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RelB Deficiency in Dendritic Cells Protects from Autoimmune Inflammation Due to Spontaneous Accumulation of Tissue T Regulatory Cells

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Foxp3$^+$ regulatory T cells are well-known immune suppressor cells in various settings. In this study, we provide evidence that knockout of the *relB* gene in dendritic cells (DCs) of C57BL/6 mice results in a spontaneous and systemic accumulation of Foxp3$^+$ T regulatory T cells (Tregs) partially at the expense of microbiota-reactive Tregs. Deletion of *nfkb2* does not fully recapitulate this phenotype, indicating that alternative NF-κB activation via the RelB/p52 complex is not solely responsible for Treg accumulation. Deletion of RelB in DCs further results in an impaired oral tolerance induction and a marked type 2 immune bias among accumulated Foxp3$^+$ Tregs reminiscent of a tissue Treg signature. Tissue Tregs were fully functional, expanded independently of IL-33, and led to an almost complete Treg-dependent protection from experimental autoimmune encephalomyelitis. Thus, we provide clear evidence that RelB-dependent pathways regulate the capacity of DCs to quantitatively and qualitatively impact on Treg biology and constitute an attractive target for treatment of autoimmune diseases but may come at risk for reduced immune tolerance in the intestinal tract. ***The Journal of Immunology*****, 2019, 203: 2602–2613.**

Regulatory T cells (Tregs) expressing the master transcription factor Foxp3 have been described as key cells for the regulation of otherwise exaggerated and potentially fatal immune responses, both to foreign- and self-antigens. More recently, it became apparent that Tregs operate in different flavors depending on coexpression of master transcription factors, cytokine, and chemokine receptors typically associated with other Th cell subsets (1). For instance, Foxp3$^+$ Tregs coexpressing the RAR-related orphan receptor γ t [ROR(γt)] describe a population of Tregs in the intestinal lamina propria that is induced only by colonization with commensal bacteria (2, 3). Likewise, T-bet–expressing Tregs prevent severe Th1-dominated autoimmunity, possibly due to colocalization with T-bet$^+$ effector T (Teff) cells (4, 5). Combined deletion of both T-bet and Gata3 in Tregs has been shown to result in a spontaneous autoimmune disorder, whereas deletion of Gata3 alone prevents Treg stability under inflammatory conditions (6, 7). Typically, Tregs derived from nonlymphoid tissues such as skin or adipose tissue show a remarkable expression of genes previously associated to type 2 immunity, including *Il1rl1* and *Gata3*, and have been termed tissue Tregs (8–10). Local Tregs have been shown to play a key role for tissue integrity because Treg-intrinsic defects can result in reduced tissue function upon damage (11, 12). Thus, type 2 immune-biased Tregs may exert a similar

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The RNA-sequencing data presented in this article have been submitted to the National Center for Biotechnology Information's Gene Expression Omnibus (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE134779) under accession number GSE134779.

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Abbreviations used in this article: cDC, conventional DC; DC, dendritic cell; EAE, experimental autoimmune encephalomyelitis; MHC-II, MHC class II; mTEC, medullary thymic epithelial cell; PEC, peritoneal cavity; ROR(γt), RAR-related orphan receptor γ t; sST2, soluble ST2; Teff, effector T; Treg, regulatory T cell; WT, wildtype.

role as steady-state innate type 2 immunity in tissue homeostasis and repair (13). However, little is known about the cell-extrinsic mechanisms that imprint a tissue Treg phenotype into T cells.

APCs and notably dendritic cells (DCs) are well known for their capacity to initiate adaptive immune responses, whereas their role for tissue homeostasis and immune tolerance has been recognized only in recent years. For instance, conditional ablation of DCs leads to aggravated autoimmunity in a murine model of multiple sclerosis termed experimental autoimmune encephalomyelitis (EAE) (14). Furthermore, DCs are able to regulate tissue-resident Tregs both during thymic differentiation and by local activation (15). Constitutive ablation of DCs did initially not reveal a major impairment of thymic-derived Treg development but leads to a potentially autoimmune myeloproliferative disorder due to a defect in central tolerance (16, 17). By contrast, the absence of DCs but not myeloid cells impairs the generation of ROR(γt)$^+$ Tregs and oral tolerance induction (2, 18). Thus, DCs have the capability to shape Treg biology in various settings.

In this study, we propose that expression of the noncanonical NF-κB pathway member RelB but not NF-κB2 in DCs has a dominant role in limiting the accumulation of Tregs with a tissue Treg signature. By contrast, commensal-induced ROR(γt)$^+$ Tregs and induction of oral tolerance are reduced after ablation of RelB in DCs. We further show that such type 2 immune-biased Tregs are functional in vitro and in vivo and that accumulation of tissue Tregs is independent of nonhematopoietic IL-33 expression. Finally, mice lacking RelB expression in DCs are almost resistant to induction of autoimmune inflammation in the CNS in the EAE model. Thus, inactivation of the noncanonical NF-κB member RelB in DCs leads to an accumulation of tissue Tregs and alters the ratio between self− versus foreign−reactive Tregs with consequences for different disease entities.

Materials and Methods

Mice

The following mouse strains were used: RelB$^{KO/KO}$ (19), NF-κB2$^{KO/KO}$ (20), IL-33–LacZ gene-trap (IL-33$^{Gt/Gt}$) knockouts (21) Foxp3.gfp knock-in (Foxp3^{tm1Kuch}) mice (22) intercrossed to MOG TCR-specific 2D2 (Tg [Tcra2D2,Tcrb2D2]^{1Kuc} [23]), and OT-II mice (Tg[TcraTcrb]425Cbn) (24) with the congenic marker CD45.1 (B6.SJL-Ptprc^a Pepc^b) were used as organs donors for adoptive transfer experiments. Mice expressing a DC-specific Cre recombinase (Tg[Itgax-cre]$^{1-1Reiz}$) mice (25) were purchased at The Jackson Laboratory and crossed with mice carrying a loxP-flanked exon 4 of the *relb* gene (RelB$^{fl/fl}$) (19) to achieve deletion of *relB* in DCs (called RelB$^{\Delta DC}$ throughout the manuscript) or mice carrying a loxP-flanked exon 1 and 2 (NF-κB2$^{fl/fl}$) (26) to achieve deletion of *nfkb2* in DCs (called NF-κB2$^{\Delta DC}$ throughout the manuscript). RelB$^{fl/fl}$ mice were crossed to Foxp3 promotor–driven BAC transgenic Cre mice (27) to generate Treg-specific RelB deletion or to a Foxn1-driven Cre transgenic mouse line (28) to generate medullary thymic epithelial cell (mTEC)-specific RelB deletion (19). For cell sorting experiments, RelB$^{\Delta DC}$ were intercrossed to Foxp3^{tm1Flv} (29) reporter mice. Treg-deficient scurfy mice (Foxp3^{sf} [30]) were used at an age of 6 d. Littermate controls were used whenever possible. All mouse strains were backcrossed to a C57BL/6 background for at least 10 generations unless otherwise stated. Soluble ST2 (sST2) was injected three times per week at a dose of 100 μg in PBS i.p. for a total of 3 wk into adult mice. All animals were kept under specific pathogen-free conditions. All interventions were performed in accordance with the European Convention for Animal Care and Use of Laboratory Animals and were approved by the local ethics committee and appropriate government authorities.

Induction of EAE

EAE was induced by injection of 200 μl of an emulsion containing 200 μg of $MOG_{35–55}$ peptide (MEVGWYRSPFSRVVHLYRNGK) and 500 μg of *Mycobacterium tuberculosis* H37Ra (BD Difco) in CFA s.c. at the base of tail. On day 0 and 2 after immunization, mice received 200 ng of pertussis toxin (Sigma). Alternatively, EAE was induced using a kit from Hooke laboratories according to the manufacturer's instructions. Clinical signs of disease were monitored according to the following scheme: score 1, tail paralysis; score 2, hind limb impairment; score 3, hind limb paralysis; score 4, front limb paralysis; score 5, death. In case hind limb movement was strongly impaired, mice were provided with a HydroGel H_20 and easily accessible wet food. For analysis of cytokine-producing T cells at peak of disease, lymphocytes were recovered from brains and spinal cords. Restimulation was either performed with $MOG_{35–55}$ peptide or PMA/ionomycin for 4 h. For the last 2 h, brefeldin A was added to the restimulated cells. When indicated, Tregs were ablated by i.p. injection of 500 μg of anti-CD25 Ab (clone PC61; BioXCell) on days -5 and -3 prior to $MOG_{35–55}$ immunization. For transfer experiments 2.5×10^6 sort-purified Foxp3/GFP$^-$2D2$^+$ Th cells were injected i.v. 24 h prior to $MOG_{35–55}$ immunization. The induction of MOG-specific 2D2$^+$Foxp3/GFP$^+$ Tregs was analyzed by flow cytometry at day 7 after $MOG_{35–55}$ immunization in inguinal lymph nodes.

