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Bcl6 Controls the Th2 Inflammatory Activity of Regulatory T Cells by Repressing Gata3 Function

Deepali V. Sawant,* Sarita Sehra,† Evelyn T. Nguyen,‡ Rohit Jadhav,‡ Kate Englert,§ Ryo Shinnakasu,¶ Giao Hangoc,* Hal E. Broxmeyer,* Toshinori Nakayama,¶ Narayanan B. Perumal,* Mark H. Kaplan,*† and Alexander L. Dent*†

The transcriptional repressor Bcl6 is a critical arbiter of Th cell fate, promoting the follicular Th lineage while repressing other Th cell lineages. Bcl6-deficient (Bcl6−/−) mice develop a spontaneous and severe Th2-type inflammatory disease, thus warranting assessment of Bcl6 in regulatory T cell (Treg) function. Bcl6−/− Tregs were competent at suppressing T cell proliferation in vitro and Th1-type colitogenic T cell responses in vivo. In contrast, Bcl6−/− Tregs strongly exacerbated lung inflammation in a model of allergic airway disease and promoted higher Th2 responses, including systemic upregulation of microRNA-21. Further, Bcl6−/− Tregs were selectively impaired at controlling Th2 responses, but not Th1 and Th17 responses, in mixed chimeras of Bcl6−/− bone marrow with Foxp3−/− bone marrow. Bcl6−/− Tregs displayed increased levels of the Th2 transcription factor Gata3 and other Th2 and Treg genes. Bcl6 potently repressed Gata3 transcriptional transactivation, providing a mechanism for the increased expression of Th2 genes by Bcl6−/− Tregs. Gata3 has a critical role in regulating Foxp3 expression and functional fitness of Tregs; however, the signal that regulates Gata3 and restricts its transactivation of Th2 cytokines in Tregs has remained unexplored. Our results identify Bcl6 as an essential transcription factor regulating Gata3 activity in Tregs. Thus, Bcl6 represents a crucial regulatory layer in the Treg functional program that is required for specific suppression of Gata3 and Th2 effector responses by Tregs. The Journal of Immunology, 2012, 189: 000–000.

Bcl6 is a potent sequence-specific transcriptional repressor originally identified as an oncogene in non-Hodgkin’s B cell lymphoma. Insights about a role for Bcl6 in the T cell lineage first came from studies in Bcl6-deficient (Bcl6−/−) mice that develop spontaneous Th2-type inflammatory disease and exhibit pronounced Th2 responses when challenged with an Ag (1–3). The most common manifestation of the inflammatory disease in Bcl6−/− mice is severe myocarditis, which is often accompanied by pulmonary vasculitis. Most Bcl6−/− mice die before 12 wk of age, and these mice typically show severe inflammatory disease. The mechanism by which Bcl6 regulates Th2 responses is not well understood, but there is evidence for post-transcriptional regulation of the Th2 transcription factor Gata3 (4). Bcl6 is the lineage-defining transcription factor for follicular Th cells, a subset of Th cells that provides help to B cells and promotes the germinal center reaction (5–7).

Regulatory T cells (Tregs) are an immune-regulatory subset of CD4+ T cells that is essential for the maintenance of peripheral tolerance and immune homeostasis. The transcription factor Foxp3 specifies the Treg lineage and maintains its functional program (8–10). Tregs function as potent inhibitors of T cell proliferation and T cell-mediated inflammation. Treg function is highly orchestrated, such that specific transcription factors regulate the ability of Tregs to inhibit discrete types of T cell responses. Thus T-bet uniquely controls the ability of Tregs to suppress Th1 responses (11), IRF4 regulates the ability of Tregs to suppress Th2 responses (12), and Stat3 directs the ability of Tregs to suppress Th17 responses (13). The Th2-specific factor Gata3 was recently revealed as a key regulator of Treg function and homeostasis (14, 15).

Although Bcl6 has emerged as a central regulator of Th cell differentiation, the role of Bcl6 in Treg function is not well understood, particularly with regard to suppression of inflammation. Bcl6−/− mice have normal percentages of natural Foxp3+ Tregs (7), and Bcl6 was recently demonstrated to be important for the development of Foxp3+ “follicular repressor T cells” that regulate germinal center responses (16, 17). However, the role of Bcl6 in Treg-mediated control of inflammatory T cell responses has not been elucidated. In this article, we report that Tregs deficient in Bcl6 are uniquely defective in their ability to suppress Th2 inflammation. Bcl6 is required to suppress Th2 genes in Tregs by limiting the transcriptional activity of Gata3. Thus, we identified a novel pathway of gene regulation in Tregs that is essential for Treg-mediated control of Th2 inflammation.
Materials and Methods

Mice

Bcl6−/− mice on a mixed C57BL/6-129sv background were described previously (1, 2). Bcl6−/− mice were used between 5 and 10 wk of age, and the mice used were active and relatively healthy. Mice in which an internal ribosome entry site element links GFP expression to the Foxp3 transcript (strain B6.Cg-Foxp3tm2TchJ, termed Foxp3-gfp in this article) were obtained from The Jackson Laboratory (Bar Harbor, ME). Bcl6−/− mice were mated onto this Foxp3-gfp background. Rag1−/−, Il10−/−, and Foxp3−/− mice were also originally obtained from The Jackson Laboratory. Bcl6−/−/Tcr−/− mice were described previously (18). Wild-type (WT) and Bcl6−/− Foxp3-gfp mice were genotyped by PCR, as described previously. Mice were bred under specific pathogen-free conditions at the laboratory animal facility at Indiana University School of Medicine and were handled according to protocols approved by the Indiana University School of Medicine Animal Use and Care Committee.

