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Disruption of FOXP3–EZH2 Interaction Represents a Pathobiological Mechanism in Intestinal Inflammation

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SUMMARY

We provide evidence that the physical and functional interaction between forkhead box protein 3 and enhancer of zeste homolog 2 necessary for regulatory T-cell–suppressive function can be impaired by inflammatory bowel disease–associated mutation or interleukin 6 signaling.

BACKGROUND & AIMS: Forkhead box protein 3 (FOXP3) regulatory T cell (Treg) dysfunction is associated with autoimmune diseases; however, the mechanisms responsible for inflammatory bowel disease pathophysiology are poorly understood. Here, we tested the hypothesis that a physical interaction between transcription factor FOXP3 and the epigenetic enzyme enhancer of zeste homolog 2 (EZH2) is essential for gene co-repressive function.

METHODS: Human FOXP3 mutations clinically relevant to intestinal inflammation were generated by site-directed mutagenesis. T lymphocytes were isolated from mice, human blood, and lamina propria of Crohn’s disease (CD) patients and non-CD controls. We performed proximity ligation or a co-immunoprecipitation assay in FOXP3-mutant, interleukin 6 (IL6)-treated or CD-CD4+ T cells to assess FOXP3–EZH2 protein interaction. We studied IL2 promoter activity and chromatin state of the interferon γ locus via luciferase reporter and chromatin-immunoprecipitation assays, respectively, in cells expressing FOXP3 mutants.

RESULTS: EZH2 binding was abrogated by inflammatory bowel disease–associated FOXP3 cysteine 232 (C232) mutation. The C232 mutant showed impaired repression of IL2 and diminished EZH2-mediated trimethylation of histone 3 at lysine 27 on interferon γ, indicative of compromised Treg physiologic function. Generalizing this mechanism, IL6 impaired FOXP3–EZH2 interaction. IL6-induced effects were reversed by Janus kinase 1/2 inhibition. In lamina propria–derived CD4+ T cells from CD patients, we observed decreased FOXP3–EZH2 interaction.


Keywords: Proinflammatory Cytokine; Epigenetics; Regulatory T Cells; Crohn’s Disease.

Autoimmune diseases are known to share similar pathways and mechanisms of pathogenesis as shown through genomewide association studies. Specifically, dysregulation of the host immunity, triggered by complex interactions between genetics, environmental factors, and the gut microbiota, is associated with inflammatory bowel disease (IBD) and extraintestinal manifestations. As a result, in IBD patients, increased production of proinflammatory cytokines, including interleukin (IL)6, are known to contribute to disease pathogenesis.1,2 Despite advances in mechanistic insight, a significant proportion of IBD patients remain refractory to our most effective biologic therapies, thus suggesting a role for other unknown pathophysiological mechanisms.3,4

X-chromosome–encoded forkhead domain-containing protein (FOXP3) is the lineage-defining oligomeric transcription factor required for the development of CD4+CD25high FOXP3+ regulatory T cells (Tregs).5 Tregs derived from the thymus during T-cell development (natural Tregs) or induced in the periphery are both necessary for maintaining immunologic self-tolerance and homeostasis.

Abbreviations used in this paper: CD, Crohn’s disease; ChIP, chromatin-immunoprecipitation; co-IP, co-immunoprecipitation; C232, cysteine 232; EED, embryonic ectoderm development; EZH2, enhancer of zeste homolog 2; FCS, fetal calf serum; FOXP3, forkhead domain-containing X-chromosome–encoded protein; H3K27me3, trimethylated histone H3 at lysine 27; IBD, inflammatory bowel disease; IL, interleukin; IPEX, immune dysregulation, polyendocrinopathy, enteropathy, X-linked; JAK, Janus kinase; Lz, leucine zipper; PBMC, peripheral blood mononuclear cell; PBS, phosphate-buffered saline; PLA, proximity ligation assay; PMA, phorbol 12-myristate 13-acetate; PRC2, polycomb repressive complex 2; STAT, signal transducer and activator of transcription; SUZ12, suppressor of zeste; Th, T helper; Treg, regulatory T cell; WT, wild-type.

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by restraining pathologic immune responses including autoimmunity, inflammation, and allergy. FOXP3 deletion or mutation can result in multi-organ autoimmunity in mice and human immune dysregulation, polyendocrinopathy, enteropathy, X-linked (IPEX). The immunosuppressive function of Tregs is maintained through a FOXP3-driven gene transcriptional program. The functional capacity of FOXP3, such as gene repression, critically relies on its protein–protein interactions with a broad range of cofactors via its structural domains, as shown by mass spectrometric analysis. These include sequence-specific transcription factors, chromatin modifiers, and FOXP3 itself.

