Histone Deacetylase Inhibitors Upregulate B Cell microRNAs That Silence AID and Blimp-1 Expression for Epigenetic Modulation of Antibody and Autoantibody Responses

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Histone Deacetylase Inhibitors Upregulate B Cell microRNAs That Silence AID and Blimp-1 Expression for Epigenetic Modulation of Antibody and Autoantibody Responses

Clayton A. White,*†,1,2 Egest J. Pone, † Tonika Lam,*† Connie Tat,*† Ken L. Hayama, † Guideng Li,*†,3 Hong Zan,*†,1 and Paolo Casali*†

Class-switch DNA recombination (CSR) and somatic hypermutation (SHM), which require activation-induced cytidine deaminase (AID), and plasma cell differentiation, which requires B lymphocyte–induced maturation protein-1 (Blimp-1), are critical for the generation of class-switched and hypermutated (mature) Ab and autoantibody responses. We show that histone deacetylase inhibitors valproic acid and butyrate dampened AICDA/Aicda (AID) and PRDM1/Prdm1 (Blimp-1) mRNAs by upregulating miR-155, miR-181b, and miR-361 to silence AICDA/Aicda, and miR-23b, miR-30a, and miR-125b to silence PRDM1/Prdm1, in human and mouse B cells. This led to downregulation of AID, Blimp-1, and X-box binding protein 1, thereby inhibiting CSR, SHM, and plasma cell differentiation without altering B cell viability or proliferation. The selectivity of histone deacetylase inhibitor–mediated silencing of AICDA/Aicda and PRDM1/Prdm1 was emphasized by unchanged expression of HoxC4 and Irf4 (important inducers/modulators of AICDA/Aicda), Rev1 and Ung (central elements for CSR/SHM), and Bcl6, Bach2, or Pax5 (repressors of PRDM1/Prdm1 expression), as well as unchanged expression of miR-19a/b, miR-20a, and miR-25, which are not known to regulate AICDA/Aicda or PRDM1/Prdm1. Through these B cell–intrinsic epigenetic mechanisms, valproic acid blunted class-switched and hypermutated T-dependent and T-independent Ab responses in C57BL/6 mice. In addition, it decreased class-switched and hypermutated autoantibodies, ameliorated disease, and extended survival in lupus MRL/Fas−/− mice. Our findings outline epigenetic mechanisms that modulate expression of an enzyme (AID) and transcription factors (Blimp-1 and X-box binding protein 1) that are critical to the B cell differentiation processes that underpin Ab and autoantibody responses. They also provide therapeutic proof-of-principle in autoantibody-mediated autoimmune.

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Abbreviations used in this article: 7-AAD, 7-aminoactinomycin D; AID, activation-induced cytidine deaminase; ANA, anti-nuclear Ab; Blimp-1, B lymphocyte–induced maturation protein-1; C(H)4, constant H chain; C3P, chromatin immunoprecipitation; CSR, class switch DNA recombination; FBS-RPMI, RPMI 1640 medium with 10% FBS, 50 mM 2-ME, and 10 μg/ml antibiotic-antimycotic mixture; GC, germinal center; HDAC, histone deacetylase; HDAC inhibitor; IκBα, inhibitory region of Cα gene; miRNA, microRNA; mut, mutant; PNA, peanut agglutinin; qPCR, quantitative PCR; qRT-PCR, quantitative RT-PCR; RU, relative unit; SCFA, short-chain fatty acid; SHM, somatic hypermutation; TSA, trichostatin A; UTR, untranslated region; VPA, valproic acid; Xbp-1, X-box–binding protein 1.
stimuli (e.g., IL-4, TGF-β, or IFN-γ), which induce selected intervening region (IgH)-S-C14 germline transcription, thereby directing CSR to specific isotypes (1, 15). It is then downregulated in memory B cells and plasma cells to preserve the specificity, affinity, and isotype of the expressed BCR and Ab (1, 2). Terminal plasma cell differentiation is critically dependent on the transcriptional repressor Blimp-1. This extinguishes the proliferative mature B cell gene expression program and drives the expression of X-box–binding protein 1 (Xbp-1), which induces secretory pathway genes for Ig secretion (4, 16, 17).

As we contended, an additional and critical level of regulation of AID expression would occur through epigenetic modifications and factors (2, 3, 18). As we also contended, epigenetic modifications and factors, including histone posttranslational modifications, DNA methylation, and microRNAs (miRNAs), interact with genetic programs to regulate B cell CSR, SHM, and plasma cell differentiation, thereby informing the Ab response (3). Accordingly, we suggested that, in addition to DNA methylation of the Aicda promoter (19) and histone acetylation of the Aicda locus (20), selected miRNAs provide a more important mechanism of modulation of AID expression (2, 3, 18). miRNAs likely play important roles in B cell development and peripheral differentiation, as well as T cell stage-specific differentiation and autoimmunity (18, 21–26).

Some miRNAs, including miR-155, miR-181b, and miR-361, would negatively regulate AID expression (2, 27–30), whereas miR-30a (31) and miR-125b (32, 33) would negatively regulate Blimp-1 expression. These miRNAs bind to evolutionarily conserved miRNA target sites in the 3′ untranslated region (UTR) of Aicda and Prdm1 miRNAs and cause degradation of the mRNA transcripts and/or inhibit their translation.

Histone deacetylase (HDAC) inhibitors (HDIs) were shown to alter gene expression by altering chromatin accessibility (34–37). In immune cells, these epigenetic modifiers exert modulatory effects, even at moderate concentrations. By using two well-characterized short-chain fatty acid (SCFA) HDIs, valproic acid (VPA) or sodium valproate (VPA), valproic acid and sodium butyrate (butyrate) (39), we tested the hypothesis that HDIs regulate intrinsic B cell functions that are critical in shaping effective Ab and autoantibody responses. VPA is a U.S. Food and Drug Administration–approved drug, which, as marketed under different brand names, is widely used as an anticonvulsant and a mood stabilizer. It selectively inhibits class I HDACs, particularly HDAC1 and HDAC2, and, less effectively, class IIa HDACs, of the four HDAC classes identified in mammals (38, 39). Butyrate is a major metabolite in the digestive tract, arising from bacterial fermentation of dietary fibers (41, 42), and it is widely used as an intestinal irritant. Butyrate modulates gene expression by selectively inhibiting HDAC1, and, less effectively, other members of class I and class IIa HDACs (39).

We addressed the ability of VPA and butyrate to modulate AID and Blimp-1 expression, CSR, SHM, and plasma cell differentiation in human and mouse B cells in vivo and in vitro. In addition, we analyzed the role of HDIs as epigenetic modifiers of selected B cell miRNAs that silence Aicda and Prdm1 in Ab and autoantibody responses. Finally, we evaluated the impact of VPA on NP-CGG and NP-LPS class-switched and hypermutated Ab responses in normal mice, as well as on the autoantibody response in lupus-prone MRL/Fas(+/−) mice. Our findings outline important modulations of epigenetic regulation of AID and Blimp-1 expression, unveil new approaches to modulation of T-dependent and T-independent Ab responses, and provide a proof-of-principle therapeutics study in autoantibody–mediated autoimmunity.
and biotin-anti-CD138 mAb (281-2; BD Biosciences), followed by FITC-streptavidin (11-4317-87; eBioscience) or PE-streptavidin (12-4317-87; eBioscience), FITC-anti-CD3 mAb (17A2; BioLegend), FITC-anti-CD4 (GK1.5; BioLegend), and/or allophycocyanin-anti-CD8 mAb (53-6.7; BD Biosciences). For intracellular staining, B cells were fixed in 150 μl formaldehyde (3.6%) for 10 min at 25˚C. In the case of IgE intracellular staining, cells were trypsinized and then fixed (47). Cells were then permeabilized in cold methanol (90%) for 30 min on ice before staining with biotin-anti-IgM or -IgG, followed by PE-streptavidin, PE-Cy7-anti-B220 mAb (RA3-6B2; eBioscience), FITC-anti-IgM mAb (II/41; BD Biosciences), allophycocyanin-anti-IgG1 mAb (A85-1; BD Biosciences), and/or PE-anti-IgE mAb (23G3; eBioscience). FACS was performed on single spleen cell suspensions. Cells were surface stained with PE-anti-CD19 (BD Biosciences), 7-AAD, and biotin-anti-CD138, followed by FITC-streptavidin. CD19+CD138+ B cells (consisting of a large proportion of germinal center [GC] B cells, referred to as “total” B cells) and CD19+CD138− plasma cells were then sorted using a Cytomation MoFlo cell sorter (Beckman Coulter) and frozen at −80˚C until used for gene-expression analysis. Annexin V analysis for apoptotic cells was performed using the Annexin V/FITC Apoptosis Detection Kit II (556570; BD Biosciences) followed by fluorescence-activated cell sorter (Beckman Coulter) and frozen at 37˚C. The cells were then cultured in the presence of LPS alone or LPS + IL-4 for 4 d before being stained with PE-anti-B220 mAb and PE-anti-B220 mAb, which was fixed with ethanol (35%), washed four times with PBS, and coated with 100 × 10^6 cells/mL CFSE at a density of 1 × 10^6 cells/ml and then washed in FBS-RPMI. Spleen cells were cultured in the presence of 20 ng/mL IL-2 alone or with LPS (5 μg/mL) + IL-4 (4 μg/mL), or CD154 (1 U/ml) + IL-4 (5 μg/mL) in the presence of nil, VPA (1000 μM), or butyrate (1000 μM) for 60 h. Cells were harvested and lysed in Laemmli buffer. Cell extracts containing equal amounts of protein (20 μg) were fractionated through SDS-PAGE (10%). The fractionated proteins were transferred onto polyvinylidene difluoride membranes (Bio-Rad) overnight (30 V) at 4˚C. After blocking and overnight incubation at 4˚C with anti-AID (ZA001; Invitrogen), anti–Blimp-1 mAb (6D3; eBioscience), or anti–β-actin mAb (AC-15; Sigma-Aldrich), the membranes were incubated with HRP-conjugated secondary Abs. After washing with PBS–Twee 20 (0.05%), bound HRP-conjugated Abs were detected using Western Lightning Plus-ECL reagents (PerkinElmer Life and Analytical Sciences).