Rescue of scurfy mice

A total of 2×10^6 sort-purified CD4$^+$ splenocytes from wildtype (WT) or RelB$^{\Delta DC}$ mice were injected i.p. into 3–6-d-old Foxp3$^{KO/KO}$ (Scurfy) mice. Nontreated Scurfy mice did not receive any cells. Survival and body weight were monitored for 60 d after cell transfer.

OT-II cell transfer and OVA feeding

Naive T cells from spleens and lymph nodes of OTII/CD45.1 mice were sort-purified or isolated by magnetic separation using a naive CD4$^+$ T cell isolation kit (Miltenyi Biotec), and 0.5×10^6 naive OT-II T cells were injected i.v. into WT and Relb$^{\Delta DC}$ recipients. Upon transfer mice were fed with 1.5% OVA fraction V (Sigma-Aldrich) in drinking water ad libitum for 9 d before analysis.

Bone marrow chimeras

Recipient mice were lethally irradiated by a Co-60 source with two doses of 6 Gy 4 h apart. Irradiated mice were reconstituted with 8×10^6 purified bone marrow cells of respective donors by i.v. injection. After reconstitution, mice received 0.25 mg/ml Enrofloxacin (Baytril; Bayer Vital GmbH) in drinking water for 3 wk. Bone marrow chimeras were analyzed 10–12 wk after reconstitution.

Production and use of sST2

sST2 cDNA (amino acids 1–337) was designed and ordered at Invitrogen Strings. A total of 5 μl of DNA fragment (20 ng/μl) were digested with NheI and XhoI, and digested fragment was gel-purified using the GeneJET Gel extraction kit according to manufacturer's instructions. Purified fragments were ligated with dephosphorylated NheI and XhoI digested pcDNA3.1 using T4 DNA ligase (NEB). Competent XL10 gold cells were transformed with the ligation mix according to manufacturer's guidelines and plated on agar plates containing 100 μg/ml ampicillin. Selected colonies were picked, and plasmids were isolated using the GeneJET plasmid prep mini kit and sequenced. Plasmids from a clone with the correct sequence were used to transfect Hek293 cells with Lipofectamine 3000 Reagent (Thermo Fisher Scientific). To generate stable cell lines, transfected cells were cultured in complete RPMI in presence of G418 for 4 wk. Presence of sST2 in the supernatant was confirmed by Western blot using a polyclonal goat anti-sST2 Ab (Abcam) and ELISA (R&D Systems). For large-scale production of sST2, supernatant of sST2-producing cells was affinity purified via His tag using nickel columns (HisTrap excel). sST2 was further purified using size-exclusion chromatography (HiLoad 16/600 Superdex 75 pg).

Biological activity of sST2 was proven according to standard protocols. Briefly, murine splenocytes were cultured in the presence of activating CD3/CD28 Abs in the presence of 10 ng/ml IL-33 (PeproTech). Addition of sST2 entirely suppressed the IL-33–induced production of IL-5 in a dose-dependent manner (data not shown).

Preparation of CNS mononuclear cells

At the peak of EAE, mice were sacrificed and perfused immediately with 10 ml of cold PBS through the left cardiac ventricle after opening the right ventricle. Brains and spinal cords were removed, cut into small pieces, and digested for 45 min at 37°C in 2.5 mg/ml collagenase D and 1 mg/ml DNase in DMEM. The digestion preparation was homogenized through a 70-μm cell strainer and centrifuged at $400 \times g$ for 10 min. The cell pellet was resuspended in 30% Percoll and layered onto 70% Percoll. Percoll gradient was run at $1800 \times g$ for 20 min without break, and the interphase containing mononuclear cells was collected for further analysis.

Isolation of gut lamina propria cells

Lamina propria of small intestine was prepared as described (2). Briefly, small intestine was flushed with PBS, and Peyer patches were removed. Intestines were cut longitudinally and incubated in 30 mM EDTA in PBS at pH 8 on ice for 30 min. Thereafter, tissues were vigorously washed in PBS repeatedly, minced into small pieces, and digested in RPMI containing 25 mM HEPES, 0.05 mg/ml collagenase D (Roche), and 10 μg/ml DNase I (Sigma-Aldrich) at 37°C for 1 h with intermittent pipetting and replacement of digestion media. Collected supernatants were filtered through a 70-μm cell strainer and centrifuged at 500 × *g* for 10 min. The cell pellet was resuspended in a 40% Percoll (GE Healthcare) solution and layered onto an 80% Percoll layer. The Percoll gradient was run at 1500 × *g* at room temperature for 15 min. The interlayer containing lamina propria mononuclear cells was collected and washed prior to further analysis.

Flow cytometry and cell sorting

Single-cell suspensions were prepared by digestion with collagenase D and DNase I, mechanical organs disruption, or peritoneal lavage, incubated with Fc blocking Ab (BD) and stained with the corresponding Abs on ice. Intracellular staining was performed using a Foxp3 fixation/permeabilization kit (eBiosciences) according to the manufacturer's instructions. Live/Dead exclusion was routinely performed using a kit from Life Technologies, and Tregs or Teff cells were identified as single cells as Live/Dead$^-$CD45$^+$CD3$^+$CD4$^+$Foxp3$^+$ or Live/Dead$^-$CD45$^+$CD3$^+$CD4$^+$Foxp3$^-$ cell, respectively. Conventional DCs (cDCs) were identified as Live/Dead$^-$, CD45$^+$ cells expressing high levels of MHC class II (MHC-II), and CD11c. Cell sorting was performed with a FACSAria III cell sorter (BD), and cell purity was typically around 99%. For data analysis FlowJo V7.5.2 (Tree Star) software was used.

Treg suppression assay

MHC-II$^+$ CD11c^{high} DCs were isolated from spleens of control mice and cocultured with CFSE-labeled CD4$^+$CD62L$^+$CD44^{low}naive Th cells isolated from control spleens in presence of 1 μg/ml soluble anti-CD3 for 3 d in a 96-well plate. If indicated, Tregs from control or RelB$^{\Delta DC}$ spleens were cocultured at a 1:2 ratio. Ratio of T cells to DCs was 5:1 with 1×10^5 T cells per well.

ELISA

Sandwich ELISA for total serum IgE was performed using a polyclonal sheep anti-mouse IgE (The Binding Site) for coating and biotinylated rat anti-mouse IgE (clone R35-118; BD Biosciences) for detection. After incubation with streptavidin-peroxidase (Calbiochem), tetramethylbenzidine (Fluka) was used according to the manufacturer's instructions, and absorption was measured at 450 nm. IL-2 and IL-33 serum levels were measured with a multiplex assay (Meso Scale Diagnostics) according to the manufacturer's instructions.

RNA-sequencing analysis

Total RNA was extracted from sort-purified Tregs from RelB$^{\Delta DC}$Foxp3^{RFP} mice from indicated organs using a RNeasy Micro Kit (Qiagen). Complete cDNA was synthesized from 5 μl of total RNA using the SmartScribe reverse transcriptase (Takara Bio) with a universally tailed poly-dT primer and a template-switching oligo followed by amplification for 12 cycles with the Advantage 2 DNA Polymerase (Takara Bio). After ultrasonic shearing (LE220; Covaris), amplified cDNA samples were subjected to standard Illumina fragment library preparation using the NEBnext Ultra DNA library preparation chemistry (New England Biolabs). In brief, cDNA fragments were end-repaired, A-tailed, and ligated to indexed Illumina TruSeq adapters. Resulting libraries were PCR amplified for 15 cycles using universal primers, purified using XP beads (Beckman Coulter), and then quantified with the Fragment Analyzer. Final libraries were equimolarly pooled and subjected to 75-bp single-end sequencing on the Illumina NextSeq 500 platform, resulting in ~27–47 mio reads. Reads were mapped to the mouse genome (version mm10) with GSNAP ([31]; v2018-03-11) and splice sites from Ensembl (version 81) as support. RNA-sequencing (RNA-seq) data quality was assessed with RNA-SeQC ([32]; v1.1.8). Uniquely mapped reads served as input for obtaining gene counts with featureCounts ([33]; v1.6.0) and Ensembl gene annotations (version 81). Principle component analysis and visualization was done in R using prcomp and ggplot functions. Normalization for library size and identification of differentially expressed genes was done with the R package DESeq2 ([34]; v1.18.1). DESeq2 *p* values were adjusted for multiple testing (Benjamini-Hochberg), and genes with an adjusted *p* value < 0.1 were considered as differentially expressed. RNA-sequencing data of this study are available at the National Center for Biotechnology Information's Gene Expression Omnibus database under accession number GSE134779 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE134779).