Histone modifications are known to modulate chromatin structure, thereby inducing reversible and hereditable transcriptional regulation of genes. Aberrant histone modifications have been strongly associated with the pathogenesis of human diseases. Lysine methylation of histones is one of the most characterized modifications to date, however, its role in Treg biology is not completely understood. Accumulating evidence now suggests that Treg function relies on enhancer of zeste homolog 2 (EZH2), under Janus kinase (JAK) 1/2 inhibition. Interestingly, in lamina propria–derived CD4+ T cells isolated from human CD biopsy specimens, we found a reduced presence of FOXP3–EZH2 protein complexes. Thus, our data support a model whereby loss of FOXP3–EZH2 protein interaction in Treg via diverse mechanisms is an indication of a compromised Treg physiology that may perpetuate intestinal inflammation. These observations highlight the clinical importance and approaches for improving Treg function in the context of inflammation.

**Results**

**FOXP3 Interacts With EZH2 in Murine-Induced Tregs and Freshly Isolated PBMC-Derived Human Tregs**

In murine Tregs, FOXP3 gene targets overlap with EZH2-mediated H3K27me3-repressive peaks as shown by chromatin-immunoprecipitation (ChIP) sequencing analysis, however, structural insight into the regulation of FOXP3–EZH2 protein interaction is lacking. To characterize this interaction, naive murine CD4+ T cells isolated from the spleen were differentiated into Tregs (induced) or T helper (Th)17 cells in culture under specific polarizing conditions. These cells were subjected to an in situ proximity ligation assay (PLA) and co-immunoprecipitation (co-IP) (Figure 1) using specific antibodies against endogenous FOXP3 and EZH2. By using PLA, we visually and quantitatively monitored protein–protein interactions in close proximity (<30 nm) in individual cells at single-molecule resolution detectable via fluorescent signals (shown in red) that serve as surrogate markers (Figure 1A). PLA and confocal imaging of cells showed that the majority of Tregs co-stained with FOXP3 and EZH2 antibodies showed nuclear PLA signals (red signals) (Figure 1B, third row, and quantified in 1C, % PLA+ cells) in contrast to single-antibody–stained cells, co-stained Th17, or activated undifferentiated CD4+ T cells (Figure 1, fourth and fifth rows, respectively). Congruent with the PLA studies, EZH2 co-purified with immunoprecipitated FOXP3 in murine Tregs in contrast to activated undifferentiated CD4+ T cells (Figure 1D). Similarly, in human Tregs (CD4+CD25+FOXP3+) freshly isolated from peripheral blood mononuclear cell (PBMC) donors, FOXP3 interacted with EZH2 (magenta signal) irrespective of anti-CD3/–CD28–induced T-cell–receptor activation (Figure 1E and F). As a control, CD4+CD25+ cells show diminished FOXP3–EZH2 interaction (Figure 1E, first row, and F). Taken together, our data show a constitutive interaction between FOXP3 and EZH2 in murine and human Tregs, suggesting that FOXP3 and EZH2 may form protein–protein complexes on their target loci to mediate gene repression.
**FOXP3 Constitutively Interacts With the PRC2 Complex**

To test the generalizable nature of our findings, we used a nonimmune cellular in vitro system devoid of T-cell-specific signaling pathways and putative activators. We ectopically co-expressed tagged (His, myc, DDK) plasmids encoding human FOXP3 and EZH2 proteins in HEK293T cells, and subsequently performed PLA and co-IP studies (Figure 2A–F). Cells co-expressing both His–FOXP3 and myc–EZH2 showed robust nuclear FOXP3–EZH2 interaction (green signal) (Figure 2A, fourth row, and B) in contrast to myc–EZH2– or His–FOXP3–expressing cells (Figure 2A, first and second rows, respectively, and B). This result was validated using a second EZH2 construct (Myc–DDK–EZH2).
Figure 2. FOXP3 constitutively interacts with the PRC2 complex. HEK293T cells transfected with plasmids encoding either EZH2 (myc-tagged EZH2), FOXP3 (His-tagged FOXP3), or both for 48 hours were subjected to PLA or co-immunoprecipitation using the indicated primary antibodies. (A) Representative PLA images of cells from 3 independent experiments; first 3 rows are negative control experiments and green signals indicate a FOXP3–EZH2 interaction. Scale bar: 20 μm. (B) Quantitation of nuclear PLA signals in images from panel A; n = number of cells imaged. **P < .001. Red horizontal bars indicate means ± SEM (1-way analysis of variance + Bonferroni test) from 3 independent experiments. (C) Whole-cell lysates from HEK293T cells transfected with plasmids encoding His–FOX3 and myc–DDK–tagged EZH2 were subjected to immunoprecipitation with IgG or anti-FOXP3 antibody; immunoblotted for His–FOX3 and myc–EZH2 with FOX3 and myc antibodies. Input shows protein expression in whole-cell lysates. Data are representative of 3 independent experiments. (D) Cells from panel C were subjected to PLA using His antibody (negative control) or both His and myc antibodies. Red signals indicate FOXP3 interaction; data are representative of 3 independent experiments. Scale bar: 20 μm. (E) Quantitation from 3 independent experiments of nuclear PLA signals in images from Figure 1D. **P < .001. Red horizontal bars indicate means ± SEM (1-way analysis of variance + Bonferroni test). (F) and (G) Whole-cell lysates from HEK293T cells transfected with plasmids encoding either His–FOX3 and myc–EZH2 alone in HEK293T cells or FOX3 alone in Jurkat T cells) were subjected to immunoprecipitation with IgG or anti-FOXP3 antibody; immunoblotted for His–FOX3, myc–EZH2, and the other PRC2 subunits SUZ12 and EED with the indicated antibodies. Data are representative of 3 independent experiments. DAPI, 4',6-diamidino-2-phenylindole.

