BET bromodomain inhibition suppresses T<sub>H</sub>17-mediated pathology

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Interleukin (IL) 17–producing T helper (T<sub>H</sub>17) cells have been selected through evolution for their ability to control fungal and bacterial infections. It is also firmly established that their aberrant generation and activation results in autoimmune conditions. Using a characterized potent and selective small molecule inhibitor, we show that the bromodomain and extra-terminal domain (BET) family of chromatin adaptors plays fundamental and selective roles in human and murine T<sub>H</sub>17 differentiation from naive CD<sup>4+</sup> T cells, as well as in the activation of previously differentiated T<sub>H</sub>17 cells. We provide evidence that BET controls T<sub>H</sub>17 differentiation in a bromodomain-dependent manner through a mechanism that includes the direct regulation of multiple effector T<sub>H</sub>17–associated cytokines, including IL17, IL21, and GMCSF. We also demonstrate that BET family members Brd2 and Brd4 associate with the Il17 locus in T<sub>H</sub>17 cells, and that this association requires bromodomains. We recapitulate the critical role of BET bromodomains in T<sub>H</sub>17 differentiation in vivo and show that therapeutic dosing of the BET inhibitor is efficacious in mouse models of autoimmunity. Our results identify the BET family of proteins as a fundamental link between chromatin signaling and T<sub>H</sub>17 biology, and support the notion of BET inhibition as a point of therapeutic intervention in autoimmune conditions.

The dysregulated activation and expansion of CD<sup>4+</sup> T cells lies at the core of autoimmune disorders. It is now widely recognized that T<sub>H</sub>17 cells, a subset of T helper cells which produce IL-17A, IL-17F, IL-21, IL-22, and GM-CSF, mediate autoimmune conditions including multiple sclerosis, psoriasis, rheumatoid arthritis, and Crohn’s disease, as well as the murine models of these diseases (Bettelli et al., 2006; Korn et al., 2009; Littman and Rudensky, 2010). To differentiate into T<sub>H</sub>17 cells, naive T cells require the combined exposure to TGF-β1 and IL-6, and it is now well established that these two factors work in concert to drive the induction of a transcriptional signature that is largely orchestrated by a group of transcriptional regulators that includes steroid receptor-type nuclear receptors ROR<gamma> and ROR<alpha> (Ivanov et al., 2006; Yang et al., 2008), IRF4 (IFN regulatory factor 4; Breitling et al., 2007; Ciofani et al., 2012; Glasmacher et al., 2012), AP-1 transcription factor Batf (Schranl et al., 2009), the proto-oncogene c-Maf (Baquie et al., 2009), NF-kB family member c-Rel (Chen et al., 2011; Ruan et al., 2011), and AHR (aryl hydrocarbon receptor; Veldhoven et al., 2008).

Global analysis of histone modifications in T cells has revealed remarkable differences in the chromatin structure of distinct T helper subsets and some of their signature transcription factors (Wei et al., 2009). Although these and other studies have begun to shed light on the role of chromatin dynamics in the control of immune lineage specification and function (Araki et al., 2011; Ramirez-Carrozzo et al., 2009), how these changes are integrated is still poorly understood. BET polypeptides BRD2, BRD3, BRD4, and BRDT harbor tandem bromodomain motifs that bind acetylated lysine residues in histones, thereby linking changes in chromatin structure with gene transcription. Indeed, BET proteins work as chromatin regulators that recruit transcriptional co-activators, such as P-TEFB, to promote gene transcription in inflammation (Hargreaves et al., 2009; Nicodeme et al., 2010) and cancer (Filippakopoulos et al., 2010; Dawson et al., 2011; Mertz et al., 2011; Zubari et al., 2011).

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A recent report has revealed a variety of alterations in T cell cytokine production as a consequence of BET bromodomain inhibition (Bandukwala et al., 2012). However, these studies relied on transient pharmacological inhibition shortly after activation, and therefore the role of BET bromodomains during T cell subset differentiation and their potential therapeutic application remain to be defined. In this work, we provide evidence that, through bromodomain function, the BET family of chromatin adaptors play fundamental roles in T<sub>17</sub> cell differentiation in vitro and in vivo, and thus represent a viable therapeutic entry point for a wide range of autoimmune disorders.

RESULTS AND DISCUSSION

BET bromodomains control human T<sub>17</sub> differentiation

Because BET bromodomain inhibition results in the suppression of a subset of NF-κB–dependent genes in murine macrophages (Nicodeme et al., 2010), we hypothesized that BET proteins may also play fundamental roles in other NF-κB–mediated processes, such as T cell activation and differentiation. With that aim, we examined whether BET bromodomain inhibition had any functional impact on the differentiation of naive T cells into any major subsets (T<sub>1</sub>, T<sub>2</sub>, T<sub>17</sub>, and iTreg). To address this question, we used a well characterized potent and selective BET small molecule inhibitor, JQ1 (Filippakopoulos et al., 2010).

