean ± SD of 5 and 3 animals per group for Sle and Tg samples, respectively). *, $P \le 0.05$; **, $P \le 0.01$. (D) Spleen sections from WT, B6.*Sle1.Sle3* (Sle), or B6.*Sle1.Sle3 Tcf4*$^{+/-}$ (Sle/het) mice were stained for total B cells (B220, red) and GC B cells (PNA, green). Shown is overall splenic architecture (top row: bars 100 µm) and representative GCs (bottom row: bars 20 µm). Representative of 3 spleens per genotype.

and B6.*Sle1.Sle3* multigenic model. Unlike human SLE patients, these and other mouse SLE models do not manifest a prominent IFN signature (Perry et al., 2011); hence, we could not detect a consistent reduction of IFN-inducible genes. It is therefore likely that the role of pDCs in experimental SLE and possibly in human SLE patients goes beyond IFN production. Indeed, a recent study in human systemic sclerosis revealed an important role for chemokine production by pDCs (van Bon et al., 2014). In that respect, it is notable that *Tcf4* haplodeficiency profoundly decreased autoantibody production, GC reaction, and the ensuing glomerulonephritis in both SLE models. These data suggest a particular importance of pDCs in autoreactive B cell activation and plasma cell differentiation in SLE. This function of pDCs may be mediated through direct interaction with B cells (Jego et al., 2003; Shaw et al., 2010) and/or indirectly by supporting helper T cell differentiation (Cervantes-Barragan et al., 2012).

Our results suggest that TCF4-driven pDC expression program may be relevant in human SLE. Although *TCF4* polymorphism has not been implicated in SLE by genome-wide association studies, it is likely to be constrained by critical functions of TCF4 in brain development. In contrast, major SLE-associated genes, including transcriptional (*IRF7*, *IKZF1*, *PRDM1*, and *JAZF1*) and signaling (*TNFAIP3* and *BLK*) regulators (Deng and Tsao, 2010) represent direct targets of TCF4 in pDCs (Ghosh et al., 2010). Thus, these genes might contribute to SLE predisposition in part through their activity in the pDC lineage. In addition, our results highlight the beneficial effect of functional pDC impairment on SLE pathogenesis, providing the rationale for pDC-targeted therapeutic approaches. Indeed, pDC ablation or functional impairment would be less immunosuppressive than a global blockade of IFN signaling, and would target multiple pDC functions such as secretion of chemokines. Collectively, our data suggest the targeting of the pDC lineage (e.g., by depleting antibodies) as a viable therapeutic strategy to ameliorate SLE.

MATERIALS AND METHODS

Animals. All experiments were performed according to the investigator's protocol approved by the Institutional Animal Care and Use Committee of Columbia University. *Tcf4*$^{+/-}$ animals (Zhuang et al., 1996) were on pure 129SvEvTac background (>N12); all other animals were on pure C57BL/6 (B6) background (>N12). Pristane was administered i.p. into *Tcf4*$^{+/-}$ animals or *Tcf4*$^{+/-}$ littermates as previously described (Lee et al., 2008). *Tlr7*.Tg males (Y-linked transgenic line 7.6; Deane et al., 2007) were crossed with *Tcf4*$^{+/-}$ females to generate B6129F1 *Tcf4*$^{+/-}$ *Tlr7*.Tg males or *Tcf4*$^{+/+}$ *Tlr7*.Tg littermates. Age-matched B6129F1 males bred in the same colony were used as WT controls. For conditional targeting of Tcf4, *Tlr7*.Tg males carrying the *Itgax*-Cre transgene (Caton et al., 2007) were crossed with *Tcf4*$^{flox/flox}$

females (Bergqvist et al., 2000) to generate *Tcf4*$^{flox/+}$ *Tlr7*.Tg males with or without the Cre transgene. Age-matched B6 males bred in the same colony were used as WT controls.