**Immunoblotting**

To analyze IgSHM in response to NP immunization, spleen B cells were isolated from C57BL/6 mice that were immunized with NP6-CGG and given untreated water or HDI water. Rearranged V<sub>186.2</sub>D<sub>jH</sub>−C<sub>ε</sub> DNA encoding the anti–CD19 mAb was amplified using a V<sub>186.2</sub> leader-specific forward primer together with a reverse C<sub>ε</sub>specific primer (13) and Phusion high-fidelity DNA polymerase (New England BioLabs). PCR conditions were 98˚C for 10 s, 60˚C for 45 s, and 72˚C for 1 min for 30 cycles. To analyze spontaneous SHM and deletion in MRL/Fas<sup>−/−</sup> mice, CD19+PNA<sup>−</sup> GC B cells were isolated from Peyer’s patches and used for extraction of genomic DNA. The rearranged V<sub>186.2</sub> DNA region (downstream of rearranged V<sub>186.2</sub>D<sub>jH</sub>−C<sub>ε</sub>), which is targeted by SHM but not subjected to any positive- or negative-selection pressure, was amplified by nested PCR using Phusion DNA polymerase and two V<sub>3551</sub> framework region 3′-specific forward primers and two reverse primers specific for sequences downstream of J<sub>C</sub>, which yielded DNA ~960 bp if a J<sub>C</sub> rearrangement occurred (49). Amplification conditions for both the first- and second-round PCRs were 98˚C for 30 s, 60˚C for 45 s, and 72˚C for 1 min. PCR products were cloned into the pCR-Blunt II-TOPO vector (Invitrogen) and sequenced. Sequences were compared with the germline V<sub>186.2</sub> or intrinsic J<sub>iH</sub>−ε<sub>i</sub> DNA region sequences using MacVector software (MacVector) for analysis of point mutations or deletions. For the intrinsic J<sub>iH</sub>−ε<sub>i</sub> DNA region, only a 700-bp region from rearrangements involving J<sub>iH</sub>−ε<sub>i</sub> was analyzed.

**Quantitative RT-PCR of mRNAs and miRNAs**

For quantification of mRNA, pri-miRNA, germline I<sub>C</sub>−C<sub>ε</sub>, and post-recombination I<sub>C</sub>−C<sub>ε</sub> and mature V<sub>186.2</sub>D<sub>jH</sub>−C<sub>ε</sub> transcripts, RNA was extracted from 0.2–5 × 10<sup>6</sup> cells using either TRIzol reagent (Invitrogen) or an RNeasy Plus Mini Kit (QiAGEN). Residual DNA was removed from the extracted RNA with gDNA elution columns (QiAGEN). CDNA was synthesized from total RNA with the SuperScript III First-Strand Synthesis System (Invitrogen) using oligo-dT primer. Transcription expression was measured by quantitative RT-PCR (qRT-PCR) with specific primers (Supplemental Table I) using a MyiQ Real-Time PCR Detection System to measure SYBR Green (iQ SYBR Green Supermix; both from Bio-Rad) incorporation with the following protocol: 95˚C for 15 s, 40 cycles of
94°C for 10 s, 60°C for 30 s, and 72°C for 30 s. Data acquisition was performed during the 72°C extension step. Melting-curve analysis was performed from 72 to 95°C. For quantification of mature miRNA transcripts, RNA was extracted from 0.2–5 × 10^6 cells using an miRNeasy Mini Kit and then reverse transcribed with a miScript II RT Kit (both from QIAGEN) using the miScript HiSpec buffer. A Bio-Rad MyiQ Real-Time PCR Detection System was used to measure SYBR Green (miScript SYBR Green PCR Kit; QIAGEN) incorporation, according to the manufacturer’s instructions. Mature miRNA forward primers (Supplemental Table I) were used at 250 nM in conjunction with the QIAGEN miScript Universal Primer and normalized to expression of small nuclear/nuclear RNAs (U6/RNU61/2, Snord61/SNORD61, Snord68/SNORD68, and Snord70/ SNORD70). The ΔΔCt method was used for data analysis of qRT-PCR experiments.

Histone acetylation of miRNA host genes and Aicda promoter by chromatin immunoprecipitation and quantitative PCR

Chromatin immunoprecipitation (ChIP) assays were performed as previously described (15, 48, 50). B cells (1 × 10^7) were treated with formaldehyde (1% w/v) for 10 min at 25°C to cross-link chromatin, washed once in cold PBS with protease inhibitors (Roche), and resuspended in lysis buffer (20 mM Tris-HCl, 200 mM NaCl, 2 mM EDTA, 0.1% w/v SDS, and protease inhibitors [pH 8]). Chromatin was sonicated to yield DNA fragments (~200–1000 bp in length), precleared with protein A agarose beads (Pierce), and incubated with anti-acetyl histone H3 mAb (H3K9ac/K14ac; 17-615; Millipore) at 4°C overnight. Immune complexes were precipitated by Protein A agarose beads, washed, and eluted (50 mM Tris-HCl, 0.5% SDS, 200 mM NaCl, 100 μg/ml proteinase K [pH 8]), followed by incubation at 65°C for 4 h. DNA was purified using a QIAquick PCR purification kit (QIAGEN). The miRNA host gene promoter region DNA was amplified from immunoprecipitated chromatin by quantitative PCR (qPCR) using appropriate primers (Supplemental Table I). Data were normalized to input chromatin DNA and depicted as relative abundance of each amplicon.

 Luciferase 3' UTR reporter assays

The partial 3'UTRs of Aicda mRNA (nt 691–1168 of NM_009645.2, National Center for Biotechnology Information) and Prdm1 mRNA (nt 2652–5101 of NM_007548.3, National Center for Biotechnology Information) were PCR amplified from spleen B cell cDNA and cloned into the pMIR-REPORT miRNA Expression Reporter Vector System (Invitrogen), which allows for analysis of 3'UTR-mediated regulation of firefly luciferase activity. The mutant (mut) Aicda 3' UTR containing point mutations (Supplemental Fig. 2E) was generated by PCR-based mutagenesis of the Aicda 3' UTR pMIR-REPORT vector using Phusion DNA polymerase (New England BioLabs.). Point mutations were introduced into the Prdm1 3' UTR, as described above, together with an additional deletion (nt 3680–5101) that were deleted be PCR to generate mut Prdm1 3' UTR. The sequence of constructs was confirmed by two independent sequencing reactions. Reporter constructs were cotransfected with the pRL-TK vector (Promega), which drives constitutive expression of Renilla reniformis luciferase, into mouse CH12F3 B cells by electroporation (250V and 900 μF; Bio-Rad). Transfected CH12F3 B cells were then cultured in FBS-RPMI for 1.5 h to allow for reporter gene expression. The ability of VPA to repress reporter activity was determined by firefly luciferase activity and normalized to Renilla luciferase activity, according to the manufacturer’s instructions, using the Dual-Luciferase Reporter Assay System (Promega).

 Methylation analysis of Aicda promoter DNA

Genomic DNA was treated with sodium bisulfite using the EpiTect Bisulfite Kit (QIAGEN), according to the manufacturer’s instructions. Bisulfite-treated DNA was amplified by PCR using GoTaq Hot Start Polymerase (Promega). The primers for bisulfite-sequencing PCR (Supplemental Table I) were designed using MethPrimer (http://www.urogene.mshmeriter/index1.html). PCR products were purified with a QIAquick PCR purification kit (QIAGEN) and sequenced before or after being cloned into the pCR-Blunt II-TOPO vector.

 Lupus mice: autoantibodies, pathology, and disease

MRL/Fas(+/−) mice (The Jackson Laboratory) were housed in the University of California, Irvine and the UT Health Science Center, San Antonio, vivaria and provided with autoclaved food and deionized water. MRL/Fas(+/−) mice were started on HDI water ad libitum at 6 or 17 wk of age or were on untreated water throughout their life and sacrificed when moribund. Anti-nuclear Ab (ANA) and anti-dsDNA Ab titers were determined in sera. For ANA assays, sera were serially diluted in PBS (from 1:40 to 1:160), incubated on ANA substrate slides (HeP-2 cell–coated slides; MBL-BION), and detected with a 1:1 mixture of FITC–anti-IgG1 and FITC–anti-IgG2a mAbs (R19-15; BD Biosciences). Images were acquired with a 40× objective on an Olympus CX41 fluorescence microscope. Anti-dsDNA IgG and IgG2a Ab titers were measured in sera of MRL/Fas(+/−) mice by ELISA, as previously described (14). Titters were expressed in RU, defined as the dilution factor needed to reach 50% of binding. Results were analyzed using GraphPad Prism software (GraphPad). Skin lesions were scored on a scale of 0 to 3, with 0 = none, 1 = mild (snout and ears), 2 = moderate (<2 cm snout, ears, and inscapular), and 3 = severe (>2 cm snout, ears, and inscapular). To assess kidney pathology, kidneys from MRL/Fas(+/−) mice were either frozen in Tissue-Tek O.C.T. compound (Sakura Finetek USA) on dry ice for immunofluorescence or fixed in paraformaldehyde (4%) and embedded in paraffin for H&E staining. For immunofluorescence, 4-μm sections were prepared by cryostat, loaded onto positively charged slides, fixed in cold acetone, and stained with a mixture of FITC-labeled rat mAb to mouse IgG1 or mouse IgG2a. Cover slips were mounted using ProLong Gold Antifade Reagent with DAPI before examination with an Olympus CX41 fluorescence microscope. For H&E staining, kidneys were fixed overnight in paraformaldehyde (4%), serially passed into ethanol (30%) for 1 h, ethanol (50%) for 1 h, and ethanol (70%) overnight, and embedded in paraffin; 4-μm sections were cut for H&E staining.

Statistical analyses

All statistical analyses were performed using Excel (Microsoft) or GraphPad Prism software. Differences in Ig titers, CSR, and RNA transcript expression were analyzed with a Student paired (in vitro) or unpaired (in vivo) t test, assuming two-tailed distributions. Differences in the frequency and spectrum of somatic point mutations were analyzed with χ^2 tests. Differences in lifespan between mice that were administered untreated water or HDI water were compared by Kaplan–Meier curves and calculated using the Mantel–Cox log-rank test.