Abs and FACS analysis

Flow cytometry analysis of intracellular transcription factors and cytokines was performed by staining the cells with fluorochrome-conjugated anti-Foxp3 (FKJ-16a; eBioscience), anti-Helios (22F6; BioLegend), anti-GATA3 (TWAJ; eBioscience), and anti–IL-4 (BD Biosciences) using the Mouse Regulatory T Cell Staining Kit (eBioscience). Cells were first stained with Ab for the desired cell surface markers, CD4 (RM4-5; BD Biosciences) and CD25 (PC61.5; eBioscience), followed by permeabilization with Fixation/Permeabilization buffer and intracellular staining in Permeabilization buffer. Flow analysis was performed on a FACS Calibur, and data were analyzed using FlowJo software (Tree Star).

Mouse T cell cultures and Treg assays

Naïve T cells (CD4+CD62L−) were purified from lymph nodes and spleen using magnetic beads (Miltenyi Biotec). Naïve CD4+ T cells (1 × 10⁶ cells/ml in DMEM medium supplemented with 10% FCS [Atlanta Biologicals], 2 mM glutamine, 100 U/ml penicillin-streptomycin, 25 mM nonessential amino acids, 25 mM HEPES, and 55 mM 2-ME [Life Technologies]) were activated with plate-bound anti-CD3 (5 μg/ml; 145-2C11; BD Biosciences) and anti-CD28 (10 μg/ml; 37.51; BD Biosciences). Abs to CD3 and CD28 were obtained from BD Biosciences. Recombinant human IL-2 was obtained from the Biological Resources Branch, Division of Cancer Treatment and Diagnosis, National Cancer Institute-Frederick Cancer Research and Development Center.

For Treg assays, CD4+CD25− T cells were purified from WT and Bcl6−/− Foxp3-gfp mice using magnetic beads, followed by FACS sorting for pure GFP+ Tregs using a FACS Aria cell sorter (Becton Dickinson). The CD4+CD25− T cell fraction from magnetic bead isolation was used as responder T cells (Tresps). Tresps were prepared from the spleens of Tcr−/−mice. For Treg suppression assays, WT or Bcl6−/− Tresps (50 × 10⁶/well) were cocultured separately with WT or Bcl6−/− Tregs at different ratios, as indicated, along with mitomycin C (20 μg/ml)-treated APCs (50 × 10⁶/well) plus anti-CD3 (2 μg/ml) or 10 μg/ml/μg/ml OVA 323-339 peptide or ovalbumin (OVA) (10 μg/ml) and WT Foxp3-gfp BM. 20 H2L/E cells were pulsed with 1 μCi [3H] thymidine at 48 h of culture, and cell proliferation in triplicate cultures was measured using a scintillation counter.

Induction of experimental colitis

Unfractionated CD4+ T cells (Tresps; 1 × 10⁶) from Il10−/− mice, isolated using magnetic bead selection, were adoptively transferred i.p. into Rag1−/− mice to induce a strong Th1-mediated colitogenic response in the recipients 4–8 wk posttransfer (19). Along with the transfer of Il10−/− Tresps, two cohorts of Rag−/− mice were injected i.p. with FACS-sorted CD4+CD25−Foxp3−/− Tresps (250 × 10⁶) from Bcl6−/− or WT Foxp3-gfp mice. The recipient mice were monitored for signs of intestinal pathology and were killed 9–11 d postchallenge, and the colon tissue from each animal was used for analysis.

Induction of experimental allergic airway inflammation

WT B6 female mice (recipients), as well as the Bcl6−/− and WT Foxp3-gfp mice (Treg donors), were sensitized i.p. with OVA (Sigma) adosed to 20 μg OVA2/2 mg OVA on days 0 and 7 of the protocol (20). On day 14, CD4+CD25−Foxp3−/− Tregs were FACS sorted from OVA-sensitized Bcl6−/− and WT Foxp3-gfp mice and then injected i.p. (350 × 10³ cells/mouse) into the sensitized WT B6 female recipients (21). Three hours following immunization, recipient mice were challenged intranasally with OVA for 5 consecutive days (100 μg/d). Mice were sacrificed by i.p. injection of pentobarbital (5 mg/mouse) 48 h after the final intranasal challenge. The trachea was cannulated, and lungs were lavaged three times with 1 ml PBS to collect the bronchoalveolar lavage (BAL) fluid. Cells recovered from the BAL fluid and the lung mediastinal lymph nodes (MLNs) were counted with a hemocytometer. Eosinophils, neutrophils, T cells, B cells, and mononuclear cells in the BAL fluid were distinguished by cell size and by expression of CD3, B220, CR3, CD11c, and MHC class II, analyzed by flow cytometry as described (20). For quantitative PCR (QPCR) analysis, lung tissues were homogenized in a tissue lyser (Qiagen), and RNA isolated with an RNeasy kit (Qiagen) was used for synthesis of cDNA for subsequent analysis. Paraffin-embedded sections were stained with H&E for evaluation of the infiltration of inflammatory cells by light microscopy.