Human CD4<sup>+</sup>CD45RA<sup>+</sup> naive T cells were purified from peripheral blood and differentiated under standard polarizing conditions in the presence of DMSO or 150 nM JQ1 (inhibitory concentration of 90% response [IC<sub>90</sub>] in a THP-1 cell-based LPS-induced IL-6 release assay; unpublished data). As a control for specificity we used the inactive enantiomer of JQ1 (JQ1(−)). As shown in Fig. 1, we found a strikingly selective effect on T<sub>17</sub> differentiation. After 6 d of culture, cells treated with DMSO or JQ1(−) exhibited a pheno-type consistent with human T<sub>17</sub> cells, as indicated by up-regulation of CCR6, IL-17A, and IL-22 (Fig. 1 A). However, in the presence of JQ1, the number of CCR6<sup>+</sup> cells was severely reduced, both IL-17A and IL-22 expression were suppressed (Fig. 1 A), and the expression of RORγt (encoded by RORC), RORα, and a subset of T<sub>17</sub> lineage-enriched transcripts were significantly inhibited (Fig. 1 C and Fig. 2 A). Under our differentiating conditions, T<sub>17</sub> cells produce some IL-10, and this was also inhibited by JQ1. BET bromodomain inhibition had no effect on total cell numbers (Fig. 1 D), ruling out the possibility of T<sub>17</sub> suppression as an indirect effect on T cell proliferation. JQ1 had no impact on the differentiation of T<sub>11</sub> (assessed as number of IFN-γ<sup>+</sup> cells and TBX21 expression), T<sub>12</sub> (IL-4<sup>+</sup> cells and GATA3 expression), or Treg (FOXP3<sup>+</sup> cells and FOXP3 expression) cells (Fig. 1, B, E, and F). Thus, BET bromodomains play essential roles in the differentiation of human T<sub>17</sub> cells but not other T cell lineages. The defect in T<sub>17</sub> differentiation uncovered by pharmacological inhibition of BET proteins was recapitulated in siRNA experiments. Because JQ1 binds to the bromodomains of all BET family members, T cells were transfected with combinations of siRNAs targeting BRD2 and BRD4 (BRD3 and BRDT are not expressed in T<sub>17</sub> cells; unpublished data). The combined knockdown of BRD2 and BRD4 for 48 h resulted in significant inhibition of RORA and IL17A expression (unpublished data), confirming the data obtained with JQ1 and further ruling out a nonspecific effect of the small molecule inhibitor. Notably, BRD2 and BRD4 have nonredundant functions in T<sub>17</sub> cells, as knocking down either transcript individually was sufficient to recapitulate the phenotype observed with JQ1 or with double RNA interference (Fig. 2 B). Collectively, these results highlight a critical role for BET bromodomains in promoting human T<sub>17</sub> cell differentiation.

BET bromodomains are necessary for the transcription of multiple T<sub>17</sub> lineage-associated cytokines, including the T<sub>17</sub> autocrine amplification factor IL-21

We consistently observed a complete suppression of IL-21 transcript and protein in JQ1–treated T cells, and in fact as early as 4 h after naive T cell culture under T<sub>17</sub> differentiating conditions, IL21 was one of the top 20 transcripts most down-regulated upon BET inhibition (unpublished data). IL-21 is required for the generation of T<sub>17</sub> cells as an autocrine factor that induces activation of STAT3 and consequently induction of RORγt (Nurieva et al., 2007; Zhou et al., 2007). Thus, we hypothesized that BET inhibition might control T<sub>17</sub> differentiation, at least in part, by directly regulating IL-21 expression. To address this possibility, we cultured human naive T cells with recombinant IL-21, and explored the impact of BET bromodomain inhibition on IL-21 mRNA expression. As previously reported (Nurieva et al., 2007; Zhou et al., 2007), exogenous IL-21 was sufficient to induce its own transcription (Fig. 2 C). This response was dependent on functional BET bromodomains, as JQ1 completely suppressed IL21 expression (Fig. 2 C). Moreover, BET bromodomains were also essential for the background IL21 expression observed in the absence of added IL-21 protein (Fig. 2 C, compare lanes 1 and 3). From these observations, we conclude that autocrine IL-21 expression in T cells requires functional BET bromodomains. We next determined the impact of BET inhibition on STAT3 activation and RORγt expression. Early in T<sub>17</sub> differentiation, STAT3 phosphorylation is dominated by the IL-6 present in the culture medium, but over time T cell–derived IL-21 significantly contributes to this process. STAT3 activation downstream of the IL-6 receptor was not affected by BET inhibition, as JQ1 had no impact on STAT3 phosphorylation in naive cells incubated with IL-6 and TGF-β for 90 min (Fig. 2 D, top). However, BET inhibition resulted in a severe impairment of STAT3 activation and RORγt induction in cells examined after 5 d of culture under T<sub>17</sub> differentiating conditions (Fig. 2, D [bottom] and F [top left]), without affecting STAT3 expression (Fig. 2 E). Addition of exogenous IL-21 almost completely restored STAT3 activation and RORγt expression (Fig. 2, D [bottom] and F [top left]), demonstrating that by directly regulating IL-21 mRNA transcription, BET controls a fundamental amplification loop that contributes to the expression of RORγt and therefore drives optimal T<sub>17</sub> differentiation.
IL-21 results in impaired STAT3 activation, and in RORC and BATF expression. We propose that the combination of these effects of BET bromodomain inhibition results in effective suppression of TH17 lineage differentiation.