Results

CSR and SHM in Ab responses are inhibited by HDIs

To address the effect of HDIs on a T-dependent response, we injected C57Bl/6 mice with NP_{16}-CGG, which preferentially induces NP-binding IgG1, 1 d after starting them on the HDI water; these mice drank HDI water at a comparable or higher rate than did mice drinking untreated water. Mice drinking HDI water showed a reduced IgG1 (including high-affinity NP-binding IgG1), but not IgM, response to NP, even after a second injection of NP_{16}-CGG (Fig. 1A, 1B); reduced class-switched NP-binding IgG1 titers occurred in the context of reduced total IgG1, IgG3, and IgG2b (IgG2b data not shown) but not IgM (Fig. 1C). They were associated with reduced proportions of GC IgG1*, but not IgM*, B cells and a reduced frequency of somatic point mutations (by >65%) in V_{H}L-D_{H}C_{V}Y1 transcripts, with no significant alteration in spectrum of the residual mutations (Fig. 1D, 1E, Supplemental Fig. 1A), suggesting that this HDI reduced AID expression to impair the class-switched and hypermutated Ab response. In these mice, HDI had no significant effect on T (CD3*) or B (B220*) cell number (Fig. 1F). A “direct” HDI effect on B cells was indicated by the reduced T-independent IgG3 response in HDI-treated mice injected with T-independent NP-LPS. These mice showed reduced titers of (high-affinity) NP-binding IgG3, as well as fewer total IgG3* B cells and NP-binding IgG3 Ab-forming cells (Fig. 1G, H). Thus, HDIs can dampen class-switched–specific T-dependent and T-independent Ab responses.

HDIs inhibit CSR without altering B cell viability or proliferation

To further define the impact of HDIs on CSR, we used appropriate stimuli to induce B cells to switch to IgG1, IgG3, IgA, or IgE in the presence of VPA, butyrate (0–1000 μM), or TSA (0–20 nM). These HDIs reduced, in a dose-dependent fashion, CSR to IgG1, IgG3, IgA, and IgE (Figs. 2A, 2B, 3A–C, Supplemental Fig. 1B).
without affecting B cell division (Fig. 2C, 2D), viability, or apoptosis in vivo or in vitro (Fig. 4A, Supplemental Fig. 1C, 1D). Expression of the antiapoptotic genes Bcl2, Mcl1, and Bcl2l1 (Bcl2l1 encodes Bcl-xL), which enhance B cell and plasma cell survival, was unaltered or increased by HDIs in vivo and in vitro (Supplemental Fig. 1F, 1H). The reduction in IgG1+ and IgG3+ B cells reflected a lower proportion of class-switched cells/round of cell division (Fig. 2C, 2D, Supplemental Fig. 2A) and was associated with decreased titers of IgG1, IgG3, IgA, and IgE in culture fluids (Fig. 3D, 3E). HDI inhibition of CSR was further confirmed by decreased mature V H DJ H -C γ 1, V H DJ H -C γ 3, V H DJ H -C α , and V H DJ H -C ε transcripts and postrecombination I m -C γ 1, I m -C γ 3, I m -C α , and I m -C ε transcripts in the presence of normal levels of the respective germline I H-CH transcripts, which are necessary for initiation of CSR (Supplemental Fig. 2B–D). Thus, HDIs significantly reduce CSR, without altering B cell viability or proliferation.

HDIs inhibit plasma cell differentiation but not survival

HDIs-mediated impairment of Ab responses was not due to alteration of GC development, because GC structure, GC B cell proportion, and B cell viability and proliferation were unaltered in NP-CGG–injected mice treated with VPA (Figs. 3G, 4A), nor did it stem from alteration of the cell cycle, as shown by the normal proportion of B cells in G 0 /G 1 , S, or G 2 /M upon stimulation in vitro (Fig. 4B). Rather, it reflected an HDI-mediated inhibition of B cell division (Fig. 2C, 2D), viability, or apoptosis in vivo or in vitro (Fig. 4A, Supplemental Fig. 1C, 1D). Expression of the antiapoptotic genes Bcl2, McI1, and Bcl2l1 (Bcl2l1 encodes Bcl-xL), which enhance B cell and plasma cell survival, was unaltered or increased by HDIs in vivo and in vitro (Supplemental Fig. 1F, 1H). The reduction in IgG1+ and IgG3+ B cells reflected a lower proportion of class-switched cells/round of cell division (Fig. 2C, 2D, Supplemental Fig. 2A) and was associated with decreased titers of IgG1, IgG3, IgA, and IgE in culture fluids (Fig. 3D, 3E). HDI inhibition of CSR was further confirmed by decreased mature V H DJ H -C γ 1, V H DJ H -C γ 3, V H DJ H -C α , and V H DJ H -C ε transcripts and postrecombination I m -C γ 1, I m -C γ 3, I m -C α , and I m -C ε transcripts in the presence of normal levels of the respective germline I H-CH transcripts, which are necessary for initiation of CSR (Supplemental Fig. 2B–D). Thus, HDIs significantly reduce CSR, without altering B cell viability or proliferation.

FIGURE 1. HDIs reduce CSR and SHM in Ab responses to NP-CGG and NP-LPS. Eight-week-old C57BL/6 mice were started on HDI water 1 d before injection with NP 16-CGG or NP-LPS. (A) Titters of high-affinity NP 3-binding IgM or IgG1 (RU) in serum 10 d after NP 16-CGG injection. Each symbol represents an individual mouse (n = 5). (B) NP 3-binding IgG1 titers (RU) in serum 28 d after initial NP 16-CGG injection (7 d after booster NP 16-CGG injection). Each symbol represents an individual mouse (n = 5). (C) Titters of total IgM, IgG1, or IgG3 in serum 10 d after NP 16-CGG injection (n ≥ 5 mice). (D) Surface IgM and IgG1 expression in spleen B220+PNAhi GC B cells 10 d after NP 16-CGG injection. Data are representative of three independent experiments. (E) Somatic point mutations in the V 186.2 region of V 186.2 DJ H -C γ 1 transcripts amplified from spleen B cells 10 d after NP 16-CGG injection. Sequence data were pooled from three mice in each group. Pie charts depict the proportions of sequences that carry 1, 2, 3, and so on point mutations over the 294-bp V 186.2 region of V 186.2 DJ H -C γ 1 transcripts. In the center is the number of independent sequences analyzed; listed below the pie charts is the overall mutation frequency (changes/base). (F) Surface B220 and CD3 expression in spleen cells 10 d after NP 16-CGG injection. Data are representative of three independent experiments. (G) NP 3-binding IgG3 titers (RU) in serum 28 d after initial NP-LPS injection (7 d after booster NP-LPS injection). Each symbol represents an individual mouse (n = 4). (H) ELISPOT analysis of NP 3-binding IgG3 Ab-forming cells (AFCs) in spleens 28 d after initial NP-LPS injection (7 d after booster NP-LPS injection). Data are from three independent experiments. Scale bars, 1 mm. Numbers indicate NP 3-binding IgG3 AFCs/1 × 10 6 spleen cells (n = 3 mice). The p values were determined using an unpaired t test.

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differentiation into plasma cells in vivo and in vitro (Fig. 4C–E). This was not associated with decreased plasma cell survival, as shown by normal plasma cell viability and apoptosis, as well as elevated \(Bcl2\), \(Mcl1\), and \(Bcl2\) expression (Fig. 4D, Supplemental Fig. 1E, 1G, 1I) and normal transcripts of \(Il6\) (data not shown), which enhances Blimp-1 expression (51). Thus, HDIs inhibit plasma cell differentiation without altering plasma cell survival.

The HDI-impaired Ab response was associated with reduced CSR and SHM, which are initiated by AID, and reduced plasma cell differentiation, which is orchestrated by Blimp-1. Expression of \(Aicda\), \(Prdm1\), and \(Xbp1\) [\(Xbp1\) is under control of Blimp-1 and its gene product promotes Ig secretion in plasma cells (16)] was significantly reduced by HDIs in vivo. Expression of \(Ung\), which encodes for Ung that plays a role downstream of AID in CSR and SHM (1), and \(Bcl6\), which encode Bcl-6, a master regulator of the GC reaction and a \(Prdm1\) repressor (52, 53), were unchanged (Fig. 5). Consistent with these in vivo findings, the expression of \(Aicda\), \(Prdm1\), and \(Xbp1\) was silenced in a dose-dependent fashion by HDIs in stimulated B cells in vitro (Fig. 5B–D). This contrasted with the unchanged expression of \(Irf4\) (encoding Irf4, a transcription factor that regulates CSR, SHM, and plasma cell differentiation) (54), \(Bcl6\), \(Ung\), \(HoxC4\) (encoding the AID-inducing \(HoxC4\) transcription factor) (12–14), \(Rev1\) (encoding the CSR scaffold protein Rev1) (48), and \(Bach2\) and \(Pax5\) (encoding Bach2 and Pax5, both repressors of \(Prdm1\)) (55, 56) (Fig. 5C, data not shown). The downregulation of \(Aicda\) and \(Prdm1\) transcripts greatly affected the expression of AID and Blimp-1 proteins (Fig. 5E). Thus, the inhibition of CSR, SHM, and plasma cell differentiation by HDIs reflects the HDI-mediated downregulation of AID and Blimp-1.

**FIGURE 2.** Dose-dependent inhibition of CSR by HDIs in B cells. (A) Surface expression of B220 and IgG1 or IgG3 on B cells stimulated with LPS + IL-4 or CD154 + IL-4 (for CSR to IgG1) or LPS (for CSR to IgG3) in the presence of nil or increasing doses of VPA (concentrations comparable to or lower than serum concentrations of VPA-treated mice) for 4 d. (B) Surface expression of B220 and IgG1 or IgG3 or intracellular expression of B220 and IgE in B cells stimulated with CD154 + IL-4 (for CSR to IgG1 and IgE) or LPS + TGF-\(\beta\) + IL-4 + IL-5 + anti-IgD dextran (for CSR to IgA) in the presence of nil or increasing doses of butyrate for 4 d. Proliferation of lymph node B220\(^+\) B cells labeled with CFSE and stimulated for 4 d with LPS + IL-4 in the presence of nil, VPA (500 \(\mu\)M) (C), or butyrate (500 \(\mu\)M) (D). Progressive left shift of fluorescence intensity indicates B220\(^+\) B cell division (left panels). Cell divisions are plotted by vertical lines versus IgG1 surface density, among B220\(^+\) cells (middle panels). The percentages of IgG1+B220\(^+\) B cells among total B220\(^+\) B cells that had completed the same number of divisions when cultured for 4 d in the presence of nil, VPA, or butyrate (right panels). Data are representative of three independent experiments.