For the cross with B6.*Sle1.Sle3* strain, a new null allele of *Tcf4* was derived by recombining the *Tcf4*^{flox} allele in the female germline using the *Tek*-Cre transgenic strain (The Jackson Laboratory). After crossing out the Cre transgene, *Tcf4*$^{+/-}$ animals were crossed to BcN.LmoJ animals homozygous for *Sle1*, *Sle2*, and *Sle3* loci (Morel et al., 2000; The Jackson Laboratory). The resulting *Tcf4*$^{+/-}$ animals heterozygous for *Sle1*, *Sle2*, and *Sle3* were backcrossed to BcN.LmoJ to achieve homozygosity for *Sle1* and *Sle3*. The integrity of *Sle* loci was confirmed by PCR genotyping for microsatellite markers spanning each locus. No differences in any SLE manifestations have been observed between male and female B6.*Sle1.Sle3* animals; thus, both male and female mice were included in the analysis along with age-matched B6 WT controls.

Flow cytometry. Suspensions of peripheral blood leukocytes or splenocytes were subjected to red blood cell lysis, washed, and stained with directly conjugated fluorescent antibodies to the indicated surface markers (eBioscience). The samples were acquired on the LSR II flow cytometer (BD) and analyzed using FlowJo software (Tree Star).

Autoantibody measurement. Immunoglobulin levels in the serum were determined by ELISA using alkaline phosphatase–conjugated antibodies to IgM, IgG, and IgG isotypes (SouthernBiotech). Anti-RNA and anti-dsDNA IgG concentrations were determined by ELISA as previously described (Blanco et al., 1991) using yeast RNA or calf thymus DNA as antigens.

Histopathology. 2-µm sections of formalin-fixed kidneys were stained with H&E and evaluated by a pathologist (V. D'Agati) who was blinded to sample identity. Mesangial and endocapillary proliferation, leukocyte infiltration, glomerular deposits, and apoptosis were scored separately on a scale from 0 (none) to 4 (highest) and added to yield a cumulative score. The percentage of cortical parenchyma with interstitial inflammation was also determined. To measure immune complex deposition, kidneys were fixed in 4% paraformaldehyde, dehydrated in 30% sucrose, and frozen in OCT (TissueTek). Frozen sections (5 µm) were stained with DAPI and PE-labeled goat anti–mouse IgG antibody (eBioscience). For the analysis of GC reaction, frozen spleen sections (5 µm) were stained with PE-labeled anti–mouse B220 (eBioscience) and biotin-conjugated peanut agglutinin (PNA; Vector Laboratories), followed by FITC-conjugated Streptavidin (eBioscience). Anti-nuclear antibodies were detected by staining fixed HEp-2 cells (MBL Bion) with mouse serum (1:100 dilution), followed by PE-labeled goat anti–mouse IgG and DAPI. Images were captured on a confocal fluorescent microscope (LSM 710 NLO) and processed by Zen software (Carl Zeiss).

Gene expression analysis. Total splenocytes from individual WT B6 ($n = 2$), B6.*Sle1.Sle3* ($n = 3$), or B6.*Sle1.Sle3 Tcf4*$^{+/-}$ ($n = 3$) animals at 30 wk were used for microarray analysis. Total RNA was isolated, reverse transcribed, amplified, labeled, and hybridized to Mouse Genome 1.0 ST arrays (Affymetrix). The results were gcRMA-normalized by the manufacturer's software and analyzed using the NIA Array software (Sharov et al., 2005). The qRT-PCR analysis of total splenocytes from individual mice was performed as previously described (Cisse et al., 2008; Ghosh et al., 2010).

Statistics. Unless noted otherwise, significance was estimated by nonparametric Mann-Whitney test.

Accession nos. Microarray data have been deposited in the Gene Expression Omnibus (GEO) database under the accession no. GSE57324.

Online supplemental material. Dataset S1 shows genome-wide expression analysis of splenocytes from B6.*Sle1.Sle3* mice with or without *Tcf4* haplodeficiency. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20132522/DC1.

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