BET bromodomain inhibition selectively suppresses the production of TH17 cytokines in TH17 differentiated cells

A prediction from the observed direct BET requirement for IL17, IL21, and GMCSF transcription is that BET bromodomain inhibition should also impair the production of these cytokines from already differentiated TH17 cells. To address this possibility, we differentiated naive T cells under TH17 polarizing conditions for 5 d. These newly differentiated TH17 cells were then incubated with JQ1 and restimulated for 24 h with anti-CD3 and anti-CD28 in the absence of polarizing cytokines.
Figure 2. BET bromodomain inhibition blocks human T<sub>H</sub>17 differentiation by controlling multiple T<sub>H</sub>17–associated genes. (A) Human naive T cells were cultured under T<sub>H</sub>17 conditions in the presence of 150 nM JQ1 or DMSO for 48 h and the expression of the indicated genes was investigated by qPCR. Error bars represent standard deviation. Data are representative of two to three independent experiments. Statistical significance was determined by Student’s t test (**, P < 0.01). (B) Human T cells were lentivirally transduced with hairpins targeting BRD2 (red bars) or BRD4 (blue bars) and cultured under T<sub>H</sub>17-polarizing conditions for 6 d. Two individual hairpins per gene were used (sh1 and sh2). Expression of BRD2, BRD4, and RORC was measured by qPCR; NTC, nontargeting control. IL-17A, IL-17F, and IL-21 protein was quantitated by Luminex. Data are representative of two independent experiments. Error bars represent standard deviation. Statistical significance was determined by Student’s t test (*, P < 0.05; **, P < 0.01). (C) Human naive T cells were stimulated with anti-CD3/CD28 for 24 or 48 h in the presence or absence of exogenous human recombinant IL-21 and JQ1 as indicated, and IL21 expression was measured by qPCR. Data are representative of two independent experiments and two independent donors. Error bars represent standard deviation. (D) Human naive T cells were cultured under T<sub>H</sub>17-differentiating conditions for the indicated times in the presence or absence of exogenous human recombinant IL-21 and JQ1 as indicated, and phospho-Stat3 was measured by flow cytometry. Data are representative of two independent experiments and two independent donors. (E and F) Samples from D (5 d, bottom) were analyzed by qPCR for the indicated transcripts. Data are representative of two independent experiments and two independent donors. Error bars
JQ1 blocked IL-17 production in a dose-dependent manner (not depicted), approaching full suppression at a concentration of 150 nM (Fig. 2 G). In keeping with the notion of a direct role of BET in controlling multiple effector T<sub>17</sub>-enriched cytokines, JQ1 also abrogated IL-21 and GM-CSF production (Fig. 2 G). In contrast, the ability of these cells to produce TNF protein was only modestly ameliorated (Fig. 2 H, left) and not reduced at the transcript level (Fig. 2 H, middle). Moreover, another TNF superfamily member, lymphotoxin-α, was similarly unaffected (Fig. 2 H, right). IL<sub>17</sub>, IL<sub>21</sub>, and GMCSF-transcripts were all reduced by JQ1 (unpublished data).

**BET bromodomains control murine T<sub>17</sub> differentiation**

To explore if the role of BET in T<sub>17</sub> differentiation has been conserved throughout evolution, and to enable pharmacological studies in mouse models of autoimmune diseases, we next sought to investigate if BET bromodomains also play critical roles in murine T<sub>17</sub> cell differentiation. Naive mouse T cells were cultured under T<sub>17</sub> polarizing conditions, and their phenotype upon BET inhibition was analyzed after 4 d. Early T cell activation was not affected by BET inhibition, as upregulation of the early activation marker CD69 was unchanged (Fig. 3 A). Thus, BET bromodomains are dispensable for T cell receptor (TCR) engagement and at least some downstream signaling events. However, T<sub>17</sub> differentiation was largely suppressed, as demonstrated by a significantly reduced number of IL-17<sup>+</sup> cells determined by flow cytometry and reduced IL-17A and IL-22 secretion to the culture medium (Fig. 3 B). This suppression was not generic, as TNF was unchanged upon BET inhibition (Fig. 3 B). To further demonstrate a direct and specific effect of BET on modulating T<sub>17</sub> development, we performed compound titration experiments and monitored IL-17 secretion and cell viability. IL-17 production was suppressed in a dose-dependent manner by JQ1 with an approximate IC<sub>50</sub> of 30 nM, whereas cellular viability was unaffected (Fig. 3 C). From these data, we conclude that BET bromodomains are essential for mouse T<sub>17</sub> differentiation.