HDIs upregulate miRNAs that target Aicda and Prdm1 transcripts in B cells

Enhancement of histone acetylation, a function of HDIs, which generally upregulate gene expression, is at odds with the decreased expression of AID/Aicda and Blimp-1/Prdm1 by HDIs in vivo and in vitro (Fig. 5). In fact, in B cells induced to undergo CSR, HDIs did not alter histone H3 acetylation in the \(Aicda\) promoter, nor did they alter DNA methylation [HDACs were suggested to interact with DNA methyltransferases (57)] (Fig. 6A–C), raising the possibility that HDIs upregulated the expression of gene(s), which, in turn, negatively regulated \(Aicda\) and \(Prdm1\). HDIs can modulate expression of miRNAs (36), which silence target miRNAs by inducing their degradation and/or reducing their translation. In this context, \(Aicda\) can be silenced by miR-155, miR-181b, and miR-361 (2, 3, 18, 27–30); \(Prdm1\) can be targeted by miR-23b (our prediction, using
mRNA 3

in Aicda mutation or deletion of the target sites of miR-155 and miR-181b of Aicda tors. These were used to transfect mouse CH12F3 B cells that can on HDI water or untreated water and injected with NP16-CGG for 10 d (as in Fig. 1). GC B cells were identified by staining with PE–anti-B220 mAb and Prdm1 mediated by upregulation of miRNAs that directly target transcripts Prdm1.

To prove that HDI inhibition of AID and Blimp-1 expression was transcribed by guest on June 9, 2017 http://www.jimmunol.org/ Downloaded from

FIGURE 3. HDIs inhibit CSR, as well as IgG, IgA, and IgE production, in a dose-dependent fashion, but they do not affect GC formation. (A) Surface expression of B220 and IgA in B cells stimulated with CD154 or LPS + TGF-β + IL-4 + IL-5 + anti-IgD dextran in the presence of nil or increasing doses of VPA for 4 d. (B) Intracellular expression of IgE in B cells stimulated with CD154 + IL-4 in the presence of nil or increasing doses of VPA for 4 d. (C) Intracellular expression of IgM and IgG1 in B cells stimulated with LPS + IL-4 for 4 d in the presence of nil or VPA. (D) IgG1, IgG3, IgA, or IgE in culture fluids of B cells stimulated with LPS + IL-4, LPS alone, LPS + TGF-β + IL-4 + IL-5 + anti-IgD dextran, or CD154 + IL-4, respectively, for 7 d in the presence of nil or increasing doses of VPA. (E) IgG1, IgA, and IgE in culture fluids of B cells stimulated with CD154 + IL-4 or LPS + TGF-β + IL-4 + IL-5 + anti-IgD dextran for 7 d in the presence of nil or butyrate. Data are from three independent experiments (mean and SEM). (F) Proportions of IgG1+ plasmablasts (B220+CD138+) as measured by surface expression of PNA-binding lectin, green). Spleen sections prepared from mice that were on HDI water or untreated water and injected with NP16-CGG for 10 d (as in Fig. 1). GC B cells were identified by staining with PE–anti-B220 mAb and FITC-PNA. Data are representative of three independent experiments. Scale bars, 50 μm.

TargetScan.org, mirNA.org, and miRbase.org) and was suggested to be targeted by mir-30a and mir-125b (3, 18, 31–33) (Supplemental Fig. 2E). We found that mir-155, miR-181b, miR-361, miR-23b, miR-30a, and miR-125b were upregulated by VPA in B cells in vivo; in purified B cells induced to undergo CSR and plasma cell differentiation in vitro, irrelevant miRNAs miR-19a/b, miR-20a, and miR-25, which are not known to regulate Aicda, Prdm1, or Xbp1, were unchanged in B cells in vivo and in vitro (Fig. 7A, 7B). Primary miRNA transcripts pri–miR-155 and pri–miR-181b, which are processed by Drosha and Dicer to give rise to mature miRNAs, also were upregulated, suggesting that HDIs upregulate miRNA host gene transcription (Fig. 6D). Accordingly, miRNA upregulation in stimulated B cells was accompanied by increased overall histone H3 acetylation of the host genes encoding these miRNAs (Fig. 7C). Thus, HDIs upregulate miRNAs that target Aicda and Prdm1 mRNA 3′ UTRs and, therefore, can silence these miRNAs.

Selected B cell miRNAs upregulated by HDIs silence Aicda and Prdm1 transcripts

To prove that HDI inhibition of AID and Blimp-1 expression was mediated by upregulation of miRNAs that directly target Aicda and Prdm1 mRNA 3′UTRs, we cloned either wild-type or mut 3′UTRs of Aicda and Prdm1 miRNAs (mut 3′UTRs were constructed by mutation or deletion of the target sites of mir-155 and mir-181b in Aicda mRNA 3′UTR or mir-23b, mir-30a, and mir-125b in Prdm1 mRNA 3′UTR) into pMIR-REPORT luciferase reporter vectors. These were used to transfect mouse CH12F3 B cells that can be induced to undergo CSR at a high rate. Like in primary B cells, VPA upregulated mir-155, miR-181b, miR-361, miR-23b, miR-30a, and miR-125b expression in CH12F3 B cells induced to undergo CSR (Fig. 7D). We then measured the ability of VPA to repress luciferase activity using reporter constructs containing wild-type or mut 3′UTRs of Aicda and Prdm1 mRNAs that were transfected into CH12F3 B cells (Fig. 7E; Supplemental Fig. 2E). The luciferase reporter activity was reduced by VPA in B cells transfected with reporter constructs containing wild-type Aicda or Prdm1 3′UTRs but not those transfected with reporter constructs containing Aicda or Prdm1 mut 3′UTRs (Fig. 7F). In B cells transfected with reporter constructs containing wild-type Aicda or Prdm1 3′UTRs, the degree of inhibition of luciferase activity was significant, despite the relatively low dose of VPA used (250 μM) and the omission of some additional miRNA target sites in the 3′UTR of Aicda mRNA, thereby emphasizing the potency of the HDI-mediated upregulation of miRNAs on B cell gene expression. Thus, VPA silences AID and Blimp-1 expression in B cells through upregulation of selected miRNAs that directly target Aicda and Prdm1 mRNA 3′UTRs.

HDIs silence AICDA and PRDM1 in human B cells to inhibit CSR and plasma cell differentiation

Next, we determined whether HDIs also inhibit CSR and plasma cell differentiation in human B cells. We stimulated purified human IgD+ B cells with CD154 + IL-21 and IL-4 or TGF-β. Like in mouse B cells, VPA and butyrate effectively inhibited CSR to IgG, IgA, and IgE in human B lymphocytes, as well as plasma cell
differentiation in a dose-dependent fashion without altering B cell viability (Fig. 8A–D). VPA increased expression of miR-155, miR-181b, miR-361, miR-23b, miR-30a, and miR-125b, which [as reported or as predicted by us (2, 3, 18, 27–33)] target miRNA binding sites in 3'UTR of human and mouse AICDA/Aicda or PRDM1/Prdm1, and decreased expression of AICDA, PRDM1, and XBP1 transcripts (Fig. 8E, 8F). Thus, HDIs (VPA and butyrate) modulate human B cell class-switching and plasma cell differentiation, as they do in mouse B cells.

HDIs dampen the autoantibody response, ameliorate disease, and increase survival in lupus mice

Lupus-prone MRL/Fas<sup>enu</sup> mice spontaneously upregulate AID, Blimp-1, CSR, and SHM and generate great numbers of plasma cells, which produce large amounts of anti-dsDNA IgG and other autoantibodies, and develop age-dependent disease, which includes skin lesions and kidney pathology (2, 14, 49). In our female MRL/Fas<sup>enu</sup> mice, ANAs and anti-dsDNA IgG autoantibodies appeared at 6 wk of age and reached high levels at 12 wk, in association with significant loads of point mutations and DNA deletions in the IgH locus. At 17 wk, all of these mice showed severe kidney immunopathology, and 75% of them displayed various skin lesions, which, in 55% of the cases, included the characteristic “butterfly” rash. To determine whether HDIs could inhibit the lupus class-switched and hypermutated autoantibody response, we assigned 80 3-wk-old female MRL/Fas<sup>enu</sup> mice to three groups: a “non-treatment” group consisting of 50 mice that were given untreated water throughout their lives; an “early treatment” group of 15 mice that were given untreated water for the first 6 wk of life, at which time they were started on HDI water; and, a “late treatment” group of 15 mice that were given untreated water for the first 17 wk of life, at which time they were started on HDI water.