Statistics

Data were analyzed by two-tailed Student *t* test and, unless otherwise indicated, analyzed using GraphPad Prism software. Bar diagrams show mean ± SD unless otherwise indicated. Mann–Whitney *U* test and two-way ANOVA with Tukey multiple correction test were used in EAE experiments as indicated. Statistical significance was set at: $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, and $****p < 0.0001$.

Results

NF-κB members alter Foxp3$^+$ regulatory T cells in a DC-specific manner

Complete knockout of the noncanonical NF-κB member RelB has been shown to result in severe T cell–dependent autoimmune inflammation (35–37). In most cell types, RelB typically pairs with p52, a breakdown product of NF-κB2/p100, to mediate signaling via the so-called alternative NF-κB pathway. Therefore, we first addressed whether genetic deletion of RelB or the regulatory element of the p100/NF-κB2 precursor protein (20) alters systemic Treg homeostasis. Confirming earlier observations, RelB deficiency resulted in a drastic increase of Foxp3$^+$ Tregs in the spleen (Fig. 1A). Surprisingly, bone marrow chimeras receiving p100-deficient bone marrow did not show any alteration in Foxp3$^+$ Tregs (Fig. 1A). To investigate a potential role of RelB or NF-κB2 in DCs for Treg biology, we crossed mice with a floxed allele of the *relb* gene (19) or *nfkb2* gene (26) to mice expressing the *Cre* recombinase under control of a DC-specific promoter (25) called RelB$^{\Delta DC}$ or NF-κB2$^{\Delta DC}$ mice, respectively. We first checked deletion efficacy in different cellular subsets of the spleen and bone marrow–derived macrophages. As expected, splenic DCs showed the most efficient *relB* deletion (Supplemental Fig. 1A) compared with other splenic subsets. Bone marrow–derived macrophages also partially deleted RelB (Supplemental Fig. 1A), indicating at least modest expression of CD11c and recombination in other myeloid lineages. Still, in this manuscript we will continue to talk about DCs for consistency with the current literature related to Itgax-Cre line. Interestingly, RelB$^{\Delta DC}$ mice showed a similar increase in splenic Tregs as complete RelB-deficient mice, whereas NF-κB2$^{\Delta DC}$ mice showed only a modest yet significant increase in Treg numbers (Fig. 1B). To definitively exclude a Treg-intrinsic role of RelB, we additionally ablated RelB exclusively in Foxp3$^+$ Tregs. We did not find any difference in Treg numbers of mice lacking RelB in Foxp3$^+$ cells (Fig. 1B) in line with recent findings for a T cell–extrinsic role of RelB in the regulation of Treg biology (38, 39). As both canonical and noncanonical NF-κB pathways regulate DC activation and maturation in an interactive manner (40), we addressed how splenic DCs are altered in the absence of RelB or NF-κB2. Conditional ablation of RelB but not NF-κB2 resulted in a slight reduction of overall DC frequencies and a relative increase of Sirpα$^-$CD8α$^+$ DCs that expressed high levels of DEC-205 (Fig. 1C, 1D). This confirms earlier results in which RelB has been shown to be necessary for the development of splenic myeloid-related CD8α$^-$ DCs (cDC2s) (41–43). DEC-205 has been previously associated to Treg induction, and the relative increase of DEC-205$^+$ DCs in RelB$^{\Delta DC}$ but not in NF-κB2$^{\Delta DC}$ mice may contribute to Treg accumulation (Fig. 1C, 1D and [44]). Besides DEC-205, altered expression patterns of costimulatory molecules on DCs may contribute to Treg accumulation in RelB$^{\Delta DC}$ mice. Indeed, DCs from RelB$^{\Delta DC}$ expressed less PD-L1 but more PD-L2, whereas expression of OX40L remained unchanged relative to control animals at steady-state (Fig. 1E).

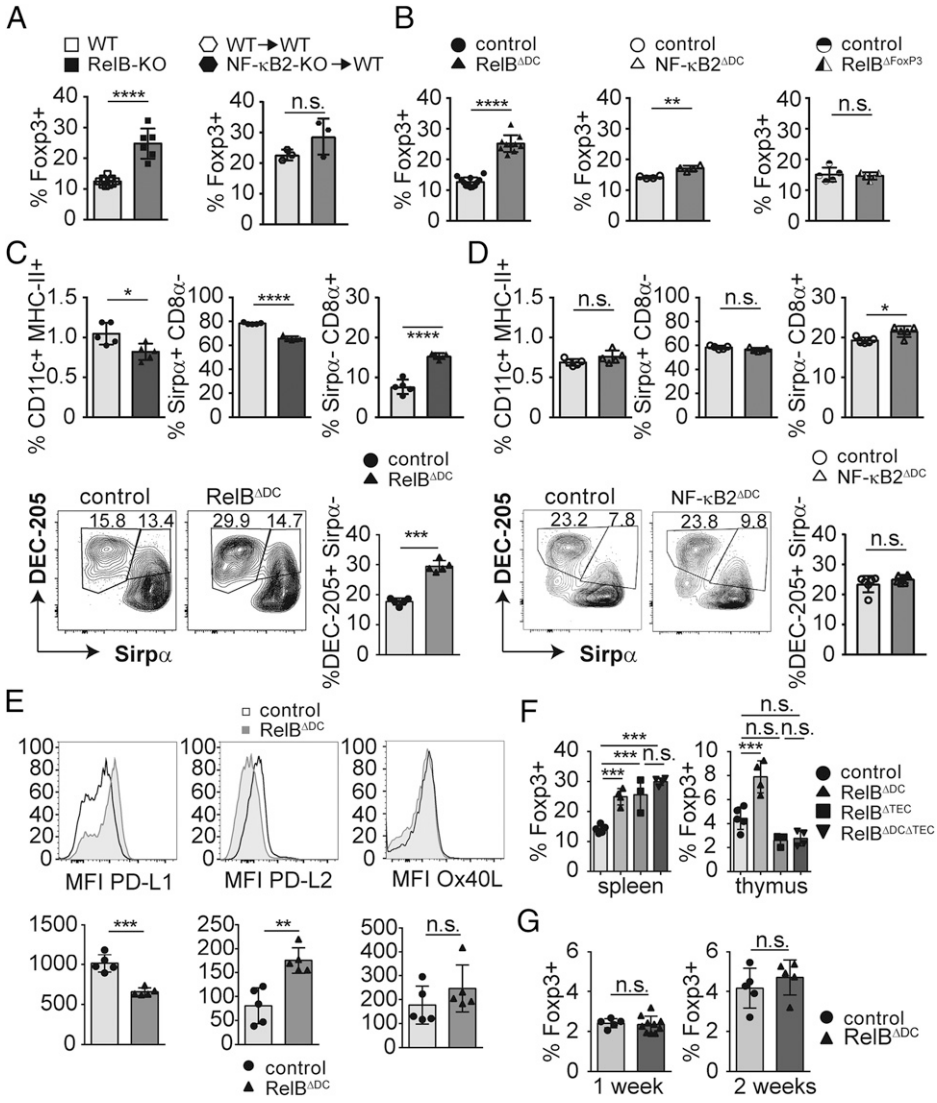

FIGURE 1. Differential impact of alternative NF-κB member on DCs and Tregs. Frequencies of Foxp3$^+$ Tregs among CD4$^+$ T cells in spleens of the indicated knockout animals or bone marrow chimeras. (**A**) Frequencies of Foxp3$^+$ Tregs among CD4$^+$ T cells in spleens of the indicated conditional knockout animals. (**B**) Frequencies of Foxp3$^+$ Tregs among CD4$^+$ T cells in spleens of the indicated conditional knockout animals. (**C**) Bar diagrams show frequencies of splenic DCs and Sirpα$^+$CD8α$^-$ and Sirpα$^-$CD8α$^+$ DC subsets (upper panels) of control and RelB$^{\Delta DC}$ mice. Contour plots (lower panels) show DEC-205$^+$Sirpα$^-$ splenic DC subsets and enumeration in control and RelB$^{\Delta DC}$ mice. (**D**) Bar diagrams show frequencies of splenic DCs and Sirpα$^+$CD8α$^-$ and Sirpα$^-$CD8α$^+$ DC subsets (upper panels) of control and NF-κB2$^{\Delta DC}$ mice. Contour plots (lower panels) show DEC-205$^+$Sirpα$^-$ splenic DC subsets and enumeration in control and NF-κB2$^{\Delta DC}$ mice. (**E**) Representative histograms and mean fluorescence intensity (MFI) of PD-L1, PD-L2, and OX40L expression on dendritic cells (CD11c$^+$MHC-II$^+$) in spleens from littermate control (filled histogram) or RelB$^{\Delta DC}$ mice (open histograms). (**F**) Quantification of Foxp3$^+$ Treg frequencies in spleen and thymus of WT or RelB$^{\Delta DC}$ mice or mice lacking RelB in medullary thymic epithelial cells (RelB$^{\Delta TEC}$) or both (RelB$^{\Delta DC\Delta TEC}$). Statistics were performed with one-way ANOVA with Tukey multiple correction test (***$p < 0.001$). (**G**) Quantification of Treg frequencies in the thymi of 1-week and 2-week-old littermate controls and RelB$^{\Delta DC}$ mice. All data show pooled results of at least two independent experiments and if not stated differently, analyzed by two-tailed Student *t* test. Bar diagrams show mean ± SD. *$p < 0.05$, **$p < 0.01$, ***$p < 0.001$, ****$p < 0.0001$.