Given the known roles of BET proteins as transcriptional co-activators, we next investigated whether BET inhibition led to changes in gene expression in T cells during T<sub>17</sub> polarization. Consistent with the failure of naive T cells to differentiate into T<sub>17</sub> cells in the presence of JQ1, we found the transcription of T<sub>17</sub> canonical genes, such as those encoding IL-17A, IL-17F, IL-21, IL-22, IL-23R, ROR<sup>γ</sup> and ROR<sup>α</sup>, to be significantly reduced by quantitative RT-PCR (qPCR) analysis (unpublished data) after 48 h of polarization. Suppression of proinflammatory gene transcription was selective, as Tnf remained unchanged in the presence of JQ1. Furthermore, JQ1 had no effect on the expression of Il6r (unpublished data), complementing the data reported above (Fig. 2 D, top) for a role of BET in T<sub>17</sub> differentiation independent of early events in IL-6 signaling. These observations suggest that pharmacological blockade of BET bromodomains does not afford general gene suppression but rather a targeted effect on specific transcriptional programs. Of note, BET inhibition did not result in e-Myc transcript reduction (Fig. 2 A and not depicted). This observation suggests a profound cell type-specific function of BET bromodomains, as BET inhibition results in complete suppression of e-Myc transcription in a wide array of cancer cell lines (Dawson et al., 2011; Mertz et al., 2011; Zuber et al., 2011). Therefore, BET proteins can control nonoverlapping transcriptional programs in different cellular contexts. To extend these observations and to gain a comprehensive view of the global transcriptional changes resulting from BET inhibition in T<sub>17</sub> cells, we did full-genome microarray analysis at 48 h of polarization. Strikingly, the transcriptional signature elicited by BET suppression was restricted to only 238 genes (176 down- and 62 up-regulated twofold or more; Fig. 3 D and Table S1). Highly reduced transcripts included those encoding T<sub>17</sub> signature genes such as Il17a, Il17f, Il23r, and Ccr6 (Fig. 3 D). Other strongly down-regulated transcripts encoded proteins that are not restricted to T<sub>17</sub> cells but have been shown to be relevant for various aspects of T<sub>17</sub> biology, including IL-1R1 (Chung et al., 2009). The expression patterns discussed above were confirmed by qPCR (unpublished data). As previously observed (Nicodeme et al., 2010; Mertz et al., 2011), BET inhibition also resulted in the up-regulation of a small subset of genes (Fig. 3 D and Table S1), suggesting that BET proteins can also act, directly or indirectly, as transcriptional repressors in certain genomic loci and cellular contexts. To further delineate the molecular pathways impinging upon the global transcriptional changes described above, we used the Gene Set Enrichment Analysis (GSEA) algorithm to identify curated gene signatures that significantly coincided with BET inhibition in our transcriptional profiling data. The NF-κB transcription factor target gene set scored as a highly significant overlap with the T<sub>17</sub> expression set (normalized enrichment score = −1.4; P = 0.003; Fig. 3 D, bottom left). This observation is consistent with published data demonstrating a role of BET proteins in mediating NF-κB–dependent gene transcription in other cellular contexts (Hargreaves et al., 2009; Nicodeme et al., 2010). Collectively, the results reported here demonstrate that BET proteins, through their bromodomain function, play a critical role in orchestrating the transcriptional program that drives T cell differentiation into the T<sub>17</sub> subset, possibly by modulating the transcriptional state of NF-κB–dependent genes. In keeping with our data from human T cells, we also observed that BET bromodomain inhibition results in a significant and dose-dependent attenuation of

[Represent standard deviation. Statistical significance was determined by Student’s t test (*, P < 0.05; **, P < 0.01); NS: not significant. (G and H) Human naive T cells were cultured under T<sub>17</sub> conditions for 6 d. After that time, cells were washed and rested for 16 h prior restimulation with anti-CD3/anti-CD28 for 48 h in the presence of DMSO control or 150 nM JQ1. Cytokine levels (luminex) or transcript levels (qPCR) are shown. Data are representative of two independent experiments. Error bars represent standard deviation. Statistical significance was determined by Student’s t test (*, P < 0.05).]
IL-17 production in fully differentiated mouse T<sub>H17</sub> cells (Fig. 3 E). Although our data clearly demonstrate that BET bromodomains selectively control T<sub>H17</sub> differentiation, it is possible that they might modulate some biological functions of other T cell lineages, as BET inhibition results in the down-regulation of multiple genes in T<sub>H0</sub> cells (unpublished data).

**BET members Brd2 and Brd4 directly bind to the <i>Il17</i> genomic locus in a bromodomain-dependent manner**

Our observation of a requirement of functional BET bromodomains for IL-17 mRNA generation (Fig. 2, A and F) prompted us to mechanistically elucidate whether the two BET family members expressed in T<sub>H17</sub> cells, Brd2 and Brd4, associated with chromatin at the <i>Il17</i> locus. With that aim, we used the mouse system as a source of large number of cells to perform chromatin immunoprecipitation (ChIP) studies under T<sub>H17</sub> polarizing conditions. After 20 h of culture, both Brd2 and Brd4 significantly associated with chromatin at the <i>Il17a</i> control region CNS2 (essential for <i>Il17a</i> transcription; Akimzhanov et al., 2007) in T<sub>H17</sub> but not T<sub>H1</sub> or T<sub>H2</sub> cells, and this binding was prevented by JQ1, significantly for Brd4 (Fig. 3 F). JQ1 had no impact on H3K4me3 or acetylation on CNS2 (Fig. 3 F), suggesting that the reduced association of BET at CNS2 was not an indirect consequence of altered chromatin structure. Furthermore, the fact that H4Ac4 levels were unaffected (Fig. 3 F) suggests that the reduced binding of BET at CNS2 is the result of JQ1-mediated release from chromatin, and not simply an absence of the bromodomain