FIGURE 4. HDIs inhibit plasma cell differentiation. (A) Proportions of B220<sup>+</sup>PNA<sup>hi</sup> GC B cells, proliferating B cells (BrdU-stained B220<sup>+</sup> B cells), viable (7-AAD<sup>−</sup>) B220<sup>+</sup> B cells, and CD4<sup>+</sup> and CD8<sup>+</sup> T cells in spleen cells from mice that were on HDI water or untreated water and injected with NP<sub>16</sub>-CGG 10 d before analysis. (B) HDI does not alter B cell cycle. Mouse IgD<sup>+</sup> B cells were stimulated for 48 h with LPS or LPS + IL-4 in the presence of nil or VPA; during the last 30 min of culture, the cells were pulse-labeled with 10 μM of BrdU. The cells were then surface stained for B220 before intracellular staining with anti-BrdU mAb and 7-AAD. B220<sup>+</sup> cells are displayed, with gates indicating the percentage of cells in G0/G1, S, and G2/M phase. (C) Proportions of B220<sup>+</sup>CD138<sup>+</sup> (plasma) cells in spleen cells from C57BL/6 mice that were on HDI water or untreated water were analyzed 10 d after NP<sub>16</sub>-CGG injection. (D) Dose-dependent inhibition by VPA of plasma cell (B220<sup>+</sup>CD138<sup>+</sup>) differentiation (upper panels) in B cells stimulated for 4 d with LPS + IL-4, without alteration of plasma cell viability, as analyzed by 7-AAD staining (lower panels, proportions of 7-AAD<sup>−</sup> viable cells among B220<sup>+</sup>CD138<sup>+</sup> cells are indicated). (E) IgG1-producing plasma cells (IgG1<sup>+</sup>CD138<sup>+</sup> or IgG1<sup>+</sup>Blimp-1<sup>+</sup>) are reduced in cultures of IgD<sup>+</sup> B cells stimulated for 7 d with LPS + IL-4 in the presence of VPA (500 μM), as shown by confocal fluorescence microscopy. Cells were permeabilized and stained with DAPI (blue) to visualize nuclei and fluorescent mAbs to visualize IgG1 (green) and CD138 (red, upper set of panels) or Blimp-1 (red, lower set of panels). Arrows indicate IgG1-producing cells (yellow; CD138<sup>+</sup>/Blimp-1<sup>−</sup>IgG1<sup>+</sup>). Data are representative of three independent experiments. Scale bars, 10 μm.
At 12 wk of age, “early” HDI-treated MRL/Faslpr/lpr mice displayed reduced levels of anti-dsDNA IgG, IgG1, IgG2a, and ANA (data not shown), but not IgM, autoantibodies; reduced overall IgG1/IgG2a but not IgM; significantly reduced (by >75%) somatic point mutations, with no significant alteration in spectrum; and a reduced load of DNA deletions in the IgH locus (Figs. 9A, 9B, 10A, 10B, Supplemental Fig. 3). They also exhibited reduced numbers of IgG2a+ B cells, as well as reduced plasma cell differentiation, in the presence of normal B220+ cell proliferation and normal B and T cell numbers (Fig. 9C–E). Early treated MRL/Faslpr/lpr mice downregulated Aicda, Prdm1, and Xbp1, but not Ung, expression in B cells or plasma cells (Fig. 9F) and increased miR-155, miR-181b, miR-361, miR-23b, miR-30a, and miR-125 in B cells (irrelevant miR-19a/b, miR-20a, and miR-25 expression was unchanged) (Fig. 9G). This did not result from altered cell viability/apoptosis (Fig. 10C, 10D) or decreased expression of antiapoptotic genes (Fig. 10E, 10F). At 17 wk of age, “early” HDI-treated MRL/Faslpr/lpr mice showed reduced skin lesions, including absence of the “butterfly” rash, as well as reduced kidney pathology (Fig. 11A, 11B, 11D) and size of spleen and lymph nodes (data not shown). They also continued to show reduced ANA and anti-dsDNA IgG1/IgG2a autoantibodies (Fig. 11C, 11E). Decreased anti-dsDNA IgG1, IgG1, and IgG2a (but not IgM) autoantibodies and amelioration of pathology (data not shown), in association with complete healing of extensive skin lesions, also were observed in the late treatment group of mice, which were started on HDI water at 17 wk, an age at which our MRL/Faslpr/lpr mice already showed significant anti-dsDNA IgG autoantibodies and disease (Fig. 11F–H). The reduced IgG2a antibody levels and disease activity in early and late HDI-treated mice resulted in a significantly extended lifespan (p < 0.0001), with 8 of the 15 early treated mice and 7 of the 15 late-treated mice still alive and apparently healthy at 40 wk of age. Only 1 of the 50 “nontreated” mice made it to 32 wk; this mouse died at 36 wk (Fig. 11I). Thus, in lupus-prone mice, HDIs upregulate selected miRNAs, which can silence B cell AID or Blimp-1 expression, thereby reducing CSR, SHM, and plasma cell differentiation and dampening the class-switched and hypermutated autoantibody response, immunopathology, and disease, significantly prolonging life.

**Discussion**

As we have argued, epigenetic changes, such as histone post-translational modifications and DNA methylation, and epigenetic factors, such as miRNAs, can interact with genetic programs to regulate B cell functions, including CSR, SHM, and plasma cell differentiation, thereby informing Ab responses that are critical for the defense against microbial pathogens and tumor cells, as well as...
autoantibody responses that mediate autoimmunity and disease (3). We showed in this study that VPA and butyrate, two SCFA HDIs, inhibited CSR, SHM, and plasma cell differentiation by modulating intrinsic B cell mechanisms. They repressed AID and Blimp-1 expression in mouse and human B cells by upregulating selected miRNAs that silenced AICDA/Aicda and PRDM1/Prdm1 mRNAs, as demonstrated by multiple qRT-PCRs (this study) and further confirmed by mRNA-Seq and microRNA-Seq (H. Zan and P. Casali, unpublished observations). AID expression and CSR also were inhibited by TSA, a hydroxamic acid HDI. The doses at which VPA and butyrate inhibited B cell class switching, hypermutation, and plasma cell differentiation were within the range of those measured in humans for these HDIs (41, 43). By inhibiting AID and Blimp-1 expression, VPA dampened class-switched and hypermutated Abs in specific T-dependent and T-independent Ab responses in normal mice. This HDI also dampened class-switched and hypermutated autoantibody levels, reduced immunopathology, and extended survival in autoimmune MRL/Faslpr/lpr mice, a well-studied model of human lupus.

SCFA HDIs were suggested to display significant selectivity for different HDACs (58). For example, VPA targets class I HDACs, particularly HDAC1 and HDAC2, and, less effectively, class IIa HDACs; butyrate targets class I HDACs, mainly HDAC1, and, less effectively, other members of class I and class IIa HDACs (38, 39). HDAC activity is primarily associated with multiprotein complexes, the role and composition of which are often cell-type specific. HDAC-associated proteins specify the selectivity of HDIs, which display different affinities for different HDAC/cofactor complexes. HDIs with diverse chemical properties target different HDACs and HDAC/cofactor complexes, thereby regulating gene expression in a locus- and cell-type-specific fashion (58). Our findings indicate that, in B cells, HDIs modulate miRNAs selectively, possibly as a result of HDACs existing in unique contexts of HDAC/cofactor complexes, as occurring in these lymphocytes, particularly when in an activated state.

HDIs also may indirectly modulate Ab responses or mitigate autoimmunity by affecting elements other than B cells, such as innate immune cells (59) and T cells (regulatory T cells and Th1 and Th17 cells), or inhibiting proinflammatory cytokines (37, 46, 60, 61). However, as shown in this study, HDIs directly regulate B cell genes that are central to peripheral differentiation of these lymphocytes and maturation of Ab and autoantibody responses. Silencing AICDA/Aicda by HDIs was intrinsic to B lymphocytes and independent of other cellular elements, as shown by our in vitro experiments using purified human and mouse B cells, as well as our in vivo studies of the T-independent response to NP-LPS. In both in vivo and in vitro B cells, the HDI-mediated downregulation of AICDA/Aicda expression was associated with a concomitant increase in the respective targeting miR-155, miR-181b, and miR-361 (2), in a tight dose-dependent manner.

FIGURE 6. HDIs do not alter DNA methylation and histone acetylation in the Aicda promoter. (A and B) CpG DNA methylation of the Aicda promoter was analyzed by bisulfite sequencing of genomic DNA from B cells stimulated for 4 d with LPS + IL-4 in the presence of increasing doses of VPA. (A) DNA sequencing of PCR products of bisulfite-treated genomic DNA. The sequence signal from dCs in CpG motifs is outlined. Because unmethylated dC nucleotides can be converted to dU (read as dT in DNA sequence), whereas methylated dC cannot, the ratio of the dC (blue)/dT (red) signal indicates the level of methylated dC at any given position. (B) Methylation pattern at each of the four dCs within CpG motifs from individually cloned sequences (each row is a unique sequence, and each dC is represented by a column of circles) is shown as an array of circles. ●, methylated dCs; ○, unmethylated dCs. (C) Abundance of acetylated histone H3 (H3K9ac/K14ac) in the Aicda promoter in B cells stimulated with LPS + IL-4 for 60 h in the presence of nil or VPA (1000 μM) was measured by ChIP and qPCR. (D) Primary (pri-) miRNA transcripts of miR-155 and miR-181b in B cells cultured for 60 h with LPS or LPS + IL-4 in the presence of nil or increasing doses of VPA were measured by qRT-PCR and normalized to Cd79b expression. Values for B cells cultured in medium containing VPA are depicted as relative to the values in B cells cultured in the absence of HDI, set as 1. Data are mean and SEM from three independent experiments. *p < 0.05, **p < 0.01 unpaired t test.
Our findings extend those suggesting a role for miR-155 in downregulating AID expression (28, 30, 62), in agreement with the demonstration that repression of this miRNA provides a mechanism of Bcl6-promoted positive regulation of AID and increased GC gene expression (30). As we showed, silencing of PRDM1/Prdm1 (and XBP1/Xbp1) by HDIs also was intrinsic to B cells and independent of other cells. Like for Aicda, HDI-mediated downregulation of PRDM1/Prdm1 was associated with a concomitant increase in the respective B cell–targeting miRNAs (miR-23b, miR-30a, and miR-125b) (2), in vivo and in vitro, and in a tight dose-dependent fashion. HDI-induced downregulation of XBP1/Xbp1 could be secondary to decreased Blimp-1 expression and/or upregulation of selected miRNAs that we tentatively identified as silencers of XBP1/Xbp1 (H. Zan and P. Casali, unpublished observations). That HDIs downregulate Blimp-1 expression by upregulating miR-23b, miR-30a, and miR-125b that silence Prdm1 was further supported by our demonstration that HDIs slightly reduced or did not essentially alter the Prdm1 repressor genes Bach2, Bcl6, or Pax5.

The selectivity of HDI-mediated silencing of AICDA/Aicda and PRDM1/Prdm1 in B cells was further emphasized by the unchanged expression of HoxC4, Irf4, Rev1, and Ung, which play important roles in AICDA/Aicda regulation and/or CSR, as well as of miR-19a/b, miR-20a, and miR-25, which are not known to regulate AICDA/Aicda or PRDM1/Prdm1. We could not rule out the possibility that HDI regulated other B cell factors (e.g., NF-kB or Id2/3), which contributed to the reduction in AID or Blimp-1. The decrease in HDI-mediated repression of luciferase activity