Thus, signaling via the NF-κB member RelB but not NF-κB2/p52 in DCs has a dominant role in controlling Treg homeostasis.

Enhanced differentiation of Tregs in the thymus could alternatively account for an accumulation of peripheral Tregs. Indeed, we found more Foxp3$^+$ Tregs in the thymus of adult RelB$^{\Delta DC}$ mice (Fig. 1F). We also observed a slight reduction of thymic Sirpα$^+$ DCs in RelB$^{\Delta DC}$ but not NF-κB2$^{\Delta DC}$ mice similar to splenic DCs lacking RelB (Supplemental Fig. 1B and [42, 43]). Given that migration of peripheral Sirpα$^+$CD8^{lo} DCs to the thymus has been proposed to efficiently induce Treg differentiation (45, 46) the observed reduction of this DC subset in the thymus of RelB$^{\Delta DC}$ mice makes it unlikely that peripheral DCs contribute to thymic Treg accumulation. In line with decreased Treg frequencies in RelB$^{\Delta TEC}$ mice (19), simultaneous ablation of RelB in DCs and mTECs prevented increased Treg frequencies in the thymus of adult mice compared with control mice, whereas Treg numbers in spleen were still increased (Fig. 1F). Treg accumulation in spleens of RelB$^{\Delta DC\Delta TEC}$ mice may be due to altered negative selection in RelB$^{\Delta TEC}$ mice resulting in autoimmunity (19) and a dominant effect of RelB-deficient DCs in the periphery. As peripherally induced Tregs can migrate to the adult thymus (47), we measured Treg frequencies in very young mice, in which peripheral Treg conversion is still very limited. However, we did not observe an increase in thymic Treg frequencies at 1 or 2 wk of age (Fig. 1G). Finally, conversion of otherwise negatively selected T cells into the Treg lineage can equally result in enhanced Treg differentiation in

the adult thymus. To test this hypothesis, we crossed RelB$^{\Delta DC}$ mice on a C57BL/6 background for one generation to a BALB/c background in which a superantigen encoding retrovirus is exclusively expressed in DCs (Mtv-6). This results in impaired negative selection of Vβ3$^+$ T cells in the constitutive absence of DCs (16). However, we did not find any difference among Vβ3$^+$ Tregs between C57BL/6 and mixed background mice in the absence of RelB in DCs (Supplemental Fig. 1C). In summary, these results indicate that accumulation of Tregs in RelB$^{\Delta DC}$ mice depends on age-dependent peripheral differentiation of Tregs by DC-intrinsic effects induced by the absence of RelB-dependent gene regulation.

Accumulated Tregs in RelB$^{\Delta DC}$ mice show a tissue Treg signature

As our results so far indicate an accumulation of Tregs by peripheral mechanisms, we performed a detailed characterization of Tregs in several tissues of RelB$^{\Delta DC}$ and NF-κB2$^{\Delta DC}$ mice. All examined organs showed an accumulation of Foxp3$^+$ Tregs in RelB$^{\Delta DC}$ and RelB$^{KO/KO}$ mice, and this was particularly pronounced among Helios$^+$ Tregs (Fig. 2A, Supplemental Fig. 2A, 2B and data not shown). This effect was almost completely blunted in NF-κB2$^{\Delta DC}$ mice (Fig. 2A, Supplemental Fig. 2A), indicating that Treg accumulation occurred in a RelB-dependent but NF-κB2–independent fashion. The high expression levels of Helios among accumulated Tregs in RelB$^{\Delta DC}$ and NF-κB2$^{\Delta DC}$ and mice argues for a preferential accumulation of Tregs specific for self-antigens because thymic and tissue-restricted neo–self-antigens have been shown to induce Tregs that express Helios (48, 49). As increased proliferation rates may contribute to Treg accumulation, we measured intracellular Ki-67 expression among Tregs of various organs. Indeed, we found higher Ki-67 expression in Tregs in spleen and lymph nodes but not thymus of RelB$^{\Delta DC}$ compared with control mice (Fig. 2B).

To gain deeper insight into the identity of accumulated Tregs in RelB$^{\Delta DC}$ mice, we performed RNA-seq analysis of sort-purified Tregs from RelB$^{\Delta DC}$ mice backcrossed to a Foxp3 reporter line. Indeed, Tregs derived from the peritoneal cavity (PEC) as one of the sites with the highest Treg accumulation revealed a number of differently expressed genes reminiscent of tissue Tregs in RelB$^{\Delta DC}$ mice, including high expression levels of *Klrg1*, *Il1rl1*, *Gata3*, *Pparg*, *Itgae*, *Nrp1*, and *Tnfrsf4* but low expression of *Bcl2* and *CCR7* (Fig. 2C, Supplemental Fig. 2C and [8]). We were able to confirm these Treg markers by flow cytometry, including KLRG1, OX40 (encoded by *Tnfrsf4*), CD103, PD-1, ICOS, GITR, and ST2 (encoded by *Il1rl1*) (Fig. 2D, Supplemental Fig. 2D). Interestingly, some of the tissue Treg signature genes were even found to be differentially expressed in Tregs isolated from the spleen and thymus of RelB$^{\Delta DC}$ mice, indicating a systemic shift in favor of tissue Tregs (Supplemental Fig. 2C). Expression of Satb1, a recently identified genome organizer necessary for proper Treg differentiation in the thymus upstream of Foxp3 expression (50), was expressed at lower levels in Tregs derived from RelB$^{\Delta DC}$ mice compared with controls in all organs (Fig. 2C, Supplemental Fig. 2C).

Barrier organs such as the intestinal tract are exposed to both self- and harmless foreign Ags that similarly rely on induction of Foxp3$^+$ Tregs for maintenance of immune tolerance. We confirmed that accumulated Tregs in RelB$^{\Delta DC}$ mice expressed higher Gata3 levels within the intestinal tract, and this was again dominant among Helios$^+$ Tregs (Fig. 2E). Surprisingly, microbiota-induced ROR(γt)$^+$ Tregs in the small intestine were reduced in RelB$^{\Delta DC}$ mice (Fig. 2F) even when excluding accumulated Helios$^+$ Tregs (Supplemental Fig. 2E). As ROR(γt)$^+$ Tregs are able to regulate type 2 immunity (2), we tested whether a comparable phenotype was observed in Teff cells of RelB$^{\Delta DC}$ mice. Indeed, Gata3$^+$ Teff cells accumulated spontaneously in the intestinal tract of RelB$^{\Delta DC}$ mice (Fig. 2G). Whether accumulation of Gata3$^+$ Th2 cells is a direct consequence of RelB deficiency in DCs or a result of the altered Treg compartment remains to be addressed. In line with these observations we found elevated levels of IgE in the serum and on the surface of FcεRI-bearing basophils and mast cells of RelB$^{\Delta DC}$ mice, a hallmark of type 2 immunity (Fig. 2H, Supplemental Fig. 3A, 3B). All of these observations could also be found in RelB$^{KO/KO}$ mice (Supplemental Fig. 3D–F) and (37). Despite this systemic type 2 immune bias in T cells and a tendency of increased blood eosinophils levels in RelB$^{\Delta DC}$ mice (Supplemental Fig. 3C), we did not find any visible signs of inflammation typically observed in RelB$^{KO/KO}$ mice (data not shown and [35–37]). Thus, both RelB$^{KO/KO}$ and RelB$^{\Delta DC}$ mice show an accumulation of Gata3^{hi} tissue Tregs partially at the expense of ROR(γt)-expressing Tregs.