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**Figure 3. BET bromodomains control mouse T<sub>H17</sub> differentiation.** (A) Mouse CD4<sup>+</sup>CD62L<sup>hi</sup> naive T cells were cultured under T<sub>H17</sub> conditions in the presence of 150 nM JQ1 or DMSO control, and their activation state was evaluated by CD69 staining by FACS after 24 h of culture. Data are representative of three independent experiments. (B) Mouse naive T cells were cultured under T<sub>H17</sub> conditions in the presence of 150 nM JQ1 or DMSO control, and IL-17 induction was measured by intracellular staining (contour plots) and ELISA (bars); IL-22 and TNF were measured by ELISA (bars). Data are representative of three independent experiments. (C) JQ1 dose response inhibition was monitored by ELISA (IL-17A) and Cell Titer Glo (viability). Data are representative of three independent experiments. (D) Mouse naive T cells were cultured under T<sub>H17</sub> conditions in the presence of 150 nM JQ1 or DMSO control for 48 h, and whole genome gene expression was evaluated on the Affymetrix exon array platform: heatmap display, log2 expression of each gene is mean-centered, and normalized to have a standard deviation of 1; GSEA plot was calculated from the same dataset. Data represent two independent biological replicates. (E) Mouse naive T cells were differentiated into T<sub>H17</sub> cells for 4 d and reactivated for 18 h with anti-CD3/CD28 in the absence (filled bars) or presence (open bars) of increasing concentrations of JQ1, and IL-17A and TNF production were monitored by AlphaLISA. Data are representative of three independent experiments (n = 4–6 mice per group). All panels, error bars represent standard deviation. Statistical significance was determined by Student’s t test (*, P < 0.05; **, P < 0.01).
molecular target. Thus, BET bromodomain inhibition results in impaired binding of Brd2 and Brd4 to the Il17a gene and its suppressed transcription.

**Inhibition of BET bromodomains blocks T_{H}17 differentiation in vivo**

We next investigated if T_{H}17 suppression by BET inhibition could be recapitulated in vivo. We used a well established model where, upon two sequential injections of anti-CD3 antibody (as a way to strongly engage the TCR), an immunoregulatory environment is generated that promotes T_{H}17 differentiation (Esplugues et al., 2011). Consistent with previous reports demonstrating migration of T_{H}17 cells into the small intestine in this model, we observed a population of IL-17–producing T cells in the duodenum. Treatment of mice with the BET inhibitor resulted in a marked suppression of this duodenal T_{H}17 population (Fig. 3 G). In accordance with these observations, we also observed a significant reduction in the levels of circulating IL-17 in JQ1–treated animals (Fig. 3 H, left). It has been established that in this model, the duodenal T_{H}17 cells acquire a regulatory phenotype that includes the coexpression of Il17 and Il10 (Esplugues et al., 2011). Consistent with those observations, we also found a significant reduction of circulating IL-10 in the plasma of these mice upon BET inhibition (Fig. 3 H, right). It is possible that this reduction in IL-10 production is a direct transcriptional effect of BET in activated effector cells (Fig. 3 D), or a consequence of reducing the numbers of T_{H}17 (regulatory T_{H}17) cells generated in this model.

Collectively, these data demonstrate a critical role for the BET bromodomains in the generation of T_{H}17 cells in vivo.

**Inhibition of BET bromodomains protects mice from autoimmunity**

The fundamental involvement of T_{H}17 cells in the pathogenesis of autoimmunity is firmly established. Because our data demonstrate that BET bromodomains are critical in the
differential and function of T\textsubscript{H}17 cells, we hypothesized that BET inhibition could be protective in mouse models of autoimmunity. To test this hypothesis, we induced collagen-induced arthritis (CIA) and experimental autoimmune encephalomyelitis (EAE) in mice, and therapeutically used JQ1 at doses predicted to afford significant target coverage based on pharmacokinetic data (Filippakopoulos et al., 2010; unpublished data). DBA/1 mice were immunized with chicken collagen-II and left untreated until clinical signs (such as paw redness and inflammation) were observed. At that point, animals were randomly assigned to treatment with vehicle or JQ1 for 2 wk. Vehicle-treated mice continued to develop increasing clinical signs consistent with moderate-to-severe arthritis (Fig. 4 A), and histological assessment of individual joints at study termination revealed significant bone and cartilage damage, as well as extensive pannus formation (Fig. 4 B). However, mice receiving a twice-per-day (BID) dose of 30 mg/kg of the BET inhibitor were significantly protected from experimental arthritis, both macroscopically (Fig. 4 A) and histologically (Fig. 4 B). Importantly, no obvious adverse events were observed in any animal during the treatment period, as determined by monitoring body weight over the course of the experiment (unpublished data). From these data, we conclude that BET bromodomains play a pivotal role in the development and maintenance of CIA.