Airway hyperreactivity to methacholine challenge was determined 24 h after the final intranasal challenge. Noninvasive unrestrained whole-body plethysmography (Buxco Research Systems) was used to record airway responsiveness with the dimensionless parameter “enhanced pause” (Penh) used for estimation of total pulmonary resistance, an indicator of bronchoconstriction. Mice were placed in whole-body plethysmographs, and baseline measurements were recorded. Saline was administered by nebulization for 2 min, followed by increasing doses of methacholine, and the enhanced-pause parameter was recorded over 5 min.

In situ hybridization

In situ hybridizations were performed on 8-μm cryosections from lungs of mice in the airway-inflammation experiment using the miRCURY locked nucleic acid (LNA) microRNA ISH Optimization Kit 2 (miR-21), according to the manufacturer’s protocol (Exiqon). In brief, the formalin-fixed, paraform-embedded slides were rinsed and digested with proteinase K for 12 min at 37°C. After protease digestion, the digoxin-labeled LNA-scrambled control probe and LNA miR-21 antisense probe (Exiqon) were hybridized to the slides at 52°C for 6 h. Following posthybridization washes with saline-sodium citrate buffer at 47°C, 100 μl rabbit anti-digoxin (Sigma-Aldrich) Ab, diluted 1/2000, was applied to the slides for 1 h at room temperature. The slides were rinsed and then incubated with 100 μl anti-rabbit alkaline phosphatase and nitrobluezenolic sulfonic acid substrate for 2 h at 30°C. Slides were counterstained with Nuclear Fast Red (Polysciences), overslipped, and mounted for viewing.

Generation of bone marrow chimeras

Donor WT BoyJ (CD45.1+) and Bcl6−/− (CD45.1−) mice on Foxp3-gfp background and Foxp3−/− mice were euthanized with CO2 asphyxiation and were subjected to lethal irradiation, and femurs and tibias were removed aseptically. Bone marrow (BM) was flushed with DMEM complete media. Recipient Rag−/− mice were sublethally irradiated (350 Gy) 16–24 h prior to reconstitution. The recipients were reconstituted with WT and Foxp3 knockout (KO) (Foxp3−/−) BM (WT:Foxp3−/− chimeras), Bcl6−/− and Foxp3−/− BM (KO:Foxp3−/− chimeras), or WT and Bcl6−/− Foxp3-gfp BM (WT:KO) chimeras (10 × 10⁶) by i.v. injection. Satisfactory reconstitution was achieved after 4–5 mo. Mice were immunized with OVA/albumin i.p. 2 wk prior to FACS sorting of the WT and Bcl6−/− CD25−Foxp3+ (Tregs) and CD25+ Foxp3+ conventional T cells (Tconvs), based on CD45.1 expression for QPCR analysis.

Affymetrix microarrays and quantitative RT-PCR

Total RNA was extracted from FACS-sorted CD4+CD25−Foxp3+ Tregs from Bcl6−/− and WT Foxp3-gfp mice following 16 h of activation in vitro with plate-bound anti-CD3 (5 μg/ml) and anti-CD28 (10 μg/ml) using the RNeasy Mini kit, according to the manufacturer’s protocol (Qiagen). The microarray studies were carried out using the facilities of the Center for Biotechnology Information Gene Expression Omnibus database at the National Center for Biotechnology Information and the Gene Expression Omnibus database (http://www.ncbi.nlm.nih.gov/geo) under accession number GSE40493.

To validate the expression array data, QPCR was performed on independently prepared Tregs from Bcl6−/− and WT Foxp3-gfp mice.
Retroviral transductions

Naive T cells (CD4+CD62L-), prepared from WT C57BL/6 or Stat6−/− mice using magnetic beads, were activated in vitro with plate-bound anti-CD3 (5 μg/ml) and anti-CD28 (10 μg/ml) for 24 h. Cells were then transduced by spin infection with bicistronic retroviral vector (RV) supernatants encoding Bcl6 and H2Kk or GATA3 and MHC class II, as described (22, 23). On the second or third day following transduction, cells infected with H2Kk RVs were stained with biotin−anti-H2Kk and streptavidin−allophycocyanin, whereas those infected with MHC class II RVs were stained for anti−hCD4-PE and then FACs sorted based on allophycocyanin or PE expression, respectively. The sorted RV+ T cells were restimulated in vitro with anti-CD3 and anti-CD28 for 4–6 h for gene-expression analysis.

Reporter assays

Jurkat T cells (10 × 10⁶ cells/250 μl) were electroporated, as described (24), in serum-free RPMI 1640 medium with an IL-5 promoter-driven luciferase reporter vector (10 μg) along with expression constructs (10 μg) for CXN, CXN-GATA3, CXN-BCL6, or CXN-GATA3 plus CXN-BCL6. After electroporation, cells were resuspended in RPMI 1640 media supplemented with 10% FCS and rested overnight. Luciferase measurements were performed 24 h after transfection following a 6-h activation of cells with PMA (10 ng/ml) and ionomycin (0.3 μg/ml) using Luciferase Assay System (Promega). M12 B cells were electroporated, as described (25), with the indicated plasmids, as above. Luciferase measurements were performed following activation of cells with PMA and dibutyryl cAMP.