Tissue Tregs in RelB$^{\Delta DC}$ mice accumulate independent of IL-33

In line with the systemic type 2 immune bias in T cells from RelB$^{\Delta DC}$ mice, we also observed higher expression of the IL-33R ST2 on Gata3$^+$ Teff cells and Helios$^+$ Tregs (Fig. 3A, 3B). Notably, ST2 expression has been previously linked to high Gata3 expression in Tregs (51). Given that IL-2/anti–IL-2 Ab complexes and particularly external IL-33 administration can boost the accumulation of ST2$^+$/Gata3$^+$ Tregs (6, 51, 52), we asked whether excessive IL-2 or IL-33 could be one of the drivers for the accumulation of tissue Tregs in RelB$^{\Delta DC}$ mice (reviewed in Ref. 53). First, we did not find differences in serum levels of IL-33 nor IL-2 in the serum of RelB$^{\Delta DC}$ mice compared with control mice (Fig. 3C). In addition, blocking IL-33 by injection of a sST2 decoy receptor over 3 wk did not reveal a major difference in total or ST2$^+$ Treg frequencies (Fig. 3D). As IL-33 is predominantly expressed by nonhematopoietic cells (21), we additionally created bone marrow chimeras with IL-33$^{KO/KO}$ animals as recipients. Again, we found a similar increase in ST2$^+$Helios$^+$ Tregs and Th2-biased Teff cells compared with WT recipients receiving bone marrow from RelB$^{\Delta DC}$ mice despite undetectable IL-33 levels in IL-33$^{KO/KO}$ recipients (Fig. 3E). Noteworthy is that constitutive IL-33–deficient mice possess normal levels of ST2$^+$ Tregs (54). This may indicate that IL-33 expands Tregs to prevent tissue damage (e.g., during ongoing type 2 immune-driven inflammation) but is not the primary driver for the tissue Treg phenotype under physiologic conditions or in RelB$^{\Delta DC}$ mice. Additionally, these results rule out a role of nonhematopoietic RelB expression (e.g., by mTECs or other radio-resistant cells of nonhematopoietic origin [42]).

In summary, these results reveal that the increase in Tregs with a tissue Treg phenotype is independent of IL-33 or other nonhematopoietic effects. Several RelB-dependent mechanisms in DCs may be in place that regulate Treg biology in an integrative manner depending on the antigenic source and/or the anatomical site.

Tregs from RelB$^{\Delta DC}$ mice are functional in vitro and in vivo

The type 2 immune bias of the accumulated Tregs observed in RelB$^{\Delta DC}$ mice raised the question of whether these Tregs are still functional because Th2 reprogramming of Tregs after excessive IL-4 or IL-33 signaling and corresponding high Gata3 expression has been proposed to impair their tolerogenic function (52, 55). Therefore, we first cocultured Tregs derived from RelB$^{\Delta DC}$ or control mice with Teff cells in the presence of WT myeloid DCs. Under these in vitro settings, we did not find a difference in their suppressive capacity (Fig. 4A). Next, we tested whether Tregs

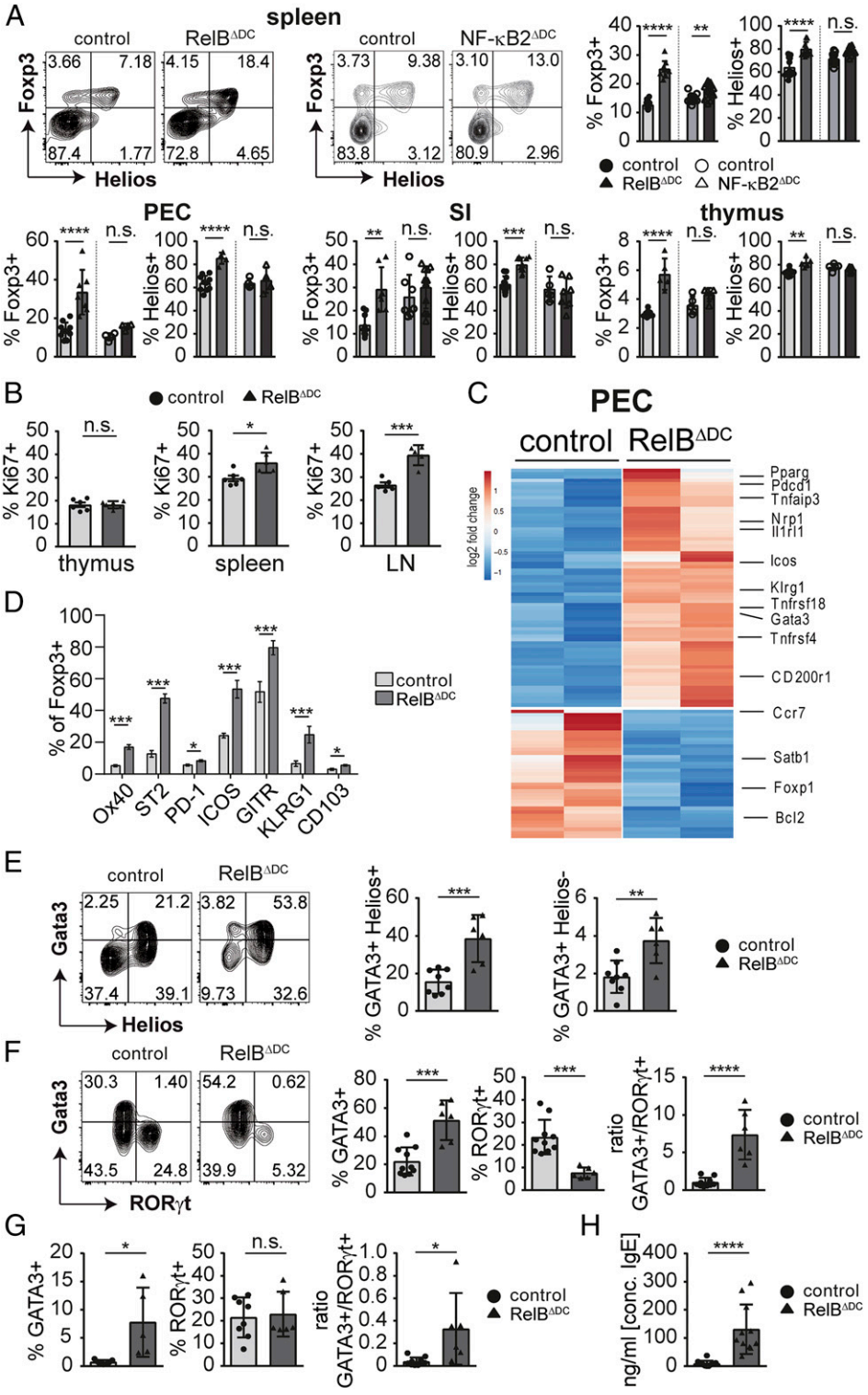

FIGURE 2. Accumulated Tregs in RelB$^{\Delta DC}$ mice show a tissue Treg signature with a type 2 immune bias. (**A**) Representative FACS plots and quantification of Foxp3$^+$ Tregs among CD4$^+$ T cells and frequency of Helios$^+$ among total Tregs in indicated organs. Statistics were performed with one-way ANOVA with Tukey multiple correction test. (**B**) Bar diagrams show frequencies of Ki-67$^+$ cells among Foxp3$^+$ Tregs in indicated organs. (**C**) Heatmap depicts selected differentially expressed genes according to RNA-seq analysis of sort-purified Tregs isolated from the PEC of control or RelB$^{\Delta DC}$ mice with a false discovery rate < 0.1 and adjusted $p < 0.1$. (**D**) Quantification of selected tissue Treg marker expression in PEC by flow cytometry. (**E**) Representative FACS plots and quantification of Gata3^{hi}Helios$^+$ and Gata3^{hi}Helios$^-$ within pregated Foxp3$^+$ Tregs isolated from the lamina propria of the small intestine. (**F**) Representative FACS plots (left) and bar diagrams (right) of RORγt and Gata3 expression within pregated Foxp3$^+$ Tregs isolated from the lamina propria of the small intestine and ratio between Gata3 and RORγt-expressing Tregs. (**G**) Bar diagrams show frequencies of RORγt$^+$ and Gata3^{hi} T cells among Foxp3$^-$ Teff cells ratio between Gata3 and RORγt-expressing Teff cells isolated from the small intestine. (**H**) Concentration of total serum IgE level of naive adult mice. All data show pooled results of at least two independent experiments and analyzed, if not stated differently, by two-tailed Student *t* test. Bar diagrams show mean ± SD. $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$.

from each genotype are able to prevent wasting disease in mice carrying the *scurfy* mutation that results in severe autoimmune inflammation due to an intrinsic Treg deficiency. When reconstituted with Tregs from RelB$^{\Delta DC}$ or control mice, scurfy mice could be rescued equally with only minor variations in survival and weight gain (Fig. 4B). So far, these data indicate that Tregs from RelB$^{\Delta DC}$ mice are functional in vitro and in vivo. Finally, we also tested whether oral tolerance induction is enhanced in RelB$^{\Delta DC}$ mice. We transferred congenically labeled naive OT-II cells into RelB$^{\Delta DC}$ or control mice and applied OVA via the drinking water. Surprisingly, we found reduced frequencies of de novo–induced Tregs derived from naive OT-II cells in RelB$^{\Delta DC}$ mice, and these Tregs additionally expressed less ROR(γt) (Fig. 4C). As we have previously shown that microbiota-induced ROR(γt)$^+$ Tregs are able to regulate Th2-dominated immune responses, we also looked for de novo differentiation of Th2 cells (2). Indeed, we found an upregulation of Gata3 both within the Treg and the Teff cell compartment in RelB$^{\Delta DC}$ mice (Fig. 4D, 4E). In summary, these results indicate that accumulated Tregs in RelB$^{\Delta DC}$ mice are functional and protect from inflammation.