Figure 1. (See previous page). FOXP3 interacts with EZH2 in murine induced Tregs (iTreg) and freshly isolated PBMC-derived human Tregs. (A) Sketch depicts PLA to detect and quantify protein–protein interactions [A] and [B] < 30 nm in close proximity or protein modifications by combining ligation of detection probes with rolling-circle amplification. (B) Mouse naive CD4⁺ T cells isolated from spleen differentiated into Tregs (induced) or Th17 cells followed by PLA. Representative confocal PLA images of CD4⁺ T-cell subsets from 3 independent experiments show endogenous FOXP3–EZH2 protein interaction (red). (C) Quantification of PLA + cells from panel B, n = number of cells imaged. **P < .001. Red horizontal bar shows means ± SEM from 3 independent experiments (1-way analysis of variance + Bonferroni test). (D) Whole-cell lysates from activated CD4⁺ T cells or iTregs in panel B were subjected to immunoprecipitation with anti-FOXP3 and immunoblotted for FOXP3 and EZH2; input shows EZH2 protein expression in whole-cell lysates. Data are representative of 3 independent experiments. (E) Representative PLA images of PBMC-derived human Tregs (CD4⁺ CD25⁺) from 3 healthy donors showing endogenous FOXP3–EZH2 interaction (magenta) before and after T-cell–receptor activation with antibodies against CD3 and CD28; CD4⁺ CD25⁺ cells were used as negative controls. Scale bar: 5 μm. Dotted white lines denote the plasma membrane as seen on differential interference contrast images. Data are representative of 3 independent experiments. (F) Quantification of nuclear PLA signals (number of dots per cell) in images from E. n = number of cells imaged. **P < .001; NS, non-significant P value. Red horizontal bars indicate means ± SEM (1-way analysis of variance + Bonferroni test) from 3 independent experiments. DAPI, 4',6-diamidino-2-phenylindole.
Because the functional relevance of this complex has not been established in human pathophysiology, we next sought to characterize known disease-inducing FOXP3 mutations by their ability to complex with EZH2.

**FOXP3 Cysteine 232 to Glycine (FOXP3–C232G) Mutation Implicated in Loss of Treg-Suppressor Function and Early Onset IBD Disrupts EZH2 Interaction and its Gene Co-repressor Function**

We previously identified a novel private mutation in FOXP3 (C232G) leading to loss of Treg-suppressive capacity and severe familial IBD, a phenotype quite distinct from the IPEX clinical phenotype. Although IPEX-inducing FOXP3 mutations, particularly in the leucine zipper (LZ) domain, have been characterized extensively, no mechanistic information relevant to C232 and in close proximity to LZ IPEX mutations, particularly within the context of EZH2, exists. Thus, we subsequently investigated the impact of disease-associated FOXP3 LZ and C232 mutations on EZH2 recruitment and function (Figure 3A).

For this purpose, we studied the core promoter of the human *IL2* gene as a model system because the human *IL2* gene is known to be rapidly modified epigenetically upon T-cell activation. We used an *IL2* luciferase construct containing 1.0 kb 5′ flanking region of the human *IL2* gene cloned upstream of the luciferase gene. As anticipated, repression of phorbol 12-myristate 13-acetate (PMA)/ionomycin-induced *IL2* promoter activity by FOXP3 as measured by luciferase expression was reduced in the presence of the specific EZH2 inhibitor GSK126 (Figure 3B), thus confirming a critical role for EZH2 in our model system.

By using this well-characterized model system, we next investigated the repressive capacity of FOXP3 C232 mutation using FOXP3–LZ mutants as relevant controls. In support of previous reports, IPEX-associated FOXP3–LZ mutants (L242P and K250D) poorly repressed the *IL2* promoter in contrast to wild-type (WT) FOXP3 (Figure 3C). Of note, the novel FOXP3 C232G mutant showed impaired *IL2*-repressive capacity similar to the FOXP3–LZ mutants (Figure 3C).
Subsequently, we assessed the ability of FOXP3–C232 mutants to co-immunoprecipitate with EZH2. Given that the mechanism of pathogenesis of LZ domain FOXP3 mutations is defined and not described to be EZH2-dependent,¹⁷,³⁸,⁴²–⁴⁴ these mutant constructs served as relevant controls. As shown by co-IP (Figure 3D) and reverse co-IP (Figure 3E), L242P and K250Δ retained EZH2 binding; however, both C232G and C232Δ mutants poorly associated with EZH2. These data suggest that C232 is critical for FOXP3–EZH2 interaction and potentially is necessary for FOXP3-mediated repressor function. We cannot completely rule out the possibility that residues within the FOX3–LZ domain are similarly important for EZH2 recruitment.