**FIGURE 7.** HDIs hyperacetylate miRNA host genes to upregulate miRNAs that silence Aicda and Prdm1 mRNAs. (A) Upregulation of miRNAs that modulate AID and Blimp-1 in “total” (spleen CD19+CD138−) B cells, naive B cells, and plasma cells from mice that were on HDI water or untreated water and injected with NP16-CGG (as in Fig. 1) was measured by qRT-PCR. (B) Expression of miRNAs that modulate AID and Blimp-1 in freshly isolated naive B cells and in B cells stimulated with LPS + IL-4 for 60 h (left panel). Dose-dependent upregulation of miRNAs that modulate AID and Blimp-1 in B cells cultured with LPS + IL-4 for 60 h in the presence of nil or VPA (250 or 1000 μM) (right panel). miRNA expression was normalized to expression of small nuclear/nucleolar RNAs Rnu6, Snord61, Snord68, and Snord70. miRNA expression in B cells isolated from mice that were on HDI water or B cells cultured with HDI were depicted as relative to the expression of each miRNA in B cells isolated from mice that were on untreated water, or B cells cultured in the absence of HDI respectively, set as 1. Data are mean and SEM from at least three mice or three independent experiments. (C) Relative abundance of acetylated histone H3 (H3K9ac/K14ac) in miRNA host genes (HGs) in purified B cells stimulated with LPS + IL-4 in the presence of nil or VPA (500 μM), as analyzed by ChIP and qPCR. (D) Mature miRNA expression in CH12F3 B cells treated with nil or VPA (250 μM) for 24 h, as measured by qRT-PCR. Values for B cells treated with VPA are depicted as relative to the expression of each miRNA in B cells treated with nil, set as 1. (E) Schematic diagram of the 3′UTRs of Aicda and Prdm1 mRNAs and their mutant (Mut) counterparts that were cloned into the pMIR-REPORT luciferase reporter vector. Open boxes indicate point mutation sequences that are putative miRNA target sites, as detailed in Supplemental Fig. 2E. (F) Luciferase activity in CH12F3 cells transfected with wild-type or mut Aicda or Prdm1 3′UTRs (cloned into pMIR-REPORT luciferase reporter vector) after a 24-h treatment with nil or VPA (250 μM). Luciferase activity was measured 1.5 h after transfection. Transfection efficiency was controlled for by normalizing to signal from cotransfected R. reniformis luciferase vector. Luciferase activity in B cells treated with VPA is depicted as relative to values in B cells cultured in the absence of VPA, set as 1. Data are mean and SEM from three independent experiments. The p values were determined using an unpaired t test. *p < 0.05, **p < 0.001 unpaired t test.
under the control of Aicda and Prdm1 mRNA 3’UTRs bearing mutated miR-155, miR-181b, miR-23b, miR-30a, and miR-125b target sites demonstrated that miRNAs are indeed direct effectors of the HDI-mediated repression of such selected genes in B cells. The role of B cell miRNAs in mediating HDI suppression of AID and Blimp-1 expression, as well as in the dampening of Ab and autoantibody responses, could be further addressed using an integrated three-prong approach involving the generation of in vivo Argonaute–miRNA–Aicda or –Prdm1 mRNA ternary complexes, knock-in mice lacking specific miRNA-targeting sites in Aicda or Prdm1 3’UTR, or mice with B cells specifically expressing “sponge” inhibitors of miR-155, miR-181b and miR-361, or miR-23b, miR-30a, and miR-125b. HDIs had no direct effect on the epigenetic status of the Aicda locus, because our acetylated histone ChIP and bisulfite sequencing experiments showed no alteration in histone acetylation or methylation of the Aicda promoter by VPA. Although it is possible that HDIs could also modify protein functions by increasing acetylation of nonchromatin proteins, our

FIGURE 8. HDIs inhibit CSR and plasma cell differentiation increases selected miRNAs and decreases target AICDA and PRDM1 mRNAs, as well as XBP1 mRNA, in human B cells. Human peripheral blood IgD+ B cells were stimulated with CD154, human IL-4, and human IL-21 (for CSR to IgG1 and IgE and plasma cell differentiation) or CD154, human IL-21, and TGF-β (for CSR to IgA) in the presence of nil, VPA, or butyrate for 60 h (for transcript or miRNA analysis) or 120 h (for flow cytometry or analysis of Ig titers in supernatants). (A) Proportions of IgG+ B cells, plasma cells (CD22+CD38+), or viable (7-AAD−) CD19+ cells. (B) Proportions of IgA+ B cells. (C) IgG and IgA titers in supernatants of B cells stimulated with CD154, human IL-4, and human IL-21 (upper panel) or CD154, human IL-21, and TGF-β (lower panel) and cultured in the presence of VPA or butyrate. Data are from three independent experiments (mean and SEM). *p < 0.05, **p < 0.01, ***p < 0.001, unpaired t test. (D) Mature VδDJHj-CA (in cells stimulated by CD154, human IL-21, and TGF-β) and VδDJHj-CA1 and VδDJHj-CA2 (in cells stimulated by CD154, human IL-4, and human IL-21) transcripts were analyzed by qRT-PCR and normalized to HPRTI transcripts. (E) AICDA, PRDM1, and XBP1 transcripts (in cells stimulated with CD154, human IL-4, and human IL-21) were analyzed by qRT-PCR and normalized to HPRTI transcripts. (F) miRNA expression was analyzed by qRT-PCR and normalized to expression of small nuclear/nucleolar RNAs RNU6-1/2, SNORD61, SNORD68, and SNORD70. Values for B cells cultured in the presence of HDIs are depicted as relative to the expression of each transcript or miRNA in B cells cultured in the absence of HDI, set as 1. Data are mean and SEM from three independent experiments. The p values were determined using an unpaired t test.
findings allow us to conclude that modulation of miRNAs leading to silencing of selected mRNAs is the mechanism by which HDIs mediate inhibition of the B cell differentiation processes that underpin the maturation of Ab responses.

Our findings in human and mouse B cells, in vitro and in vivo, greatly extend and provide a mechanistic underpinning for the limited data by Kienzler et al., suggesting that VPA reduces human naive B cell differentiation to (CD27hiCD38hi) plasmablasts and reduces IgG and IgA expression. However, at odds with our findings, they did not observe a decrease in CSR induction in human B cells in vitro by VPA. This could be explained by the different designs of their experiments compared with ours. Kienzler et al. (63) stimulated human B cells with CD154 + IL-21; we stimulated human naive B cells with CD154 + IL-21 + IL-4 or CD154 + IL-21 + TGF-β. IL-4 or TGF-β, both critical CSR-inducing stimuli, were missing in Kienzler et al.’s experiments, possibly resulting in relatively lower AICDA and PRDM1 expression. Analysis of the molecular events underpinning CSR was also missing, making it virtually impossible to provide a thorough explanation for the putative discrepancy between the data of Kienzler et al. and ours.

In vivo HDI inhibition of CSR and plasma cell differentiation “freezes” B cells at an IgM+ stage, as indicated by the higher proportion of IgM+ lymphocytes in human or mouse B cell cultures exposed to HDIs. Whether these IgM+ B cells remained “naive” B cells or underwent some degree of memory B cell differentiation is unclear. The much-reduced IgH locus mutational load in HDI-treated normal and lupus-prone mice supports the contention that those IgM+ B cells expressed primarily unmutated IgM natural Abs. These still would have been available for the response to microbial pathogens and might have played a protective role in systemic autoimmunity (64). In addition, in both normal and autoimmune mice, HDI treatment allowed for some residual AID expression, which resulted in a significant reduction in, but not ablation of, secondary Ab isotypes. Even at low titers, these can mediate a protective antimicrobial immunity, as suggested by the apparently normal risk for infections in Aicda−/− mice with reduced AID levels (65). Thus, in normal and

FIGURE 9. HDIs impair class-switched and hypermutated autoantibody response, increase selected miRNAs, and decrease target Aicda and Prdm1 mRNAs, as well as Xbp1 mRNA, in MRL/Fas−/− mice. Female MRL/Fas−/− mice were started on HDI water or untreated water at the age of 6 wk and analyzed at the age of 12 wk. (A) Titers of circulating anti-dsDNA IgM, IgG, IgG1, and IgG2a and total IgM, IgG1, and IgG2a (n = 5 mice/group). (B) Frequency of somatic point mutations was reduced by 75% in MRL/Fas−/− mice given HDI water. A 700-bp intronic JH4-iE4 DNA in CD19+PNA+ B cells in GC was amplified and sequenced (sequence data were pooled from three mice in each group). Pie charts depict the proportions of sequences that carried 1, 2, 3, and so forth point mutations (center of pie shows the number of independent sequences analyzed). Listed below the pie charts are overall mutation frequencies (changes/base). (C) Proportions of IgG2a+ B cells and proliferation of spleen B220+ cells (analyzed by administration of BrdU in drinking water at 10 wk of age). (D) CD19+CD138+ plasma cells in spleens. Data are representative of three independent experiments. (E) Surface CD19 and CD3 expression in spleen cells. Data are from one of three independent experiments yielding comparable results. (F) Aicda and Umg transcripts (in spleen CD19+CD138− B cells, normalized to Cd79b transcript) and Prdm1 and Xbp1 transcripts (in spleen CD19+CD138− plasma cells, normalized to Gapdh transcript) were measured by qRT-PCR. Values from mice that were on HDI water are depicted as relative to the expression of each transcript in mice that were on untreated water, set as 1. Data are mean and SEM from four independent experiments. (G) miRNA expression in CD19+CD138− spleen B cells was measured by qRT-PCR and normalized to expression of small nuclear/nucleolar RNAs RNU6-1/2, SNORD61, SNORD68, and SNORD70. miRNA expression in the B cells from mice that were on HDI water are depicted as relative to the expression of each miRNA in the B cells from mice that were on untreated water, set as 1. Data are mean and SEM from three independent experiments. The p values were determined using an unpaired t test.
DNA deletions in intronic JH4-iE or untreated water (from 6 to 12 wk of age, at which time the mice were sacrificed, as in Fig. 9 and Supplemental Fig. 3). Relative to the expression of each transcript in the cells from mice that were on untreated water, set as 1. Data are mean and SEM from three independent experiments. Epigenetic dysregulation can compound genetic susceptibility to mediate autoantibody responses and autoimmunity (3). Epigenetic changes associated with autoimmune responses have been investigated in T cells but only marginally in B cells (68). We (14) and other investigators (69) showed that highly upregulated AID and Blimp-1 expression is an important feature of lupus patients and lupus-prone mice, including MRL/Fas<sup>lpr/lpr</sup> mice. In these mice, dysregulation of AID and Blimp-1 causes aberrant rates of CSR and SHM, leading to increased loads of somatic point mutations and deletions/insertions in the IgH locus, as well as heightened Ig- secretion rates that result in abundant production of pathogenic autoantibodies. Accordingly, increased AID and Blimp-1 expression in lupus patients is associated with high levels of mutated IgG autoantibodies, which heighten disease activity (14, 69). Converse analysis showed that highly upregulated AID and Blimp-1 expression is an important feature of lupus patients and lupus-prone mice, including MRL/Fas<sup>lpr/lpr</sup> mice. In these mice, dysregulation of AID and Blimp-1 causes aberrant rates of CSR and SHM, leading to increased loads of somatic point mutations and deletions/insertions in the IgH locus, as well as heightened Ig- secretion rates that result in abundant production of pathogenic autoantibodies. Accordingly, increased AID and Blimp-1 expression in lupus patients is associated with high levels of mutated IgG autoantibodies, which heighten disease activity (14, 69). Conversely, AID deficiency in MRL/Fas<sup>lpr/lpr</sup> Aicda<sup>−/−</sup> mice protected against disease (64, 70), and decreased AID expression in MRL/Fas<sup>lpr/lpr</sup> HoxC4<sup>−/−</sup> and MRL/Fas<sup>lpr/lpr</sup> Aicda<sup>−/−</sup> mice, which display 30–60% of the AID level of MRL/Fas<sup>lpr/lpr</sup> Aicda<sup>+/−</sup> mice, reduced autoantibody titers and delayed disease (14, 71). A role in promoting GC formation and generation of class-switched autoantibodies was suggested for miR-155 (62, 72, 73), and reduced autoantibody production and autoimmunity were reported in miR-155–deficient B6/Fas<sup>lpr/lpr</sup> mice (74). However, this likely resulted from dysregulation of a variety of genes in multiple immune cells, including derepressed expression of SHIP-1 in B cells, which led to mitigation of B cell activation, proliferation, and autoantibody production. In our hands, HDIs did not...
yield obvious alterations in GC formation or B cell SHIP-1 transcripts (data not shown).