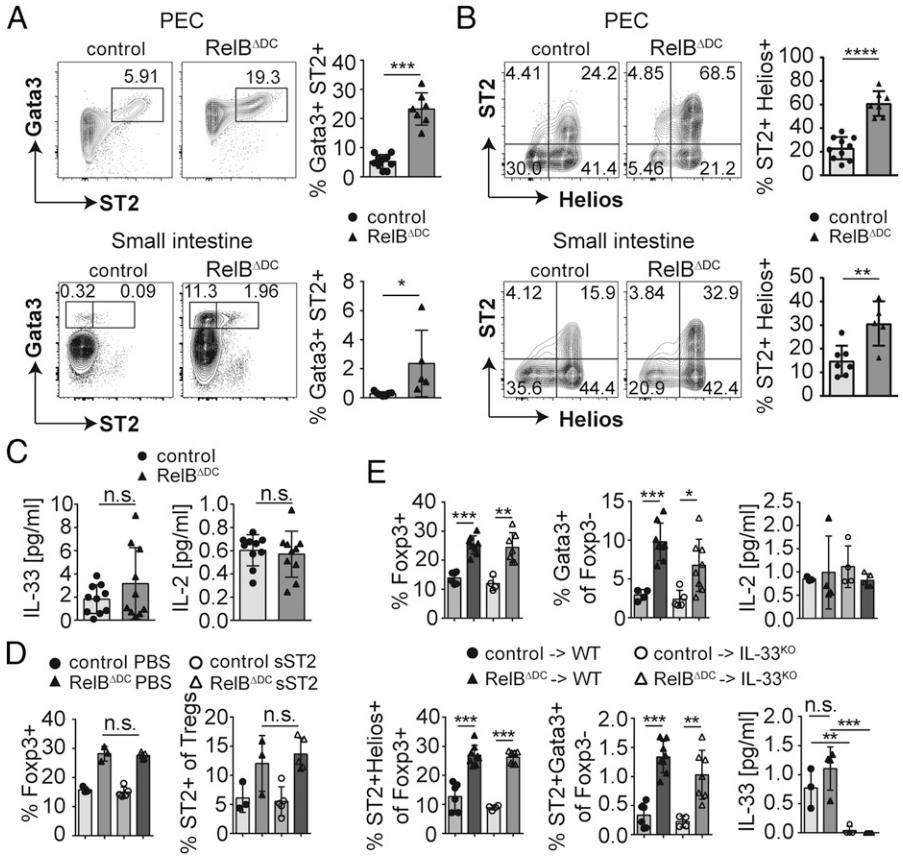

FIGURE 3. RelB$^{\Delta DC}$ mice accumulate ST2$^+$ tissue Tregs independent of IL-33. (**A**) Representative FACS plots (left) and quantification (right) of Gata3$^+$ST2$^+$ cells within Foxp3$^-$ T cells in PEC or small intestine of littermate control and RelB$^{\Delta DC}$ mice. (**B**) Representative FACS plots (left) and quantification (right) from littermate control and RelB$^{\Delta DC}$ mice showing ST2$^+$ Helios$^+$ cells among Foxp3$^+$ Tregs from PEC and lamina propria of the small intestine. (**C**) IL-33 and IL-2 serum levels of control littermates and RelB$^{\Delta DC}$ mice. (**D**) sST2 or PBS was injected i.p every other day into control or RelB$^{\Delta DC}$ mice for 3 wk. Bars indicate Foxp3$^+$ Treg numbers and ST2 expression among Tregs in the spleen at the end of the experiment. Statistics were performed with one-way ANOVA with Tukey multiple correction test. $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$. (**E**) Treg frequencies and expression of Helios, ST2, and Gata3 in the spleen from bone marrow chimeras receiving either bone marrow from littermate or RelB$^{\Delta DC}$ animals. WT or IL-33$^{KO/KO}$ animals served as recipients as indicated. Lower plots show serum levels of IL-33 or IL-2 in the described bone marrow chimeras. Statistics were performed with one-way ANOVA with Tukey multiple correction test. $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$. All data show pooled results of one (E) or at least two independent experiments and analyzed if not stated differently, by two-tailed Student *t* test. Bar diagrams show mean ± SD. $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$.

However, this occurs at the expense of impaired de novo Treg differentiation capacity and accumulating Th2 cells in the intestinal tract in response to foreign oral Ags similar to what has been found in germ-free mice (56).

Accumulation of tissue Tregs protects from autoimmunity

Overall, our data indicate a specific accumulation of Tregs with a tissue Treg signature in RelB$^{\Delta DC}$ mice. Given that Gata3$^+$ Tregs are still present in the absence of microbial stimulation by bacterial symbionts (2), we reasoned that most of the accumulated Tregs in RelB$^{\Delta DC}$ mice are specific for self-antigens and may thus protect from autoimmune inflammation. We therefore induced EAE in both RelB$^{\Delta DC}$ and control mice and followed disease scores. Intriguingly, RelB$^{\Delta DC}$ mice were almost completely protected from disease, whereas littermates showed severe signs of autoimmune inflammation (max. mean score: 2.4 [control] versus 0.58 [RelB$^{\Delta DC}$] [Fig. 5A]). In line with the low EAE scores we found reduced absolute numbers of pathogenic cytokine-producing T cells in the spinal cord (Fig. 5B, Supplemental Fig. 4A). Moreover, less of these infiltrating T cells were specific for MOG protein because restimulation with MOG$_{35–55}$ peptide revealed reduced numbers of CD154$^+$ Ag-specific T cells in the CNS of RelB$^{\Delta DC}$ mice (Supplemental Fig. 4B). We also found more Gata3$^+$ T cells and Tregs in the CNS at the peak of the disease (Fig. 5C, Supplemental Fig. 4C, 4D) and as expected increased numbers of Helios$^+$ Tregs expressing ST2 (Fig. 5D, Supplemental Fig. 4E).

Next, we wanted to exclude a potential DC-intrinsic defect during the priming phase in the absence of RelB and therefore adopted a protocol of Ab-mediated depletion of Tregs prior to EAE induction (57). As expected, Treg depletion aggravated disease scores in control animals (Fig. 5E). Despite the only moderate Treg depletion efficiency in RelB$^{\Delta DC}$ mice at the time of immunization and rapid Treg recovery at the peak of disease (Supplemental Fig. 4F, 4G), we observed similar disease scores in Treg-depleted RelB$^{\Delta DC}$ and control animals (Fig. 5E). This was again associated with an accumulation of pathogenic cytokine-producing Teff cells in the CNS (Fig. 5F). Thus, RelB-deficient DCs are capable of inducing a full-blown pathogenic immune response in the absence of an excess of polyclonal tissue Tregs. Notably, treatment of mice with rIL-33, which is known to boost accumulation of tissue Tregs, is equally able to reduce EAE disease scores (58). To address whether RelB$^{\Delta DC}$ mice support increased de novo production of self-reactive Tregs during EAE in vivo, we transferred sort-purified MOG-specific 2D2Foxp3$^-$ naive T cells into RelB$^{\Delta DC}$ or control mice prior to EAE induction. Interestingly, 2D2 T cells started to upregulate Foxp3 in RelB$^{\Delta DC}$ but not control mice