To establish a mechanistic link between C232Δ-induced disruption of FOXP3–EZH2 interaction and EZH2-mediated gene silencing, we performed chromatin immunoprecipitation of the H3K27me3-repressive mark on the IFNG promoter locus, an IBD-relevant gene and an established FOX3 target.²³ We initially evaluated the repressive function of the C232Δ mutant and confirmed that this mutant similarly displayed impaired repression of the IL2 promoter (Figure 3F). In addition and comparable with the C232G mutant, the C232Δ mutant lacked the capacity to efficiently suppress PMA/ionomycin-induced IL2 cytokine production, as evident by increased frequency of C232Δ⁺/IL2⁺-expressing cells in contrast to WT (Figure 3H, quadrant 2 [Q2], bottom row). We directly tested the ability of FOX3–C232Δ mutant to recruit EZH2 to its target IFNG promoter by chromatin immunoprecipitation assay. As anticipated, C232 deletion within FOX3 led to markedly diminished H3K27me3 at the IFNG promoter (Figure 3G).

Thus, although IPEX-inducing FOX3 mutations, particularly within the LZ domain, have been characterized extensively, we report a FOX3 mutation that impairs protein association with EZH2.

**IBD-Associated IL6-Induced Membrane-to-Nucleus Signaling Pathway Similarly Disrupts FOX3–EZH2 Interaction in a Manner Reversible by JAK1/2 Inhibition**

Thus far in our in vitro models, we have linked the pathogenesis of genetically induced IBD to destabilized FOXP3–EZH2 interaction, which is driven by FOXP3–C232 mutation. FOX3⁺ Tregs are known to respond to micro-environmental signals, and proinflammatory cytokines have been directly implicated in the pathogenesis of gastrointestinal inflammation.⁴⁵–⁴⁹ Indeed, our recently published data set showed the IL6 signaling pathway to be one of the top up-regulated pathways in CD4⁺ T cells from inflamed terminal ileum of a previous cohort of CD patients.⁵⁰ Thus, given the reported destabilizing effects of IL6 on Treg development and function,⁵¹–⁵⁴ we chose the IL6 signaling pathway as our model system for subsequent experiments. Acute IL6 treatment of PBMC-derived Tregs, in a time-dependent manner, disrupted FOX3–EZH2 protein interaction (Figure 4A, third and fifth rows, and as quantitated in B and C) in contrast to vehicle-treated cells (Figure 4A, second row, and as quantitated in B and C). In addition, disruption of FOX3–EZH2 interaction directly correlated with increasing concentration of IL6 (Figure 4A, third and seventh rows, and as quantitated in B and C). Flow cytometric analysis of cells confirmed that IL6 had no obvious