**PRDM1** has been identified as one of the risk loci for lupus in human genetic-association studies (75, 76), and increased Blimp-1 expression was shown to parallel a surge in circulating plasma cells during disease flares (77). Blimp-1 is required for generation of short-lived and long-lived plasma cells. Unlike short-lived plasma cells, long-lived autoreactive, malignant, or allergen-specific (IgE+) plasma cells are refractory to immunosuppression and irradiation (78). In our *MRL/Fas*<sup>lpr/lpr</sup> mice, HDI-mediated upregulation of miR-30a and miR-125b, which are highly expressed in GC B cells and downregulated in plasma cells (32, 79), along with HDI-mediated upregulation of miR-23b, which is reduced in lupus (80), silenced Blimp-1 expression, thereby impairing plasma cell differentiation and compounding the negative effect of decreased CSR and SHM on the production of high-affinity class-switched autoantibodies. Because Blimp-1 is required for formation and maintenance of plasma cells (4), HDI-mediated downregulation of Blimp-1 can lead to significantly long-lasting lower levels of autoantibodies by decreasing autoantibody-producing plasma cells. Accordingly, our preliminary data (data not shown) suggest that the beneficial effect of HDIs is long lasting after withdrawal of the drug from treated autoimmune mice.

Butyrate is one of the SCFAs produced by gut commensal bacteria through dietary fiber fermentation (41) and is the most potent HDI among the SCFAs. It modulates the function of intestinal macrophages (81) and acts on naive T cells to promote epigenetic changes that regulate the expression of genes responsible for differentiation into regulatory T cells and IL-10–producing T cells (42, 82). Our demonstration that butyrate (at a dose as low as 250 μM) inhibits the expression of genes responsible for differentiation into regulatory T cells and IL-10–producing T cells (42, 82)
modulates AID expression and CSR to IgG, IgA, and IgE, as well as plasma cell differentiation through direct activity on B cells, indicates that this HDI can play an important role in modulating Ab responses of gut lymphoid organs (in which butyrate occurs at 1–20 mM). This would be particularly true of the cecal patch, a major intestinal lymphoid organ in the proximal colon, as well as in Peyer’s patches, which are highly represented in the ileum, the portion of intestine that is immediately afferent to the proximal colon. Both the cecal patch and Peyer’s patches contain vast numbers of B cells committed to the production of IgA, and to a lesser extent, IgE (83, 84). Butyrate may also play an important role in limiting AID expression in the inflamed colonic mucosa, in which AID is induced by proinflammatory cytokines (85). By suppressing AID, butyrate could suppress inflammation-mediated neoplastic transformation, leading to colorectal cancer (86), a process in which AID-mediated oncogenic mutagenesis plays a significant role.

Metabolites from intestinal microbiota are key determinants of host–microbe mutualism and, consequently, the health or disease of the intestinal tract, as well as other organs and tissues (87–89). It was suggested that SCFAs produced by gut commensal bacteria can distribute systemically and shape the immunological environment in the lung, thereby influencing the severity of allergic inflammation. Mice fed a high-fiber diet had increased circulating levels of SCFAs and were protected against allergic inflammation (mediated by IgE) of the lung, whereas a low-fiber diet decreased levels of SCFAs and increased allergic airway disease (87). A diverse microbial population, which would produce an appropriate amount of SCFA HDIs, particularly butyrate, is required to maintain a baseline immune-regulatory state, including IgG, IgA, and IgE levels. Elevated serum IgE and CSR to IgE in B cells at mucosal sites in the absence of microbial colonization in germ-free mice and in mice with low-diversity gut microbiota further emphasize the important role for gut commensal bacteria–produced butyrate in modulating IgE levels (90, 91). Altered composition and decreased bacterial diversity of gut microbiota would lead to changes in absolute and relative levels of SCFA HDIs (89) and, therefore, changes in systemic IgG, IgA, and IgE specificities and levels, which contribute to altered immunity and increased susceptibility to immune-mediated diseases.

Despite involving no human patient, our study provides a strong rationale and a mechanistic basis for the use of HDIs as epigenetic modulators of Ab responses, as well as therapeutics for systemic autoimmunity and, possibly, IgE-mediated allergic responses. In our experiments, HDI was administered in drinking water, rather than parenterally as in previous studies (46), resulting in steady and well-tolerated therapeutic levels of HDIs. These were comparable to those in patients taking HDIs per os (43) and without the concentration spikes associated with HDI injections (46). HDI administration in drinking water likely contributed to the effectiveness of the modulation of T-dependent and T-independent Ab responses in healthy mice, as well as to the dampening of the systemic autoantibody response, reduction in immunopathology, and extended survival in lupus mice. Overall, our studies suggest a new and important therapeutic indication for VPA and butyrate, and, likely, other HDIs, such as TSA and suberoylanilide hydroxamic acid (approved by the U.S. Food and Drug Administration for the treatment of cutaneous T cell lymphoma). They also provide novel and significant mechanistic insights into epigenetic mechanisms of immunoregulation, as mediated by direct modulation of B cell–intrinsic functions, thereby offering new clues for further therapeutic approaches, as specifically targeted to B cells.


Supplemental Figure 1

A) Mutations from LPS + IL-4 stimulation shown in B cells (LPS + IL-4). Total mutations analyzed: 601.

B) Flow cytometry analysis of B cells (LPS + IL-4) showing expression of IgG1.

C) Flow cytometry analysis of B220 hi CD138 + cells showing cell count and Annexin V expression.

D) Flow cytometry analysis of B220 lo CD138 + cells showing cell count and Annexin V expression.

E) Flow cytometry analysis of B220 lo CD138 - cells showing cell count and Annexin V expression.

F) Relative expression of B cells (LPS + IL-4) after HDI (VPA) treatment.

G) Flow cytometry analysis of CD19 + CD138 - cells showing cell count and Annexin V expression.


Supplemental Figure 1. HDI inhibit CSR and Aicda expression but do not alter the spectrum of somatic point-mutations as well as viability and apoptosis of B cells and plasma cells in vivo and in vitro. (A) Spectrum of somatic mutations in the V_{186.2} region of V_{186.2}DJ_{H}-C_{\gamma 1} transcripts from mice that were on HDI-water or untreated water, as in Figure 1E. Values are expressed as the actual numbers of different nucleotide substitutions (top panels) or as the percentage of total point-mutations (bottom panels). (B) Dose-dependent inhibition of CSR and Aicda expression by HDI TSA in B cells. Mouse naïve B cells were stimulated with LPS plus IL-4 in the presence of 0, 10 or 20 nM (0, 3 or 6 ng/ml) TSA. IgG1+ B cells were analyzed 4 days after the stimulation. Aicda transcripts were measured by qRT-PCR and normalized to Cd79b expression, 60 hours after the stimulation. Values in B cells cultured in the presence of TSA are depicted as relative to Aicda transcript level in B cells cultured in the absence of TSA, set as 1. (C-F) Mouse naïve B cells were stimulated for 4 days with LPS plus IL-4 in the presence of nil or increased doses of HDI (VPA) to assess viability and apoptosis. Proportions of (C) viable (7-AAD–) or (D) apoptotic (Annexin V+) B220+ B cells are indicated. (E) Proportions of Annexin V+ B220+CD20+CD138+ plasma cells are indicated. (F) Expression of anti-apoptotic genes Bcl2, Mcl1 and Bcl2l1 measured by qRT-PCR and normalized to Gapdh expression. Values in cells treated with VPA are depicted as relative to the expression of each transcript in cells treated with nil, set as 1. Data are presented as mean and SEM from three independent experiments. (G-I) C57BL/6 mice on HDI-water or untreated water were injected with NP_{16}-CGG 10 days before analysis. Proportions of (G) 7-AAD+ viable cells or Annexin V+ apoptotic cells among spleen B220+CD138+ plasma cells are indicated. Expression of Bcl2, Mcl1 and Bcl2l1 transcripts in (H) CD19+CD138− B cells and (I) CD19+CD138+ plasma cells were measured by qRT-PCR and normalized to Gapdh expression. Values in cells treated with HDI or cells isolated from mice that were on HDI-water are depicted as relative to the expression of each transcript in cells cultured in the absence of HDI, or cells isolated from mice that were on untreated water, respectively, set as 1. Data are presented as mean ± SEM from three independent experiments.
**Aicda mRNA 3’UTR**

-3

5’...UGAAAGCACCUCCUGGAAGUUC...GACCCGCAUAUCCUCAAAAGCAUAUAU...3’

3’...AGGGUUGGUCCUGUUACUACAA...miR-181b

5’

mut Aicda mRNA 3’UTR

5’...UGAAAGCACCUCCUGGAAGUUC...GACCCGCAUAUCCUCAAAAGCAUAUAU...3’

3’...AGGGUUGGUCCUGUUACUACAA...miR-181b

5’

Prdm1 mRNA 3’UTR

5’...AUGUUAAAACGUGCAGUGGCCAGCAGAUAAGAAGAGCUCAG...GAGUUCUUGGCUAAUCGGCAGG...AGUGUGAGAAGGUCUAC...UUGUGUGUGUACAGG...UAGUGUUAGUAC...3’