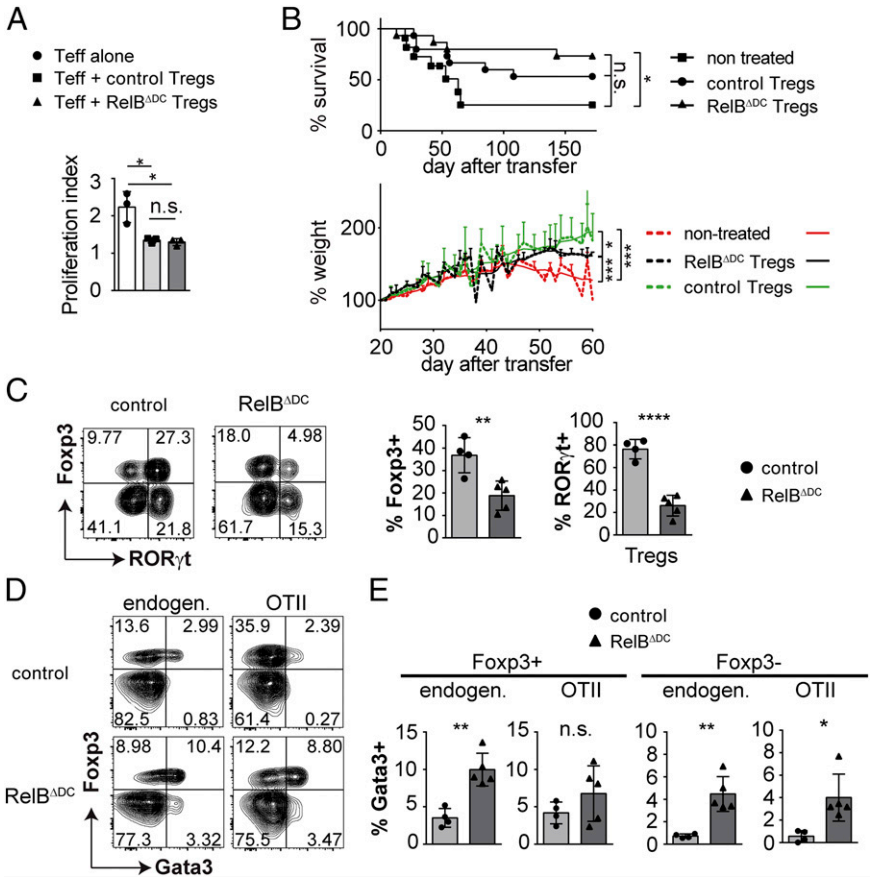

FIGURE 4. Tregs from RelB$^{\Delta DC}$ mice are functional in vitro and in vivo but de novo induction of Tregs in the intestinal tract is impaired. (**A**) Proliferation index from an in vitro suppression assay with DCs and Teff cells isolated from WT mice and Tregs isolated from littermate control or RelB$^{\Delta DC}$ mice. (**B**) Six-day-old mice with the scurfy mutation received bulk CD4$^+$ T cells isolated from littermate control or RelB$^{\Delta DC}$ mice by i.p. injection. Upper plot indicate survival rate, lower plot indicate mean percentage of initial body weight at day 20. (**C**) Littermate control and RelB$^{\Delta DC}$ mice received congenically labeled naive OT-II T cells by i.v. injection and were exposed to 1.5% chicken OVA containing drinking water for the following 9 d. Representative contour plots (left) and quantification (right) of Foxp3$^+$ and ROR(γt)$^+$Foxp3$^+$ among OT-II cells isolated from the lamina propria of the small intestine are shown. (**D**) Comparison of endogenous and transferred T cells for Foxp3 and Gata3 expression among T cells isolated from the lamina propria of the small intestine from the experiment in (C). (**E**) Quantification of the data shown in (D). All data show pooled results of at least two independent experiments and were analyzed by two-tailed Student *t* test. Bar diagrams show mean ± SD. $*p < 0.05$, $**p < 0.01$, $***p < 0.001$, $****p < 0.0001$.

by day 7 after immunization in the draining inguinal lymph node before any sign of disease onset (Fig. 5G). In summary, these data reveal a key role of tissue Tregs for preventing autoimmune inflammation, which can be achieved through selected deletion of the NF-κB family member RelB in DCs.

Discussion

APCs and notably DCs have been known as initiator cells for the induction of immune responses to foreign Ags, whereas their role for active tolerance induction with therapeutic potential has been recognized only at the beginning of this century (59). Particularly the mutual relationship between DCs and Tregs through increasing DC numbers and a simultaneous increase of Tregs indicates a critical role of DC–T cell interactions for dictating Treg populations (60). Treg homeostasis and function in the periphery is further dependent on continuous triggering of the TCR by (auto-) Ags most likely constantly presented by DCs. Yet, this effect is independent from Treg hallmarks like Treg signature gene expression or the ability to use IL-2 but alters expression of a number of tissue Treg-associated genes, including Helios and Gata3 (61, 62). In this study, we have identified one pathway within the DC compartment that limits the proliferation and therefore also accumulation of tissue Tregs: Ablation of RelB but not NF-κB2 within CD11c$^+$ cells leads to a drastic increase in Treg numbers that predominantly show a tissue Treg phenotype. Most likely, the majority of such accumulated Helios$^+$ Tregs in RelB$^{\Delta DC}$ mice are specific for self-antigens, as both thymic and tissue-restricted neo–self-antigens are able to induce Helios$^+$ Tregs, whereas Treg-specific Helios expression has not been described in Tregs with TCR specificities for foreign Ags (48, 49). Thus, it remains possible that both enhanced generation of Tregs in the thymus and increased de novo generation in the periphery contribute to the increase in Tregs although the latter possibility may be more relevant in RelB$^{\Delta DC}$ mice according to de novo Treg induction of 2D2 T cells (Fig. 5F) and low expression of Satb1 and Bcl2. Accumulated Tregs in RelB$^{\Delta DC}$ mice show hallmarks of tissue Tregs, including expression of ST2, Gata3, and Helios and are able to almost completely protect from autoimmune inflammation of the CNS. DCs have been previously associated with maintenance and induction of self-reactive Tregs. However, Batf3-dependent CD8α$^+$ DCs were dispensable for the induction of prostate-specific Tregs (15). In line with these results, RelB$^{\Delta DC}$ mice show a reduction mainly in Sirpα$^+$CD8α$^-$ DCs but not CD8α$^+$ (Batf3-dependent DCs) due to cell-intrinsic developmental defects in the absence of RelB (42, 43). This results in a dominant accumulation of DEC-205$^+$ DCs that have been previously shown to be ideal targets for Ag-specific tolerance applications via induction of Foxp3$^+$ Tregs (44). Notably, therapeutic targeting of MOG expression to DCs was able to induce PD-1$^+$ Tregs and protect mice from EAE, whereas conditional ablation of DCs resulted in a more severe inflammation of the CNS (14).

Mechanistically, ST2 deficiency has been shown to prevent Gata3 expression in Tregs, and exogenous IL-33 is able to induce accumulation of ST2$^+$ Tregs (8, 51, 63). However, accumulated tissue Tregs in RelB$^{\Delta DC}$ mice were independent from non-hematopoietic IL-33 and also neutralization of IL-33 by sST2 did not reduce Treg levels significantly although it remains possible that DCs themselves are able to provide IL-33 (e.g., within the immunological synapse for expansion of type 2–biased Tregs in RelB$^{\Delta DC}$ mice that we were unable to neutralize [Fig. 3] and [52, 64]). Noteworthy is that IL-33–deficient mice possess normal levels of ST2$^+$ Tregs (54). This may indicate that IL-33 expands Tregs to prevent tissue damage (e.g., during ongoing type 2 immune-driven inflammation) but is not the primary driver for the tissue Treg phenotype under physiologic conditions. Alternatively,