Gene-expression analysis

Total cellular RNA was prepared using the TRIzol method (Life Technologies), and cDNA was prepared with the Transcriptor First Strand cDNA synthesis kit (Roche). QPCR reactions were run by assaying each sample in triplicates using the Fast Start Universal SYBR Green Mix (Roche Applied Science) with a Stratagene Mx3000P Real-Time QPCR machine. Samples with limiting RNA were assessed for gene expression using TaqMan assays (ABI). Levels of mRNA expression were normalized to β-actin mRNA levels, and differences between samples were analyzed using the ddCT method. For quantitative RT-PCR analysis of microRNAs, RNA was extracted from lung tissue or serum samples using mirNeasy Mini kit, according to the manufacturer’s protocol (QIAGEN), and gene expression was assessed using TaqMan microRNA assays (Applied Biosystems). Normalization was performed using snor202, snor234, and U6 as controls, with U6 as the sole control for samples with limiting RNA. The following PCR primer sequences were used: Il10, forward (F): 5′-GCGTGCGATGGTGGTGCATGA-3′ and reverse (R): 5′-TGTGGCTGGCTGCTGTCA-3′; Il4, forward (F): 5′-CCCTGCTGTCCTCATGGTGG-3′ and reverse (R): 5′-CCCTGCTGTCCTCATGGTGG-3′; AcoT, forward (F): 5′-GAAGCCCTACAGACGAGCTCA-3′ and reverse (R): 5′-GAAGCCCTACAGACGAGCTCA-3′; Il2, forward (F): 5′-AAAGTGCGTGGACTCTTCATT-3′ and reverse (R): 5′-AAAGTGCGTGGACTCTTCATT-3′; Ib2, forward (F): 5′-GGGTGCAAGCCCTATCGCA-3′ and reverse (R): 5′-GGGTGCAAGCCCTATCGCA-3′.

Results

Bcl6−/− Tregs fail to suppress allergic airway inflammation in vivo

Because Bcl6−/− mice develop spontaneous Th2-type inflammation, we next tested whether Bcl6−/− Tregs were defective in their ability to suppress Th2 responses. We used a model in which Th2 airway inflammation is induced by repeated intranasal administration of OVA following initial i.p. priming with OVA (20, 21). Prior to the OVA challenge, OVA-primed CD4+ CD25+ Foxp3+ Tregs from WT or Bcl6−/− mice with intact suppressor function in vitro (Supplemental Fig. 1C) were injected to test their ability to suppress airway inflammation. After the last OVA challenge, the mice were analyzed by weight loss, changes in colon length, and histological assessment. Bcl6−/− Tregs suppressed the development of disease as effectively as did WT Tregs (Fig. 1C–F). Together, these data show that Bcl6−/− Tregs are competent at suppressing T cell proliferation in vitro and Th1-type colitogenic responses in vivo.
functioning to suppress airway hyperresponsiveness. To further analyze the airway inflammatory response, we measured the cellularity of BAL and of the draining MLNs for the three treatment groups. Strikingly, although WT Tregs suppressed BAL and MLN cell counts compared with control mice with airway disease, Bcl6−/− Tregs promoted a several-fold increase in BAL and MLN cellularity compared with control mice (Fig. 2B). Analysis of the specific types of cells in the BAL revealed that the bulk of the increase in cellularity was due to eosinophils, a cell type characteristic of Th2 responses (Fig. 2C). The in-airway inflammation by histology and scored the inflammation by differential cell counts. As shown in Fig. 2D and 2E, although WT Tregs suppressed inflammatory cell accumulation around the airways, Bcl6−/− Tregs failed to suppress the inflammation. These data indicate that Bcl6−/− Tregs are not just severely defective in the ability to suppress Th2 inflammation, they also actively exacerbate Th2 inflammation, leading to greater recruitment of eosinophils and reduced lung function.

**Bcl6−/− Tregs exacerbate Th2 immune responses in allergic inflammation in vivo**

To further characterize the Th2 inflammatory response mediated by Bcl6−/− Tregs in the airway inflammation model, we analyzed gene expression in the lungs by QPCR. We found that the Th2 cytokines Il4, Il5, and Il13 were most strongly expressed in the lungs of mice that received Bcl6−/− Tregs (Fig. 3A). The increased Th2 cytokines can explain the increased infiltration of eosinophils, impaired lung function, and increased IgE levels in the mice that received the Bcl6−/− Tregs (Supplemental Fig. 2A). We tested Foxp3 expression as a marker for Tregs and found the highest levels in the lungs from mice injected with Bcl6−/− Tregs (Fig. 3B). Thus, defective homing of the Bcl6−/− Tregs to the inflamed lungs or loss of Treg stability in the context of the inflammatory Th2 milieu is unlikely to account for the augmented Th2 responses seen with Bcl6−/− Tregs.