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**Figure 3. (See previous page).** FOX3 cysteine 232 to glycine (FOX3–C232G) mutation implicated in loss of Treg-suppressor function and early onset IBD disrupts EZH2 interaction and its gene co-repressor function. (A) Schematic depicts structural domains within 50 kilodalton human FOXP3 (1–431 amino acids), detailing genetic mutations associated with IBD and IPEX syndrome. Within 50 domains include the following repressor domain (RD), zinc finger (ZnF), LZ, and forkhead (FKH)-DNA binding. Red and black arrows indicate amino acids mutated in IBD and IPEX patients. C232G, cysteine 232 to glycine; L242P, leucine 242 to proline; K250Δ, lysine 250 deletion. (B) Jurkat cells transfected with IL2 firefly and renilla luciferase plasmids plus either empty vector or His–FOX3 plasmids were treated with 0.4% dimethyl sulfoxide (DMSO)–vehicle control or indicated concentrations of EZH2 inhibitor GSK126. Thirty-six hours later, cells were treated with 0.4% DMSO–vehicle control or PMA/ionomycin for 12 hours to activate the IL2 promoter as measured by firefly luciferase expression normalized to the renilla internal control. Bottom panel: Whole-cell lysates from transfected and GSK126-treated cells were immunoblotted for H3K27me3; the same membrane was stripped and rebotted for H3 as control. Red horizontal bar denotes the mean IL2 firefly/renilla ratio ± SD from 3 replicates. ****P < .001 (1-way analysis of variance + Bonferroni test). Result is representative of 3 independent experiments. (C) Jurkat cells expressing vector or FOX3 (WT or mutants) plus luciferase plasmids were treated with DMSO or PMA/ionomycin as in panel B. Red horizontal bar denotes the mean IL2 firefly/renilla ratio ± SD from 3 replicates. ***P < .001 (1-way analysis of variance + Bonferroni test). (D) Whole cell lysates from HEK293T cells co-expressing myc-tagged EZH2 and His–FOX3 WT or mutants were subjected to FOX3 immunoprecipitation, immunoblotted for His–FOX3 and myc–EZH2 using the indicated antibodies. Red arrows and gray arrows emphasize C232 mutants within FOX3. Data shown are representative of 3 independent experiments. (E) Jurkat cells expressing empty vector or His–FOX3 (WT or C232 mutants) and indicated luciferase plasmids were treated with 0.4% DMSO or PMA/ionomycin. Red horizontal bar denotes the mean IL2 firefly/renilla ratio ± SD from 3 replicates; ***P < .001 (1-way analysis of variance + Bonferroni test). Result is representative of 3 independent experiments. (G) Chromatin from Jurkat cells expressing FOX3–WT or –C232A were incubated with IgG control or anti-H3K27me3 antibody, polymerase chain reaction (PCR) for the IFNg promoter was performed to assess the presence of H3K27me3 repressive mark. Data shown are representative of 3 independent experiments. (H) Jurkat cells overexpressing empty His-vector plasmid (control), His–FOX3 WT or His–FOX3 mutants (C232G and C232Δ) were treated with 0.2% DMSO (top row) or PMA/ionomycin (bottom row) for 12 hours. Cells were permeabilized and then stained with fluorescently conjugated IL2 and His antibodies against intracellular IL2 and His-tagged FOX3. Dot plot in quadrant 2 (Q2) depicts the frequency, in percentage, of IL2 and His co-expressing cells as measured by flow cytometry. Data shown are representative of 3 independent experiments.
effect on either FOXP3/EZH2 protein expression (Figure 4I) or the frequency of FOXP3\(^+\) and EZH2\(^+\) Tregs (Figure 4H). Given the clinical efficacy and interest in the use of small-molecule JAK inhibitors for the treatment of human immune-mediated diseases such as rheumatoid arthritis, IBD, and myelofibrosis,\(^\text{53}\) we chose to further characterize the involvement of the IL6-dependent JAK-signal transducer and activator of transcription (STAT) pathway through tyrosine phosphorylation assays and ruxolitinib-mediated JAK1/2 inhibition. First, corroborating our data in primary cells, we validated the IL6-induced disruption of FOXP3–EZH2 interaction in HEK293T cells via co-IP (Figure 5A and B, lanes 2 compared with lanes 3). Interestingly, the effect of IL6 was dynamic, with the interaction restored at later time points potentially owing to a negative feedback mechanism (Figure 5A and B, lanes 4 and 5 compared with lanes 2). Primary Tregs then were treated with IL6 in the presence of the JAK1/2 inhibitor ruxolitinib, which prevented IL6-induced disruption of FOXP3–EZH2 complexes (Figure 4A, fourth and sixth rows, and as