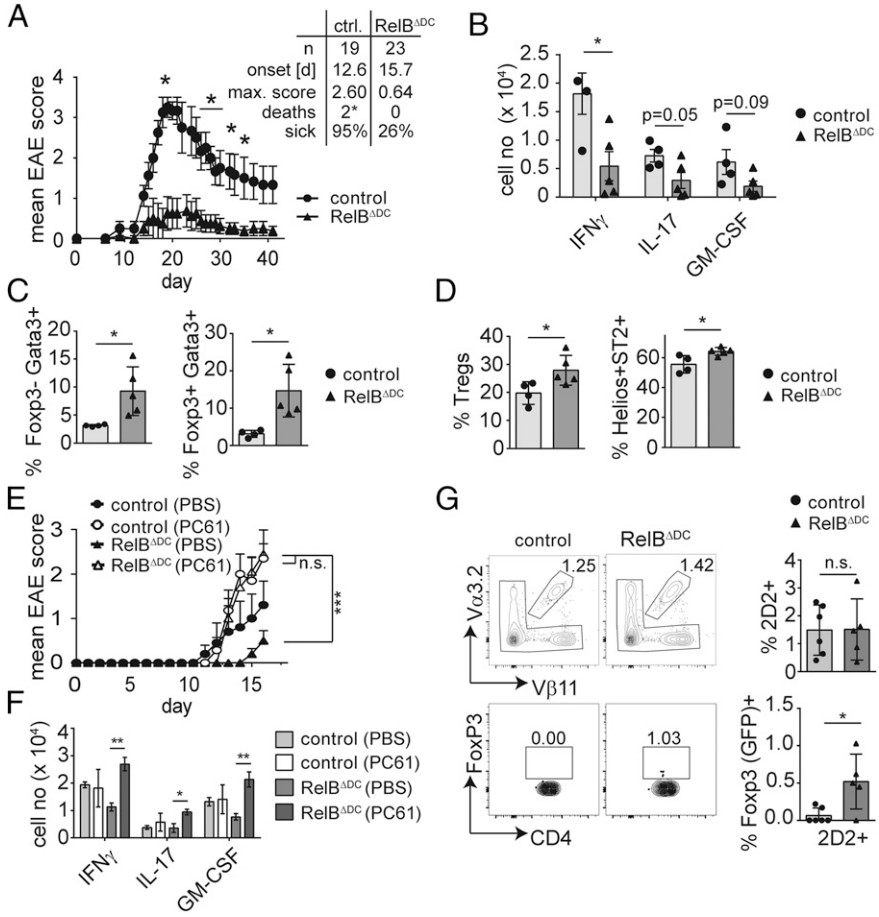

FIGURE 5. RelB$^{\Delta DC}$ mice are protected from EAE due to accumulation of Tregs EAE was induced by immunizing littermate control or RelB$^{\Delta DC}$ mice with MOG_{35-55} in CFA as described in *Materials and Methods*. (**A**) EAE clinical score in WT and RelB$^{\Delta DC}$ mice shown as mean ± SEM of one representative experiment. Table depicts summary of all experiments. Sick, score of at least one. Mice that had to be sacrificed because of high disease scores are indicated as deaths. (**B**) Total numbers of cytokine-expressing Th cells in the CNS at peak of disease after PMA/ionomycin restimulation of one representative experiment. (**C**) Frequency of Foxp3$^-$Gata3$^+$ and Foxp3$^+$Gata3$^+$ Th cells in the CNS at peak of disease. (**D**) Frequency of Foxp3$^+$ cells within CD4$^+$ T cells or frequency of Helios$^+$ ST2$^+$ cells within Foxp3$^+$ Tregs in the CNS at peak of disease. (**E**) Clinical score of EAE in littermate control and RelB$^{\Delta DC}$ mice treated with an anti-CD25 Ab (open symbols) or PBS (filled symbols) prior induction of EAE as described in *Materials and Methods* section. Diagram shows mean ± SEM. (**F**) Total cell number of cytokine-expressing Foxp3$^-$ CD4$^+$ T cells in the CNS at the peak of EAE. (**G**) Littermate control and RelB$^{\Delta DC}$ mice received 2.5×10^6 sort-purified MOG-specific Foxp3/GFP$^-$2D2 T cells prior EAE induction via i.v. injection. Upper plots (left) and quantification (right) indicate frequency of Vα3.2$^+$Vβ11$^+$ 2D2 cells among CD4$^+$ T cells isolated from draining inguinal lymph nodes at day 8 after EAE induction. Lower plots indicate frequency (left) and quantification (right) of Foxp3/GFP$^+$ cells among Vα3.2$^+$Vβ11$^+$ 2D2 T cells isolated from draining inguinal lymph nodes at day 8 after EAE induction. Bar diagrams show mean ± SD of at least two independent experiments unless otherwise indicated. Statistical analysis was performed using Mann–Whitney *U* test (in [A]) or two-way ANOVA with Tukey multiple correction test in (E). Otherwise, unpaired two-tailed Student *t* test was used. $*p < 0.05$, $**p < 0.01$, $***p < 0.001$.

IL-2/anti–IL-2 Ab complexes are able to induce high numbers of Gata3-expressing Tregs, and activation of T cells by RelB-deficient DCs has been shown to result in increased IL-2 production by T cells or DCs (6, 63, 65), but we did not find any difference in systemic IL-2 or IL-33 cytokine levels in the serum or peritoneal lavage of RelB$^{\Delta DC}$ mice.

In line with their assumed specificity for self-antigens, tissue Tregs have been shown to regulate a number of physiological processes, including muscle repair, lung integrity after influenza infection, and metabolic disorders in fat tissues (10–12). We now demonstrate that increasing tissue Treg numbers through ablation of DC-intrinsic RelB is also able to prevent autoimmune inflammation (Fig. 5). Notably, treatment of mice with rIL-33, which among other effects is known to boost accumulation of tissue Tregs, is able to equally reduce EAE disease scores (58). It remains to be addressed how tissue Tregs could fulfill this task but three general possibilities seem plausible: First, tissue Tregs could modulate DCs to prevent effective priming toward bona-fide self-antigens. This possibility has been proposed as a general concept for Treg function but could be dangerous for simultaneous immune responses of different origins and directed toward distinct specificities. Second, accumulation of tissue Tregs could enhance tissue integrity and prevent (e.g., break of the blood-brain barrier) as has been shown for other tissues like lung and muscle (11, 12). Finally, Tregs may prevent Ag-specific T cell responses directly. This would require expansion of de novo–induced Tregs (Fig. 5G) or necessitate the accumulation of MOG-specific Tregs at steady-state in RelB$^{\Delta DC}$ mice. How RelB deficiency in DCs can result in enhanced de novo induction and accumulation of self-reactive Tregs but at the same time result in impaired de novo to orally supplied, foreign Ags remains to be identified, but different functional programs exploited by different DC subsets adapted to their local environment and tissue function are likely in place.

Protection from autoimmune inflammation in RelB$^{\Delta DC}$ mice comes at a high cost, as we have observed impaired tolerance

induction in response to oral Ags and particularly in the numbers of ROR(γt)$^+$ Tregs. This Treg subset is now seen as a major factor for tolerance of symbiotic microbes and is essential for the efficient suppression of different forms of colitis (2, 3, 66, 67). Interestingly, RelB$^{\Delta DC}$ mice show a type 2 bias both within the Treg and the Teff compartment in PEC and small intestine and also after oral Ag exposure. This may be attributed due to cell-intrinsic defects in tissue-resident DCs but also to the lower numbers of ROR(γt)$^+$ Tregs counteracting type 2 immunity (2). Related to these results, DC-specific ablation of TRAF6, a key adaptor protein for the integration of TLR and some TNFR members into NF-κB activation, leads to a spontaneous inflammation of the small intestine characterized by impaired Treg differentiation in response to oral Ag and a marked type 2 immune bias, including accumulation of Th2 cells and eosinophils (68). TRAF6 can also signal via the classical NF-κB pathway, but recent evidence suggests that NF-κB signaling in DCs cannot be strictly divided into classical and alternative signaling pathways (40). Our observation that deletion of NF-κB2 in DCs did not fully recapitulate the RelB$^{\Delta DC}$ in terms of Treg accumulation (Fig. 2A) supports the importance of RelB/p50 or complexes or NF-κB2 homodimers in DCs cross-regulation via classical NF-κB pathways.

Full knockout of RelB results in a fulminant autoimmune inflammation that is dependent on the adaptive immune system (37). However, this can be attributed to the essential role of RelB in mTECs and as a consequence impaired negative selection (19). Indeed, patients suffering from RelB deficiency have to undergo hematopoietic stem cell transplantation due to severe immune deficiency (69). Noteworthy is that at least in one case increased frequencies of Tregs were observed in a RelB-deficient patient before hematopoietic stem cell transplantation (personal communication to Chaim Roifman, The Hospital for Sick Children, Toronto, Canada). Thus, increased Treg numbers cannot control autoimmune inflammation due to impaired central tolerance per se. The reasons for this observation may lay in potential differences and sources of respective self-antigens.

This observation supports our results that RelB could be an attractive target to enhance the number of tissue Tregs for the treatment of autoimmune diseases although not at zero cost. Indeed, infusion of RelB-silenced DCs have been used to treat ongoing myasthenia gravis and shown to prolong allograft tolerance, which was again associated with a Th2 and Treg bias (70–72). Likewise, transfer of WT DCs into RelB-deficient hosts has been shown to reverse airway inflammation and counteract the type 2 bias observed in these mice (73). Finally, type 2–biased Tregs have been found to accumulate in tumorigenic environments and may contribute to prevent effective antitumor immunity (74). Such "negative" functions of type 2 immune-biased Tregs may help to explain why the number of tissue Tregs is limited by RelB-dependent DCs. In summary, the inverse association of RelB-expressing DCs with the accumulation of Th2-biased tissue Tregs proves a dominant effect of tissue Treg numbers for effective protection from autoimmunity.

Acknowledgments

This work is dedicated to Falk Weih who regrettably departed from this life before the end of this study. He will be remembered as as a passionate scientist, a wise group leader, and, first and foremost, a good friend. We thank Benjamin Schnautz and Johanna Grosch for technical assistance and Boris Reizis, Veit Buchholz, Dirk Baumjohann, and Ursula Zimber-Strobl for providing mice.

Disclosures

The authors have no financial conflicts of interest.

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