3’...AGUGUUAAAACGUGCAGUGGCCAGCAGAUAAGAAGAGCUCAG...GAGUUCUUGGCUAAUCGGCAGG...AGUGUGAGAAGGUCUAC...UUGUGUGUGUACAGG...UAGUGUUAGUAC...5’

mut Prdm1 mRNA 3’UTR

5’...AUGUUAAAACGUGCAGUGGCCAGCAGAUAAGAAGAGCUCAG...GAGUUCUUGGCUAAUCGGCAGG...AGUGUGAGAAGGUCUAC...UUGUGUGUGUACAGG...UAGUGUUAGUAC...3’

3’...AGUGUUAAAACGUGCAGUGGCCAGCAGAUAAGAAGAGCUCAG...GAGUUCUUGGCUAAUCGGCAGG...AGUGUGAGAAGGUCUAC...UUGUGUGUGUACAGG...UAGUGUUAGUAC...5’
Supplemental Figure 2. (A-D) HDI-mediated inhibition of CSR as indicated by reduced mature V\textsubscript{H}DJ\textsubscript{H}-C\textsubscript{H} and post-recombination I\textsubscript{\mu}-C\textsubscript{H} transcripts in HDI-treated B cells. (A) Purified spleen B cells were labeled with CFSE and stimulated with LPS for 4 days in the presence of nil or HDI (VPA, 500 \mu M). The percentage of B220\textsuperscript{+}IgG3\textsuperscript{+} B cells among total B220\textsuperscript{+} B cells that had completed the same number of divisions when treated with nil or HDI is depicted in the scatter plot. Data are representative of three independent experiments. (B) Germline I\gamma\textsubscript{3}C\gamma\textsubscript{3} transcripts in B cells stimulated for 60 hours with LPS in the presence of nil or increasing doses of VPA, measured by qRT-PCR and normalized to Cd79b transcripts (all other germline I\textsubscript{\gamma}-C\textsubscript{H} transcripts were also normal, not shown). (C and D) B cells were stimulated with LPS plus IL-4 (for IgG1 and IgE), CD154 plus IL-4 (for IgE), LPS (for IgG3), or LPS or CD154 plus TGF-\beta, IL-4, IL-5 and anti-IgD dextran (for IgA) for 60 hours in the presence of nil or increasing doses of VPA. (C) Mature V\textsubscript{\mu}DJ\textsubscript{H}-C\gamma\textsubscript{1}, V\textsubscript{\mu}DJ\textsubscript{H}-C\gamma\textsubscript{3}, V\textsubscript{\mu}DJ\textsubscript{H}-Ca and V\textsubscript{\mu}DJ\textsubscript{H}-C\varepsilon transcripts and (D) post-recombination I\textsubscript{\mu}-C\gamma\textsubscript{1}, I\textsubscript{\mu}-C\gamma\textsubscript{3}, I\textsubscript{\mu}-Ca and I\textsubscript{\mu}-C\varepsilon transcripts, which are both hallmarks of completed CSR were analyzed by qRT-PCR and normalized to Cd79b transcripts. Data are from three independent experiments (mean and SEM). Values in B cells cultured in medium containing HDI are depicted as relative to the expression of each transcript in B cells cultured in the absence of HDI, set as 1. Data are presented as mean and SEM from three independent experiments. *p < 0.05, **p < 0.01, ***p < 0.001, unpaired t-test. (E) Alignment of unmutated and mut Aicda and Prdm1 mRNA 3’UTR sequences used in luciferase reporter assays and the miRNAs that target them. Unmutated and mut 3’UTRs of the Aicda and Prdm1 mRNA 3’UTRs that were cloned into luciferase vectors for experiments in Figure 7E and 7F are diagramed. Base pairing of miRNAs that target the Aicda and Prdm1 mRNA 3’UTRs is represented by vertical lines. Grey boxes indicate the seed sequence of miRNAs. Mutations to predicted and known miRNA target sites were designed to disrupt miRNA binding to mRNA 3’UTRs and are shown in red. The latter three miRNA target sites in mut Prdm1 mRNA 3’UTR were deleted (rather than mutated).
Supplemental Figure 3. Spectrum and distribution of point-mutations in the intronic J₄-iEμ region of MRL/Faslpr/lpr mice is not altered by HDI. A 700 bp sequences (outlined by pink line) of intronic J₄-iEμ DNA in CD19⁺PNA⁺GC B cells from Peyer's patches of 12-week-old lupus-prone MRL/Faslpr/lpr mice that were on HDI-water or untreated water (starting at 6 weeks of age, as in Figure 9) were analyzed for nature and distribution of mutations. Red letters above the black germline sequence depict point-mutations in sequences from MRL/Faslpr/lpr mice that were on untreated water, blue letters below the germline sequence show point-mutations in sequences from mice that were on HDI-water.
Supplemental Table 1. Primers for qRT-PCR, detection of mature miRNA transcripts and bisulfite PCR.

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<tr>
<th>Mouse genes</th>
<th>Forward primer</th>
<th>Reverse primer</th>
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<tr>
<td>Aicda</td>
<td>5'-AGAAAGTCACGCTGGAGACC-3'</td>
<td>5'-CTCCTCTTACCAGCTAGCA-3'</td>
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<tr>
<td>Ung</td>
<td>5'-TAATCAAGCTCAGCGCCTGCT-3'</td>
<td>5'-TTGAGGAGAGGCACCTTG-3'</td>
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<td>IL-6</td>
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</tr>
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<td>Prdm1</td>
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<td>5'-GGAGAGGAGGCGCCTTCACA-3'</td>
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<td>Xbp1</td>
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<td>Revl</td>
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<td>Gapdh</td>
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<td>5'-GGGGCTCTCTGGAATTCAG-3'</td>
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<td>Bcl211</td>
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<td>pri-miR-181b</td>
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<td>Iγ-Cγ3</td>
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<td>5'-AGCAAGGGAACACACAGGATAC-3'</td>
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<tr>
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<tr>
<td>Iγ-Cε</td>
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<td>5'-ACCAAGGGATAGACAGGATGGG-3'</td>
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<tr>
<td>VκDJκ-Cα</td>
<td>5'-CATCTGGAAGACCTCGNCNGNTCTCAT-3'</td>
<td>5'-TAATCGTAACAGGACAGC-3'</td>
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<tr>
<td>VκDJκ-Cε</td>
<td>5'-CATCTGGAAGACCTCGNCNGNTCTCAT-3'</td>
<td>5'-ACAGGGCTTCAAGGGGTAGA-3'</td>
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Mature miRNA and sn/snoRNA forward primers (used with Qiagen miScript Universal Primer as reverse primer)

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<th>mmu-miR-155-5p</th>
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<td>5'-AACATCATTGGTGGTGTTGGTG-3'</td>
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<td>miR-361-5p</td>
<td>5'-TTATCGAATCTTCAGGGGGTAC-3'</td>
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<td>miR-23b-3p</td>
<td>5'-ATCACATTGGCAGGGATTAC-3'</td>
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<td>miR-30a-5p</td>
<td>5'-TGTAACACATCCTCAGTGGA-3'</td>
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miR-125b-5p  5'-TCCCTGAGACCTAACTTGTGA-3'
miR-19a/b-3p  5'-TGTCACCATCTCTGAACACCTG-3'
miR-20a-5p   5'-AAAGTGCTTTAGTGAGTAGT-3'
miR-25-3p    5'-CATGTCATTGTCCTG-3'
Rnu6/RNU6-1/2 5'-GCTCGGAGGACAGCATCTAATAAT-3'
Snord61/SNORD61  5'-CCACTGATCTCCTGACATGA-3'
Snord68/SNORD68 5'-GCTGTACTGACTTGATGA-3'
Snord70/SNORD70 5'-TTTTGGAACATGAACTTGATTTT-3'

Human genes

V_{nDJH} FR3-C_{γ1} 5'-GACACGGGCTGTTTTAATCTGTGCG-3'  5'-AGTAGTCTTTGACCCAGGCAGCC-3'
V_{nDJH} FR3-C_{ε}   5'-GACACGGGCTGTTTTAATCTGTGCG-3'  5'-GGGAGGTGGCATTGGAGG-3'
V_{nDJH} FR3-C_{α}   5'-GACACGGGCTGTTTTAATCTGTGCG-3'  5'-GTGGGAAGTTTCTGGCGGT-3'
AICDA           5'-GATCTCGGACTGGGACCTAGA-3'  5'-GGTTCCCTGGGACAGGGATCC-3'
PRDM1           5'-AGCCTGACATCTGAGGAC-3'  5'-TTCTGATCGGCCATCTTGACTC-3'
XBP1            5'-GCAGGCCCCAGTGCACTCACC-3'  5'-CTCAGGCGCTCTGGGGAAGGTACGG-3'
HPRT1           5'-TGCTCGAGATGTGAAGAGG-3'  5'-TCCCTTGTGACTGTACCTTCAA-3'

Somatic mutations

V_{186.2-C_{γ1}} 5'-CATGCTCCTTCTTGCGACAGCAACACG-3'  5'-GTGCACACCGTGGGACAGGGATCC-3'
JX13F-JX4R 5'-AGCCTGACATCTGAGGAC-3'  5'-CCTGATCGGCCATCTTGACTC-3'
JX15F-JX5R 5'-CATCTGAGGACTCTGCAGTCTAT-3'  5'-CCTCACCTCCATTCTGGGTTAAA-3'

miRNA host gene (HG) promoter ChIP

miR-155 HG  5'-AAGGTGTAGCTGATCAGGCAAGGAC-3'  5'-TGTGCATCTGTGATCAGGCTCT-3'
miR-181b HG  5'-GGAGTTGAAATTCTGAAGGCTTACG-3'  5'-ACTGCAAGGACGAATGAGATGCT-3'
miR-361 HG   5'-ACATGCCTTGGTTCTGGAGG-3'  5'-GGAGGTGACAGTTATGGGACGC-3'
miR-23b HG   5'-CCTGCTCGGACTGGGACCTAGA-3'  5'-GGTTCCCTGGGACAGGGATCC-3'
miR-30a HG   5'-TGCAAAAAGACTAGATGATCTGTC-3'  5'-GTGAAAGGCTCCTGATGAGG-3'
miR-125b HG-1 5'-TCCCTCAGGCGACTGCTG-3'  5'-ACAGGCGCTTATGGAACACAC-3'
miR-125b HG-2 5'-CGTGTGGCGCTCCCCCTC-3'  5'-ATGCAAAAGGACACCGCAAC-3'

Bisulfite PCR

Aicda promoter  5'-TGATTTTTGTTATTTTGATATTTG-3'  5'-TACTCTTTAAAAACTCTCCCTTC-3'