A previous study associated increased miR-21 with Th2 inflammatory responses in three different mouse models of allergic airway inflammation (31). miR-21 was mainly localized to cells of
the myeloid lineage, and the increased miR-21 was shown to indirectly prime for Th2 responses by targeting the IL-12a subunit of the Th1 cytokine, IL12. To test the relevance of this finding to the exacerbated Th2 responses following transfer of Bcl6<sup>−/−</sup> Tregs, we assessed miR-21 expression in the lungs of mice in our airway inflammation model. Surprisingly, although miR-21 expression was not different between control and WT Treg-treated mice, miR-21 was greatly increased in the total RNA of lungs taken from the Bcl6<sup>−/−</sup> Treg-treated mice (Fig. 3C). Therefore, the increased miR-21 in the lungs of Bcl6<sup>−/−</sup> Treg-treated mice strongly supports the idea that Bcl6<sup>−/−</sup> Tregs actively promote severe Th2 inflammation, because miR-21<sup>−/−</sup> mice develop reduced allergic inflammation (32). Although miR-21 was detected at a low level in myeloid inflammatory cells in our model of airway inflammation, similar to the study by Lu et al. (31), we also observed very high miR-21 expression in airway epithelial cells (Fig. 3D, Supplemental Fig. 2B). Mice given Bcl6<sup>−/−</sup> Tregs showed a similar lung pattern of miR-21 expression as did control and WT Treg-injected mice, but they had more intense miR-21 staining, correlating with higher overall lung miR-21 expression. Further, expression of the reported miR-21 target gene, Il12a, was reduced in the lungs of Bcl6<sup>−/−</sup> Treg-treated mice (Supplemental Fig. 2C), consistent with increased lung miR-21 levels in this group. Interestingly, we also observed a significant increase in circulating or serum miR-21 in the Bcl6<sup>−/−</sup> Treg-treated group (Fig. 3E). Thus Bcl6<sup>−/−</sup> Tregs promote exacerbated Th2 responses in the airway inflammatory setting, associated with a novel systemic upregulation of miR-21 that can further augment Th2 responses by inhibiting Th1 differentiation (32).

**Bcl6<sup>−/−</sup> Tregs are selectively impaired in controlling systemic Th2 responses**

To test the ability of Bcl6<sup>−/−</sup> Tregs to control inflammatory T cell responses in another in vivo setting, we set up mixed BM chimeras in which BM from Foxp3<sup>−/−</sup> (scurfy) mice was injected into irradiated Rag1<sup>−/−</sup> recipient mice along with BM from WT Foxp3<sup>−/−</sup> Foxp3<sup>−/−</sup> Foxp3-gfp mice (KO:Foxp3<sup>−/−</sup> chimeras) or Bcl6<sup>−/−</sup> Foxp3<sup>−/−</sup> Foxp3-gfp mice (KO:Foxp3<sup>−/−</sup> chimeras) (Fig. 4A). Because of a spontaneous mutation in Foxp3, Foxp3<sup>−/−</sup> or scurfy mice lack functional Tregs and develop a severe autoimmune pathology mediated by both Th1 and Th2 cells (11, 33, 34). WT:Foxp3<sup>−/−</sup> chimeric mice have a mixture of WT and Foxp3<sup>−/−</sup> Tconvs and a functional WT Treg subset, whereas KO:Foxp3<sup>−/−</sup> chimeric mice have a mixture of Bcl6<sup>−/−</sup> and Foxp3<sup>−/−</sup> Tconvs and complete deficiency of Bcl6 in the Treg subset. After 16–20 wk to allow lymphoid constitution, both types of chimeric mice were immunized with OVA-Alum to provoke an immune response, and Tconvs were purified and tested for gene expression, following activation with anti-CD3 and anti-
CD28 Abs in vitro. As shown in Fig. 4B and Supplemental Fig. 3A, Tconv5 from KO:Foxp3KO chimeras showed a striking increase in the expression of Th2 cytokines compared with Tconv5 from WT:Foxp3KO chimeras, whereas Il13a and Il17a levels were not significantly different between the two chimer types. These findings further confirm that Bcl6−/− Tregs have a selective failure to control Th2 responses, but not Th1 and Th17 responses, despite the presence of Bcl6-sufficient Foxp3−/− lymphoid and myeloid cells. Additionally, considering the abnormal development of Th1 and Th2 cells in Foxp3−/− mice (11, 33, 34), the specific increase in Th2 cytokines, but not Th1 cytokines, with the KO:Foxp3KO chimeras is especially noteworthy. Thus, our results with the KO:Foxp3KO chimeras and the Th1 and Th2 disease models clearly demonstrate a critical role for Bcl6 in Treg-mediated control of Th2 inflammatory responses in vivo.