In a separate set of experiments, mice were immunized with a myelin oligodendrocyte glycoprotein (MOG) peptide, and when the initial signs of disease became evident (clinical score = 1) animals were treated with vehicle, JQ1, or dexamethasone (as a generic antiinflammatory control). JQ1-treated animals were significantly protected from EAE, whereas vehicle-treated animals continued to develop disease (clinical scores, body weight, and disease incidence; Fig. 4 C). To mechanistically delineate the impact of BET inhibition in this model, we isolated T cells from draining cervical lymph nodes at study termination (day 22) and reactivated them ex vivo for 3 d with MOG peptide. T cells obtained from JQ1-treated animals produced normal levels of IFN-γ but were impaired in their production of IL-17 (Fig. 4 D). At peak disease (day 17), central nervous system-infiltrating lymphocytes from vehicle-treated mice produced IL-17A, IL-17F, IL-21, and IFN-γ, whereas JQ1-treated animals showed a selective decrease in the number of cells producing IL-17A/F and IL-21, but not IFN-γ (Fig. 4 E). These results suggest that BET inhibition protects against EAE by selectively impairing the generation and/or function of T\textsubscript{H}17 cells. Of note, T cells from dexamethasone-treated animals were impaired in the production of both IL-17A and IFN-γ (Fig. 4, D and E), with no improvement in clinical scores compared with JQ1-treated mice, highlighting the critical role of T\textsubscript{H}17 cells in this model.

In summary, we have shown that BET proteins, through their bromodomain motifs, play critical roles in the control of T\textsubscript{H}17 differentiation in vitro and in vivo by integrating signals that drive naïve T cells into the T\textsubscript{H}17 lineage. We have also defined a role for BET bromodomains in the selective activation of T\textsubscript{H}17 cells once they are fully differentiated. Because T\textsubscript{H}17 cells are essential effectors of autoimmunity, our data suggest that interfering with BET-dependent chromatin signaling may provide clinical benefit to patients suffering from this group of diseases.

**MATERIALS AND METHODS**

**Antibodies and intracellular cytokine staining.** Mouse anti-CD4 (RM4-5) and anti-CD69 (H1.2F3) were purchased from BD. Human anti-CCR6 (17-1969-42) and mouse anti-CCR6 (S57976) were purchased from ebioscience and BD, respectively. For intracellular staining, cells were restimulated with 50 ng/ml PMA (Sigma-Aldrich) and 500 ng/ml ionomycin (Sigma-Aldrich) for 5 h with the addition of GolgiPlug (BD). After restimulation, the cells were washed and stained for extracellular markers, followed by fixation, permeabilization using the Cytofix/Cytoperm kit (554714; BD), and staining for intracellular cytokines to detect mouse IL-17A (S55902; BD), IL-17F (561631; BD), IL-21 (12-7211-82; ebioscience), IFN-γ (554411; BD), human IL-17A (S60487; ebioscience), IL-22 (12-7229-42; ebioscience), IL-10 (554707; BD), IFN-γ (17-7319; ebioscience), IL-4 (12-7049-42; ebioscience), Foxp3 (12-4777-41; ebioscience), and phosphoStat3 (557814; BD). For Foxp3 intracellular staining, cells were fixed and permeabilized using the Foxp3/Transcription Factor Staining kit (00-5523-00; ebioscience). For phospho-Stat3 intracellular staining, cells were fixed and permeabilized using Phostflow Lyse/fix Buffer (558050; BD) and Permeabilization buffer III (558049; BD). Cells were acquired on the FACSCalibur (BD) and data analyzed using Flowjo Software.

**Human T cell cultures.** Leukopak samples were obtained from the Biologic Speciality Corporation and PBMCs were isolated by ficoll (GE Healthcare) density gradient centrifugation. CD4⁺CD45RA⁺ T cells were isolated from PBMCs by magnetic depletion of non–T\textsubscript{H}17 cells and memory T cells using the human naïve CD4⁺ T Cell Isolation kit II (130–094-131; Miltenyi Biotech). For the induction of T\textsubscript{H}17 differentiation, naïve CD4 T cells were activated using Human T-Activator CD3/CD28 Dynabeads (Invitrogen) and cultured in DMEM (Invitrogen) in the presence of the following cocktail: 2.5 ng/ml TGF-β1 (R&D Systems), 30 ng/ml IL-6 (R&D Systems), 20 ng/ml IL-23 (R&D Systems), 25 ng/ml IL-1β (R&D Systems), 10 µg/ml anti–human IFN-γ (clone B140; ebioscience), and 10 µg/ml anti–human IL-4 (clone 8D4-8; ebioscience) for 2–6 d. Human recombinant IL-21 was added to cell cultures when indicated at 50 ng/ml (CR172A; Cell Sciences). For T\textsubscript{H}1 conditions, the following cocktail was used: 10 ng/ml IL-12 (R&D Biosystems), 20 ng/ml IL-2 (R&D Biosystems), and 10 µg/ml anti-human IL-4 (clone 8D4-8; ebioscience) for 2–6 d. Human recombinant IL-2 was added to cell cultures when indicated at 50 ng/ml (CR172A; Cell Sciences). For T\textsubscript{H}17 conditions, the following cocktail was used: 10 ng/ml IL-12 (R&D Biosystems), 20 ng/ml IL-2 (R&D Biosystems), and 10 µg/ml anti–human IL-4 (clone 8D4-8; ebioscience) for 2–6 d. Mouse T cell cultures. Single cell suspensions of splenocytes were prepared using 70-µm nylon cell strainers (BD). Red blood cells were lysed using ammonium chloride lysing buffer (R7757; Sigma-Aldrich) and washed with cRPMI 10% FBS (61870-036; Invitrogen). Naïve CD4 T cells were purified using magnetic-activated cell sorting beads (130-093-227; Miltenyi Biotech). Purity of sorted naïve cells was >90%. Naïve CD4 T cells from C57BL/6 mice were cultured in 24-well plates (10⁶ cells/ml) and stimulated with anti-CD3/CD28-coated beads (Dynabeads 11452D; Invitrogen) for 4 d under the following T\textsubscript{H}17 polarizing conditions: 5 ng/ml TGF-β1 (100-B; R&D Systems), 20 ng/ml IL-6 (406-ML; R&D Systems), 20 ng/ml IL-23 (1887-ML-010; R&D Systems), 10 µg/ml anti–IFN-γ (clone B140; ebioscience), and 20 ng/ml Treg TGF-β1 (R&D Biosystems), and 10 ng/ml IL-2 (R&D Biosystems). Naïve CD4 T cells were polarized under respective conditions for 2–6 d.