Figure 4. (continued). IBD-associated IL6-induced membrane-to-nucleus signaling pathway similarly disrupts FOXP3–EZH2 interaction in a manner reversible by JAK1/2 inhibition. (A) Confocal microscopic PLA images shows endogenous FOXP3–EZH2 interaction (red signals) in the nucleus of CD4\(^+\)CD25\(^+\) cells (Tregs) before (0.2%–0.4% dimethyl sulfoxide [DMSO]), after IL6 (50 or 100 ng/mL, 2\(\times\)) or after IL6 and JAK1/2 inhibitor ruxolitinib pretreatment (10 \(\mu\)mol/L). CD4\(^+\)CD25\(^+\) cells were used as negative controls. Scale bar: 5 \(\mu\)m. Result is representative of 3 independent experiments using freshly isolated PBMC-derived Tregs from 3 different donors. (B) Quantitation of nuclear PLA signals in images from panel A (rows 2–7). n = number of cells imaged. \(*P < .001, *P < .05\). Red horizontal bars indicate means ± SEM (1-way analysis of variance + Bonferroni test) from 3 independent experiments. (C) Quantitation of red fluorescent intensities displayed by representative cells shown in panel A. Data are representative of 3 independent experiments. (D) Representative confocal microscopic PLA images of intestinal CD4\(^+\) T cells from 3 CD patients showing reduced FOXP3–EZH2 complexes (white signals) in comparison with non-CD control cells. Dotted white lines denote the plasma membrane as seen on differential interference contrast images. Scale bar: 2–5 \(\mu\)m. Simple endoscopic scores for CD patients were as follows: patient 1, 18; patient 2 (on 30 mg of prednisone), 10; and patient 3 (on 8 mg of budesonide 1 time daily), 8. (E) Lamina propria CD4\(^+\) T cells from panel D were stained with fluorescently conjugated FOXP3 antibody and subjected to flow cytometric analysis. Histogram overlay compares FOXP3 expression in isolated CD4\(^+\) T cells (control vs CD patients 2 and 3). (F) Quantitation of nuclear PLA signals/CD4\(^+\) T cells from individual CD patients (patients 1, 2, or 3) vs non-CD CD4\(^+\) T cells. n = number of cells imaged. Red horizontal bars denote means ± SEM. \(* * *P < .001\); NS, 1-way analysis of variance + Bonferroni test. (G) Quantitation of nuclear PLA signals/CD4\(^+\) T cells from all 3 CD patients vs non-CD control as shown in panel F. n = number of cells imaged. \(* * *P < .0001\). Red horizontal bars indicate means ± SEM (Student t test). (H) PBMC-derived human Tregs were treated with DMSO, IL6 (50 ng/mL), or IL6 (50 ng/mL) plus 10 \(\mu\)mol/L ruxolitinib (ruxo.) for 2 hours in serum-free media as in panel A, and then permeabilized and stained for FOXP3 or EZH2 with fluorescently conjugated FOXP3 antibody and subjected to primary antibody, respectively. Dot plots show the frequency, in percentage, of cells expressing FOXP3 (top row: quadrant 7 [Q7] or EZH2 (bottom row: quadrant 3 [Q3]) as measured by flow cytometric analysis. For negative controls, IgG isotype or fluorescently conjugated secondary antibody were used to stain cells. (I) Histograms depict FOXP3 or EZH2 expression in cells from panel H. Data are representative of 3 independent experiments. DAPI, 4’,6-diamidino-2-phenylindole; FI, fluorescent intensity; SSC, side scatter.
Figure 5. IL6-induced disruption of FOXP3–EZH2 protein interaction correlates with increased STAT3 activation and FOXP3 tyrosine phosphorylation. (A) HEK293T cells ectopically expressing plasmids encoding His–FOXP3 and myc–EZH2 were treated with IL6 (50 ng/mL) for the indicated duration under reduced-serum conditions. Whole-cell lysates were subjected to immunoprecipitation with IgG or FOXP3 antibody and immunoblotted for His–FOXP3. The same membrane was stripped and reblotted for myc–EZH2. For input, lysates were immunoblotted for His–FOXP3, myc–EZH2, STAT3, and p-STAT3 (Y705) with their corresponding antibodies. (B) Reverse co-immunoprecipitation of experiment in panel A using myc antibody for EZH2. Data are representative of 3 independent experiments. (C) Representative confocal PLA images of human CD4+CD25++ cells (Tregs) shows tyrosine phosphorylated FOXP3 (red) in response to IL6 (50 ng/mL) alone or in combination with ruxolitinib (Ruxo.) (10 μmol/L) for the indicated time points. To detect FOXP3 tyrosine phosphorylation, cells were stained with pan p-Tyr antibody and specific FOXP3 antibody as indicated. Data are representative of 3 independent experiments. Scale bar: 2 μm. (D) Quantitation of nuclear PLA signals in images from panel C. n = number of cells imaged. ***P < .001; NS, non-significant P value. Red horizontal bars indicate means ± SEM (1-way analysis of variance + Bonferroni test) from 3 independent experiments using cells from PBMC donors. (E and F) PBMC-derived human Tregs were treated with IL6 or both IL6 and JAK1/2 inhibitor ruxolitinib (Ruxo.) for the indicated time points. PLA and confocal microscopic imaging were performed to detect and visualize phosphorylated (p) residues (p-Y705 and p-S727) on STAT3 (red signals) by staining cells with the indicated antibodies. Representative images from 3 independent experiments are shown from 3 different donors. White dotted lines mark the cytoplasm of cells while 4',6-diamidino-2-phenylindole (DAPI) stains the nuclei blue. Red PLA signals indicate phosphorylated tyrosine residue (Y) 705 on STAT3 in cells stained with both STAT3 and p-STAT3-Y705 antibodies or phosphorylated serine residue (S) 727 on STAT3 in cells stained with both STAT3 and p-STAT3-S727 antibodies. Scale bar: 5 μm. (G and H) Quantitation of nuclear PLA signals from images in panels E and F, respectively. n = number of cells imaged. Red horizontal bars denote means ± SEM. **P < .01 and ***P < .001 (1-way analysis of variance + Bonferroni test) from 3 independent experiments across 3 different donors.
quantitated in B and C). The demonstrated loss of FOXP3–EZH2 interaction correlated with increased tyrosine phosphorylation of FOXP3 (Figure 5C, as quantitated in D), and increased STAT3 activation (Figure 5A, lane 3, and E–H). Thus, using healthy donor Tregs, our data suggest that IL6-induced activation of JAK1/2 destabilizes FOXP3–EZH2 interaction.

Finally, we studied FOXP3+ cells isolated from the intestinal lesions of human CD, a pathologic condition we previously identified to be associated with dysregulated EZH2-dependent FOXP3 transcriptional gene networks. Specifically, we investigated whether the disruption of the FOXP3–EZH2 protein complex is a molecular feature of human CD via PLA using freshly isolated CD4+ T cells from patient biopsy specimens. Inflamed colonic biopsy specimens were taken during endoscopy from 3 patients (patients 1, 2, and 3) diagnosed with severe to moderate CD based on simple endoscopic scoring for CD of 18, 10, and 8, respectively, as previously reported as a reliable assessment for disease severity. Consistent with our hypothesis, CD CD4+ T cells showed reduced FOXP3 and EZH2 protein interaction (white signals) in contrast to that of healthy controls (Figure 4D) as quantitated in Figure 4F and G. As relevant controls, total FOXP3 expression was comparable in non-CD and CD CD4+ T cells (Figure 4E). Collectively, these observations suggest that the CD-associated inflammatory milieu potentially disrupts the constitutive binding of FOXP3 to EZH2 in Tregs. This consequently may impair Treg function in vivo, thereby perpetuating intestinal inflammation. Taken together with the JAK1/2 inhibition studies, our data suggest that this disease-relevant biochemical process potentially can be reversed by currently available JAK1/2 inhibitor therapy.