Bcl6 represses the expression of both Treg and Th2 genes in the Treg lineage

To understand the functional defects that can explain the selective failure of Bcl6−/− Tregs to control Th2 inflammatory responses, we performed a gene-expression microarray using mRNA from highly purified CD4+CD25+Foxp3+ Tregs from WT and Bcl6−/− mice, activated in vitro. We found a large number of gene differences between WT and Bcl6−/− Tregs, with 833 genes upregulated >1.5-fold in Bcl6−/− Tregs in a statistically significant manner. Several of these upregulated genes were those critical for Treg function, such as Foxp3, Il12a, Cldn4, and Tgfb1 (Fig. 5). Transcript for Ebi3, a component of the suppressive cytokine IL-35 (35, 36), was elevated, whereas Il12a, encoding the other component of IL-35, was mildly decreased. Il10 and granzyme b (Gzmb) were markedly upregulated in Bcl6−/− Tregs (Fig. 5) and were previously reported as Bcl6 targets in T cells (4, 37), indicating that Bcl6 is a repressor of gene expression in Tregs. Many of the genes increased in Bcl6−/− Tregs were also increased in CD25+CD4+ T cells isolated from Bcl6−/− mice (17). However, CD25+CD4+ T cells in Bcl6−/− mice are contaminated with Foxp3+ Th2 effector cells and are not a pure Treg population (data not shown). Our data using purified CD4+CD25+Foxp3+ Tregs identify genes regulated by Bcl6 specifically in Tregs. The increased expression of Treg suppressor genes, particularly Il10, in Bcl6−/− Tregs can explain the enhanced ability of Bcl6−/− Tregs to limit T cell proliferation in vitro and colitis in vivo, but does not explain the effect of Bcl6−/− Tregs on Th2 inflammation. Strikingly, however, we noted increased expression of multiple Th2 lineage genes in Bcl6−/− Tregs (Fig. 5), most notably Gata3, cmaf, Corp, and the Th2 cytokines Il4, Il5, and Il13. Importantly, only Th2 lineage genes, but not Th1 and Th17 lineage genes, were
significantly upregulated in Bcl6−/− Tregs (Fig. 5A). Several chemokine receptor genes were upregulated in the Bcl6−/− Tregs, as well as other genes with important immune functions, such as Csf1, Batf, and Klrq1. These data indicate that Bcl6 is critical for limiting the effector profile of Tregs and, specifically, that Bcl6 is required for repression of the TH2 gene program in Tregs. Moreover, the specific upregulation of TH2 cytokines, multiple chemokine receptors, and the macrophage growth factor Csf1 might all contribute to the promotion of augmented TH2 responses by Bcl6−/− Tregs in the airway inflammation model and the KO:Foxp3KO chimeras. In the microarray, “KO2” showed a much higher expression of both Treg genes and TH2 genes than did “KO1,” consistent with KO2 having a greater severity of TH2 inflammation than KO1, as assessed by histology of the heart and lungs (data not shown). TH1 and TH17 genes were also modestly upregulated in KO2, but not KO1, consistent with the reported role for Bcl6 in inhibiting TH1 and TH17 differentiation (6, 7). However, the role of Bcl6 in inhibiting TH2 responses is more dominant for the inflammatory phenotype of Bcl6−/− mice, because Tregs from both the healthy and sick Bcl6−/− mice show an increase in TH2 gene expression. This indicates that, in addition to an intrinsic role for Bcl6 in regulating TH2 gene expression in Tregs (as shown by healthier KO1), the TH2 inflammatory disease further contributes to remodeling of the Tregs (as shown by sicker KO2), and both of these effects contribute to defective control of TH2 responses by Bcl6−/− Tregs.

TH2 genes are intrinsically repressed by Bcl6 in Tregs

Under inflammatory conditions, Tregs can downregulate Foxp3 expression and convert to proinflammatory cells capable of producing effector cytokines (38). Using intracellular staining, we determined that the elevated GATA-3 and IL-4 expression in the Bcl6−/− Treg population was in the Foxp3+ cells and was not simply due to Tregs that lost Foxp3 expression following activation or contaminating TH2 effector cells (Fig. 6). Thus, Foxp3+ Tregs in the Bcl6−/− mice upregulate TH2 genes, suggesting that Bcl6 represses TH2 genes in Tregs via a Foxp3-independent mechanism. The next question was to definitively address whether the upregulated TH2 genes in Bcl6−/− Tregs were due to intrinsic regulation by Bcl6 in the Treg lineage or to an indirect effect from the TH2-inflammatory disease in the Bcl6−/− mice. To test this, we generated mixed BM chimeras in which BM from CD45.1+ WT Foxp3-gfp mice (WT: Foxp3KO) and Bcl6−/− BM mixed with Foxp3KO BM (KO:Foxp3KO). Data show average expression from four mice for the WT: Foxp3KO group and three mice for the KO:Foxp3KO group. Error bars represent SEM. **p < 0.01, ****p < 0.0001, Student t test.

Bcl6 represses Gata3 transcriptional activity

To mechanistically understand how Bcl6 intrinsically regulates TH2 cytokine expression, we analyzed the regulation of Gata3 by Bcl6.
Although previous work from our laboratory showed that Bcl6 could repress Gata3 protein expression in a posttranscriptional manner (4), the degree to which Bcl6 represses Gata3 transcriptional function has remained unclear. Therefore, we tested the ability of Bcl6 to repress Gata3 transactivation. We initially used an approach in which Stat6^(-/-) T cells were transduced with Gata3-expressing retrovirus, with and without cotransduction of Bcl6-expressing retroviruses. As shown in Fig. 8A, transduction of Bcl6 essentially ablated the induction of Il4 and Il5 by Gata3, showing that Bcl6 could strongly repress Gata3-dependent Th2 cytokine expression. Bcl6 did not repress Tnfa, indicating a restricted role for Bcl6 in the repression of Th2 cytokine genes that are activated by Gata3. To further examine the repression of Gata3 function by Bcl6, we used a transient transfection assay in which luciferase expression is under control of the Il5 promoter. As shown in Fig. 8B and 8C, Gata3 alone strongly activates the Il5 promoter, and Bcl6 alone weakly represses Il5 promoter activity. When expressed together, Bcl6 potently represses Gata3-induced Il5 promoter activity, showing that Bcl6 can directly target and inhibit the transcriptional activity of Gata3. This repressive function occurs even in B cells (Fig. 8C), thus showing that Bcl6 inhibits Gata3 independent of endogenous Gata3 and does not require other T cell-specific factors. These data indicate a model wherein increased levels of Gata3 transcriptional activity in the absence of Bcl6 would lead to increased Th2 lineage gene expression in Tregs. Also, because Gata3 can autoactivate its own expression (39), this could further solidify the Th2 lineage gene program in Bcl6^(-/-) Tregs.