**Mouse T cell cultures.** Single cell suspensions of splenocytes were prepared using 70-µm nylon cell strainers (BD). Red blood cells were lysed using ammonium chloride lysing buffer (R7775; Sigma-Aldrich) and washed with cRPMI 10% FBS (61870-036; Invitrogen). Naïve CD4 T cells were purified using magnetic-activated cell sorting beads (130-093-227; Miltenyi Biotech). Purity of sorted naïve cells was >90%. Naïve CD4 T cells from C57BL/6 mice were cultured in 24-well plates (10⁶ cells/ml) and stimulated with anti-CD3/CD28-coated beads (Dynabeads 11452D; Invitrogen) for 4 d under the following T\textsubscript{H}17 polarizing conditions: 5 ng/ml TGF-β1 (100-B; R&D Systems), 20 ng/ml IL-6 (406-ML; R&D Systems), 20 ng/ml IL-23 (1887-ML-010; R&D Systems), 10 µg/ml anti–IFN-γ antibody (554408; BD), and 10 µg/ml anti–IL-4 antibody (554432; BD). Naïve CD4 T cells from C57BL/6 mice were polarized under the following T\textsubscript{H}1 conditions: 20 ng/ml IL-12 (419-ML-010; R&D Biosystems), 10 ng/ml IL-2 (402-ML; R&D Biosystems), and 10 µg/ml anti–IL-4 antibody (554432; BD). Naïve CD4 T cells from C57BL/6 mice were polarized under the following T\textsubscript{H}17 conditions: 20 ng/ml IL-12 (419-ML-010; R&D Biosystems), 10 ng/ml IL-2 (402-ML; R&D Biosystems), and 10 µg/ml anti–IL-4 antibody (554432; BD).
Cell viability. Cell viability was assessed using Cell Titer Glo which determines the number of viable cells based on quantification of ATP present (G7572; Promega). Live cell numbers were determined by trypan blue staining followed by analysis using Countess automated cell counter (Invitrogen).

shRNAs and lentivirus transduction of human primary T cells. Target sequences for human BRD2 and BRD4 were obtained from CellM. Sense and antisense oligonucleotides (66 nt) containing sense, loop, and antisense sequences were obtained with 5’ phosphorylation from Integrated DNA Technologies. Oligonucleotides were annealed and ligated into a lentiviral shRNA vector based on pLKO.1 obtained from CellM. In this vector, shRNA expression is driven by the U6 promoter, and both a fluorescence marker and puromycin acetyltransferase (separated by the T2A sequence) are driven by the UbC promoter. Lentiviral production was performed according to publicly available protocols (http://www.broadinstitute.org/rnai/public/resources/protocols). Naïve T cells were differentiated under Tq17 conditions for 16 h, followed by a spin infection for 1.5 h with lentivirus-expressing shRNAs against BRD2, BRD4, or a nontargeting control. 24 h after infection, cells were selected with 1 µg/ml of puromycin for 5 days and supernatants and cell pellets were collected for cytokine quantification and qPCR.

Cytokine assays. Cytokines were quantified from cell assays by ELISA (IL-22, TNF, and IFN-γ; eBioscience) or AlphaLISA (IL-17A and TNF; Perkin Elmer) according to the manufacturer’s instructions. Plates were read on the SPECTRAmax M2 ( Molecular Devices) or the EnVision 2104 Multilabel reader. Human cytokines IL-17A, IL-17F, and IL-21 were quantified from cell assays using the Multiplex MAP Human Th17 magnetic bead panel (Millipore; HTH17MAG-14K). Cytokines were quantified in plasma by MSD multi-array assays (IL-17A and IL-10; Meso Scale Discovery) according to the manufacturer’s instruction. Mouse plasma was obtained by centrifugation of blood in serum separator Microtainer tubes (365956; BD) after submandibular vein puncture or cardiac puncture.