In summary, based on our study, we infer a mechanistic model explaining the pathobiological mechanisms that can be responsible for Treg abnormality. According to this

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**Figure 5. (continued)**
model, the physical interaction between FOXP3 and EZH2 necessary for gene co-repressive function can be attenuated by IBD-associated FOXP3-C232 mutation, resulting in impaired repression of target genes. Guided by this observation, we showed the generalizability of this paradigm to sporadic forms of human IBD evident by the diminished presence of FOXP3–EZH2 protein complexes in CD-associated CD4⁺ T cells. Consistent with this paradigm, in human Tregs, IL6 signaling disrupted FOXP3–EZH2 protein interaction in a manner reversible by the JAK1/2 inhibitor ruxolitinib. Thus, we discovered a perturbed EZH2 pathway in Tregs as a clinically important epigenetic mechanism that is potentially responsible for Treg dysfunction during IBD progression.

Discussion
In a murine model, we previously showed that EZH2 expression in Tregs plays an important co-regulatory role in enforcing the immunosuppressive functions of FOXP3. However, clinical evidence linking aberrant EZH2 function to intestinal inflammation and the mechanisms involved had remained elusive. Based on our previous work, the distinct presentation of the severe familial IBD, which was induced by FOXP3–C232G–mediated Treg dysfunction, led us to postulate a novel role for Treg-specific FOXP3–EZH2 interaction in suppressing gastrointestinal inflammation. By using this IBD-related private mutation to illuminate a more generalizable mechanism relevant to IBD pathophysiology, we then studied the impact of inflammatory signaling pathways on FOXP3–EZH2 protein interaction. This report contributed 2 major advances to the current state of understanding the functional relationship between FOXp3 and EZH2. First, we have now uncovered a novel pathobiological mechanism caused by loss of FOXP3 protein interaction with its obligatory co-factor EZH2 in the context of a genetic FOXP3–C232G mutation previously associated with early onset human IBD. Second, generalizing this observation, we show that CD lesion–derived lamina propria CD4⁺ T cells isolated from patients show reduced FOXP3–EZH2 interaction. In primary human Tregs, the proinflammatory cytokine IL6 abrogates FOXP3–EZH2 interaction in a manner that correlates with increased post-translational modification of FOXP3. Exploring the mechanism, we showed that IL6-induced effects were reversible by inhibition of JAK1/2 activity. Collectively, our study advances insight into EZH2-mediated epigenetic function in Tregs and its involvement in human IBD pathophysiology. Our data show the immune-suppressive function of the FOXP3–EZH2 protein complex and highlights the therapeutic implication of stabilizing this interaction to improve Treg function during inflammation.

Numerous studies have intensely explored mechanisms of IPEX pathogenesis by structurally and functionally characterizing the consequences of disease-inducing FOXP3 mutations, however, the mechanistic detail of how a rare FOXP3–C232G mutation is linked to IBD had remained uncharacterized. Driven by this fundamental gap in knowledge, we sought to study the molecular mechanism of pathogenesis of this rare human mutation in the context of EZH2 function. In this study, via biochemical and functional approaches, we established a physical and functional interaction between FOXP3 and EZH2. To structurally characterize mechanisms that mediate this constitutive physical interaction as well as its clinical relevance, we used naturally occurring and disease-causing FOXP3 mutations associated with IPEX and IBD to identify residues required for EZH2 binding. IBD-associated FOXP3–C232G and FOXP3–C232Δ mutations impaired FOXP3’s ability to bind EZH2 and therefore caused deficiencies in the repression of IL2. Moreover, the H3K27me3-repressive mark on the EZH2 target gene IFNG was reduced in the chromatin of cells isolated from FOXP3–C232Δ–expressing cells compared with that of wild-type FOXP3, which is indicative of EZH2 dysfunction. Our study is consistent with the paradigm of how molecular mechanisms of disease pathogenesis can be driven by genetic mutations or nongenetic events. For example, basic zipper transcription factor–regulon, which we previously found to be differentially expressed in CD lesion–derived CD4⁺ T cells, recently was reported to be associated with an IPEX-inducing FOXP3–A384T mutation evident from loss of basic zipper transcription factor expression and function.