**Discussion**

In the past few years, Bcl6 has emerged as a central regulator of Th cell differentiation. However, the role of Bcl6 in Treg function has not been completely elucidated, particularly in terms of controlling inflammation. In this study, we showed that Bcl6 function is specifically required for Tregs to suppress Th2-type inflammation. These results provide an explanation for the Th2-type inflammation that is a hallmark of Bcl6^(-/-) mice (1–3). The inflammatory disease in Bcl6^(-/-) mice is dependent upon T cells (Supplemental Table I), and our results indicate that the Th2 inflammatory responses increase in severity as the result of defective Treg activity in Bcl6^(-/-) mice. Moreover, in the absence of Bcl6, Tregs develop a Th2-type proinflammatory phenotype, showing that Bcl6 is a key transcriptional regulator of Treg function.

Other transcription factors were shown to control the ability of Tregs to regulate specific types of T cell responses. Irf4^(-/-) Tregs fail to suppress autoimmune Th2 responses (12). Unlike Bcl6^(-/-) Tregs, Irf4^(-/-) Tregs have decreased expression of Th2 genes, and the inability of Irf4^(-/-) Tregs to control Th2 responses fits with a model in which Tregs co-opt the regulatory program of the specific Th cell response that they are suppressing (11–13). Ad-

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**FIGURE 5.** Bcl6^(-/-) Tregs exhibit a hybrid Treg–Th2 phenotype. (A) Heat map depiction of gene transcripts differentially expressed between sorted Tregs from Bcl6^(-/-) or WT Foxp3-gfp mice, analyzed by expression microarrays. Gene expression is represented as log2-transformed values; red represents expression greater than mean, and green represents expression less than the mean, as shown in the color scale below (n = 2 mice/group, with two replicates each mouse represented as an average). KO1, healthy; KO2, sick. Average fold-change in KO/WT gene expression is noted next to each gene row. *p < 0.05, **p < 0.01, ***p < 0.001, ****p < 0.0001, average fold change in KO/WT, Student t test. (B) QPCR validation of differentially expressed genes between Bcl6^(-/-) (KO) Tregs and WT Tregs selected from the microarray analysis following activation for 16 h with anti-CD3 and anti-CD28 (Treg genes: Foxp3, Il10, Tgfb1, and Gzm b) and Th2 genes (Il4, Il5, Il13 and Ccr8), with expression normalized to btub. Data are average expression from at least three mice/group.
ditionally, Irf4 expression is not changed in Bcl6$^{−/−}$ Tregs (Fig. 5A), consistent with Bcl6 and Irf4 operating through distinct mechanisms in Tregs. Foxp3 itself is a critical inhibitor of Th2 cytokine expression; in two mouse models of attenuated Foxp3 expression, Tregs expressed Th2 cytokines and promoted Th2 responses (40–42). Bcl6$^{−/−}$ Tregs express both Th2 cytokines and elevated levels of Foxp3 (Fig. 5). Thus, Bcl6 represses Th2 gene expression through a Foxp3-independent pathway by repressing Gata3 function.

An important issue is how Bcl6$^{−/−}$ Tregs exacerbate Th2 responses in the airway inflammation model. The fact that Foxp3 expression is higher in lungs receiving Bcl6$^{−/−}$ Tregs than in WT Tregs (Fig. 3B) indicates that Bcl6$^{−/−}$ Tregs are not simply downregulating Foxp3 when exposed to an inflammatory environment. Thus, one possibility is that Bcl6$^{−/−}$ Tregs promote Th2 inflammation by secreting Th2 cytokines that mimic Th2 effector activity and/or amplify further Th2 differentiation and that, in vivo, this effect overrides the suppressive functions. Although we

**FIGURE 6.** Bcl6 represses Th2 genes in Tregs, independent of Foxp3 expression. (A) Representative FACS plot depicting expression of GATA3 in freshly isolated Foxp3$^+$ and Foxp3$^-$ CD4$^+$CD25$^+$T cells from Bcl6$^{−/−}$ and WT mice (left panel). Bar graph representing percentage of GATA3$^+$ Foxp3$^+$ Tregs in Bcl6$^{−/−}$ (KO) and WT mice ($n = 3$ /group) (right panel). (B) Representative graph depicting expression of GATA3 on freshly isolated Bcl6$^{−/−}$ and WT cells gated on CD4$^+$CD25$^+$Foxp3$^+$ T cells (left panel). Mean fluorescence intensity (MFI) for GATA3 staining in the Bcl6$^{−/−}$ (KO) and WT mice (right panel). Foxp3$^+$ fraction is quantified ($n = 3$ /group). (C) Representative FACS plot depicting expression of IL-4 on Bcl6$^{−/−}$ (KO) and WT CD4$^+$CD25$^+$Foxp3$^+$ fraction following stimulation with PMA and ionomycin (left panel). Scatter plot represents percentage of IL-4$^+$Foxp3$^+$ Tregs in Bcl6$^{−/−}$ and WT mice ($n = 5$ /group) (right panel). Error bars represent SEM. *$p < 0.05$, Student $t$ test.