Real-time RT-PCR. RNA was purified from cells using an RNaseasy Mini kit (QiAGEN) according to the manufacturer’s protocol. First-strand cDNA was synthesized using SuperScript III reverse transcription. Quantitative real-time PCR was performed using FastStart Universal Probe master mix (Roche) and TaqMan probes for transcripts encoding the proteins IL-17A, IL-17F, IL-21, IL-22, IL23R, RORγt, RORα, c-Myc, TNF IL6R, CCR6, BATE CM-CSE, AHR, IRF4, GATA3, TBET, FOXP3, STAT3, BRD2, BRD3, and BRD4 on the Stratagene MxPro3005p. Mouse samples were normalized using GAPDH primer/probe sets (5046211001; Roche). Human samples were normalized using GAPDH primers and universal probe library probes (Roche).

Global expression profiling. Naïve CD4+ T cells were treated with 150 nM JQ1 or DMSO under Tq17 polarizing conditions for 48 h. Total RNA was prepared using an RNaseasy kit with on-column DNAse digestion according to the manufacturer’s instructions. Samples were processed and hybridized on Affymetrix exon arrays, and data were acquired, at ALMAC Diagnostics. CEL files were processed with the RMA algorithm on core probe sets using the Expression Console program (Affymetrix). Duplicate log2 expression values were averaged and subtracted to obtain log fold change. For the heat maps, genes having at least twofold change and an unadjusted Student’s t test with p-value <0.10 was selected. Profiles were normalized for each gene across both time points for the purpose of display; only the relevant time point is shown. The gene expression data are available at the Gene Expression Omnibus with accession no. GSE37270. For gene function analysis, all genes with twofold change were selected. For Gene Set Enrichment Analysis (GSEA), mouse genes were mapped to human genes using the human and mouse orthology from The Jackson Laboratory (HMD_Human5.rpt). GSEA was run with MSIGDB set c3.all.v3.0.bsymbols.gmt.

ChIP assays. T cells treated with DMSO or 150 nM JQ1 were cross-linked with 1% formaldehyde at a density of 2 × 10^6 cells/ml for 10 min at room temperature. Chromatin preparation and ChIP were performed as previously described (Mertz et al., 2011) with the following antibodies: anti-H4 tetra-acetyl (Active Motif), anti-Brd2 (Bethyl Laboratories, Inc.), anti-Brd4 (Bethyl Laboratories, Inc.), IgG (Jackson ImmunoResearch Laboratories), and H3K4me3 (Abcam). The sequences for CNS2a primers were: forward, 5’-CAGCGTGTGGTTTGGTTTAC-3’, and reverse, 5’-CTAGGTGGG- TTCCTCACTGG-3’. The enrichment was normalized to input DNA.

In vivo T cell stimulation and intestinal lymphocyte isolation. C57BL/6 mice were purchased from Charles River and kept under specific pathogen-free conditions in the animal care facility at VivoSource Laboratories, Inc. Experimental procedures were approved by VivoSource’s Institutional Animal Care and Use Committee (IACUC). 8–10-wk-old C57BL/6 female mice were injected with 30 µg anti-CD3 (145 2C11) twice, 1 h after compound treatment and again 48 h later. Eight mice per group were treated with 15 mg/kg JQ1 or vehicle control by i.p. injection twice a day. Serum was collected 6 h after the first anti-CD3 injection and at the end of the study. Mice were sacrificed 4 h after the final anti-CD3 injection. Isotype control or PBS was injected as controls. The intraepithelial lymphocytes were collected as follows: small intestines were removed and Peyers’ patches were dissected. The first 3 cm of the small intestine were considered as duodenum. Intestines were cut longitudinally and then cut into 1-cm strips. Tissues were washed in Hanks’s buffered saline and incubated in the presence of 0.1 nM EDTA at 37°C for 20 min while stirring. The released cells were processed through a nylon wool column to enrich for T cells. The eluate was loaded onto a Percoll gradient and centrifuged. The cells between 40 and 100% Percoll were collected and used as intestinal epithelial lymphocytes.

CIA. CIA studies were performed at Biomere, Inc. and were approved by Biomere’s IACUC. DBA1/ female mice were immunized by subcutaneous injection via the tail vein using purified chicken type II collagen emulsified at a 1:1 ratio (vol/vol) in CFA, and then boosted 3 wk later using chicken type II collagen emulsified at a 1:1 ratio (vol/vol) in IFA. Approximately 2 wk after the boost, animals began to show disease signs and treatment was initiated (day 0), and it continued for 14 d.

EAE. EAE studies were performed at WuXi App Tech Ltd and were approved by WuXi’s IACUC. C57BL/6 mice were randomized into four groups and immunized subcutaneously via the tail vein using purified chicken type II collagen emulsified at a 1:1 ratio (vol/vol) in CFA, and then boosted 3 wk later using chicken type II collagen emulsified at a 1:1 ratio (vol/vol) in IFA. Approximately 2 wk after the boost, animals began to show disease signs and treatment was initiated (day 0), and it continued for 14 d.

Chemical compound synthesis. JQ1 was synthesized according to published methods (Filippakopoulos, et al., 2010).

Online supplemental material. Table S1 shows the effect of BET bromodomains inhibition on gene expression in Tq17 cells. Online supplemental material is available at http://www.jem.org/cgi/content/full/jem.20130376/DC1.

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