**FIGURE 7.** Bcl6 intrinsically represses Th2 genes in Tregs. (A) Scheme for mixed BM chimeras (WT:KO); Tregs were gated as CD4$^+$CD25$^+$Foxp3$^+$ (GFP$^+$) T cells prior to gating WT and KO based on CD45.1 expression. (B) QPCR analysis of Gata3, Il4, Il10, Il5, Ifng, and Foxp3 in sorted BM chimera-derived Bcl6$^{−/−}$ (CD45.1$^+$) and WT (CD45.1$^+$) Tregs, with expression normalized to tubb5. Data are average expression from six mice/group. Error bars represent SEM. *$p < 0.05$, ***$p < 0.001$, Student $t$ test.
observed that supernatants from Bcl6<sup>−/−</sup> Tregs can promote Th2 differentiation of naive CD4<sup>+</sup> T cells, the amount of IL-4 and IL-5 secreted by Bcl6<sup>−/−</sup> Tregs is much less than what is made by activated Th2 cells in vitro (data not shown) and is unlikely to be higher than what is produced by activated Th2 cells in vivo. Another possibility is that Bcl6<sup>−/−</sup> Tregs migrate more efficiently to the inflamed organ than do other cell types, as the result of increased expression of several chemokine receptors (Fig. 5). Once in the lungs, the increased Th2 cytokines made by the Bcl6<sup>−/−</sup> Tregs are likely to upset the normal regulatory balance. For instance, IL-4 can desensitize effector T cells to the inhibitory effects of Tregs (43). Bcl6<sup>−/−</sup> Tregs may produce other factors in addition to IL-5 that promote eosinophil recruitment; however, eotaxin-1 (Ccl11), eotaxin-2 (Ccl24), and eotaxin-3 (Ccl26) mRNAs were not significantly increased in the Bcl6<sup>−/−</sup> Tregs (data not shown). Interestingly, we observed a fold-increase in miR-21 expression in the lungs of Bcl6<sup>−/−</sup> Treg-treated mice, which has been linked to promotion of Th2 responses by inhibiting Th1 polarization (32). Thus, by targeting Il12a, miR-21 may be part of a positive-feedback loop for Th2 inflammation; thus, increased miR-21 and reduced Il12a in the lungs of Bcl6<sup>−/−</sup> Treg-treated mice can explain the augmented Th2 responses. We found that miR-21 is also increased in Bcl6<sup>−/−</sup> Tregs (D.V. Sawant and A.L. Dent, manuscript in preparation), and reduced Il12a expression in Bcl6<sup>−/−</sup> Tregs due to miR-21 targeting may lead to less production of the Treg immunosuppressive cytokine IL-35 (36), despite increased levels of Ebi3 expression in Bcl6<sup>−/−</sup> Tregs (Fig. 5A). Bcl6<sup>−/−</sup> Tregs may have an impaired ability to control Th2 responses, because IL-35 was shown to potently suppress Th2-type allergic airway inflammation (44). Several of these mechanisms can also explain the lack of repression of Th2 responses in the KO:Foxp3KO chimeric mice.

The Th2 factor Gata3 plays a key role in Treg fitness by maintaining high levels of Foxp3 expression (14, 15). Gata3<sup>−/−</sup> Tregs have lower Foxp3 expression and decreased expression of Foxp3 target genes (14, 15). Mice with Gata3<sup>−/−</sup> Tregs develop Th1- and Th17-type inflammation that is likely due to reduced Treg activity (14). Wohlfert et al. (15) reported that Gata3 is induced in Tregs at mucosal surfaces; however, WT Gata3-expressing Tregs do not express Th2 cytokines. In both mouse and human Tregs, Gata3 expression is regulated by IL-2 and TCR signals, independent of IL-4/Stat6 signaling (15). Previously, we demonstrated that Bcl6 regulates Gata3 and Th2 responses independently of IL-4 and Stat6 (1). In this study, we show that Bcl6 can potently repress Gata3 transcriptional activity and is required to inhibit Th2 cytokine expression by Tregs. The increased Gata3 expression seen in Bcl6<sup>−/−</sup> Tregs may be partially explained by an augmented ability of Gata3 to autoactivate its expression in the absence of Bcl6 (39), but it also probably reflects the Th2 environment and the degree of Treg stimulation through the TCR. From our current findings, we propose that Bcl6 controls Gata3 expression in Tregs, independently of IL-4 and Stat6, by dampening Gata3 transcriptional activity and modulating the ability of Gata3 to autoactivate its own expression.

Acquisition of specific T effector transcriptional programs allows Tregs to effectively curb immune responses (11–13); however, this regulatory mechanism can lead to pathogenic consequences because of the presence of self-reactive TCRs on Tregs. Thus, Treg-
acquired effector features need to be under tight control; in this study, we showed that a Bcl6-mediated brake on Gata3 activity in Tregs is essential for their ability to control Th2-type inflammation. Bcl6 is unique among transcription factors that regulate the ability of Tregs to control Th2 responses in that it represses Gata3 and Th2 responses in Tregs at the same time that it is required for Tregs to properly control Th2 cell responses. Thus, Bcl6 prevents Tregs from acquiring Th2 effector-like characteristics by repressing Gata3 function.

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Disclosures

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References