Although adoptive transfer studies in animal models of colitis have shown a critical role for Tregs in suppressing chronic intestinal inflammation, the observation that ex vivo cultured human Tregs isolated from colonic mucosa of CD patients showed normal functional properties in vitro have remained thought-provoking. This discrepancy has been attributed to the ex vivo culturing conditions in which human Tregs were expanded before conducting in vitro functional assays. Here, we report that human CD lesion–derived lamina propria CD4⁺ T cells show minimal FOXP3–EZH2 protein interaction in contrast to non-CD control cells. This is consistent with our previously described observation that gene networks co-regulated by FOXP3 and EZH2 were up-regulated in intestinal lesion CD4⁺ T cells from CD patients. In addition, these CD4⁺ T cells showed a marked Th1/Th17 effector-like phenotype in a fashion similar to murine EZH2-deleted FOXP3⁺ Tregs cultured ex vivo. Indeed, an increase of proinflammatory cytokines, such as IL6, is a hallmark of human IBD. In murine models of autoimmune diseases, IL6 favors Th17 cell differentiation and function while opposing Treg differentiation. For example, IL6-unresponsive antigen-specific Tregs obtained via T-cell–conditional deletion of IL6R signaling subunit glycoprotein 130 showed improved protection against IL17-mediated experimental autoimmune encephalomyelitis while Treg depletion re-established the disease. Although other studies in murine cells have additionally linked the mechanism of IL6-induced inhibition of Treg function to attenuated FOXP3 protein expression, we have shown the applicability of our findings broadly to IBD pathogenesis by revealing that acute treatment of Tregs with IL6 impaired FOXP3–EZH2 protein interaction. This incomplete attenuation of FOXP3–EZH2 interaction by IL6
suggests that additional proinflammatory signals, such as tumor necrosis factor-alpha (TNF-α) and IL-21, as well as genetic aberrations, potentially are required for the maximum disruption of this interaction. For example, tumor necrosis factor-alpha-induced FOXP3 serine dephosphorylation has been associated with rheumatoid arthritis pathogenesis. In line with the idea that FOXP3–EZH2 interaction is potentially regulated by post-translational modifications, IL6 signals had no effect on the FOXP3/EZH2 protein levels but rather augmented FOXP3 tyrosine phosphorylation. Therefore, identifying cytokine-induced posttranslational modifications on FOXP3 and EZH2, and how it impacts FOXP3–EZH2 interaction and Treg function in vivo, merits further investigation. In addition, the impact of proinflammatory cytokine signaling on other transcription factors, such as T-box transcription factor (T-box), is likely a mechanism potentially involved in dampening Treg function at conditions that closely resemble those observed human IBD alterations, potentially are required for the maximum therapeutic efficacy. In our study, we associated reduced FOXP3 levels with the idea that FOXP3 signaling on other transcription factors, such as T-box, is likely a mechanism potentially involved in dampening Treg function at conditions that closely resemble those observed in human IBD alterations.

In conclusion, our findings highlight the importance of FOXP3–EZH2 protein interaction in gene-silencing function. This interaction is clinically relevant in the context of genetic FOXP3 alteration that consequently abrogates EZH2 binding and its co-repressive capability. Similarly, proinflammatory cytokine signals can impair FOXP3–EZH2 protein interaction potentially through posttranslational modifications that can serve as biomarkers for Treg dysfunction and clinical response to biologics in IBD, as well as other autoimmune diseases and inflammatory conditions. These findings may guide novel efforts to develop safe therapies or approaches for desensitizing Tregs from the damaging effects of proinflammatory signals. Our study indicates potential therapeutic approaches and mechanisms for improving Treg function during IBD pathogenesis via stabilizing FOXP3–EZH2 interaction.

Materials and Methods

Human Biopsy Specimens

De-identified biopsy specimens from inflamed colonic mucosa were obtained from 3 CD patients diagnosed by established clinical, radiologic, and histopathologic criteria (2 men, ages 27 [patient 1] and 35 [patient 2] years, and 1 woman, age 54 years [patient 3]). For comparison, biopsy specimens were obtained from healthy controls (1 man and 1 woman, both ages 59). CD patient 1 had a severe level of inflammation in affected areas and was not on anti-inflammatory steroid medications whereas CD patients 2 and 3 showed moderate levels of inflammation and were on steroidal medications at the time (30 mg of prednisone, and 8 mg of budesonide 1 time/d, respectively) when biopsy specimens were taken. The study was approved by the Institutional Review Board committee-approved protocol (13-000712) and written informed consent was received from participants before inclusion in this study.

Animal Work and Ethics

C57BL/6J mice were initially purchased from the Jackson Laboratory and bred in conventional housing in the Mayo Clinic animal facility. All mice used in the experiments were males 5–10 weeks of age. Animal work was performed in accordance with reviewed and approved protocols by the Mayo Clinic Institutional Animal Care and Use Committee.

Isolation and Culture of CD4+ T Cells From Colonic Biopsy Specimens

Tissue biopsy specimens from each individual were rinsed in 0.9% NaCl and then placed in 1 mmol/L EDTA Duchmann media (RPMI 1640 supplemented with 10% fetal calf serum [FCS], 1% penicillin/streptomycin, 1% gentamicin sulfate, 10 mmol/L HEPES, and β-mercaptoethanol) for 15 minutes in a 37°C CO2 incubator to remove epithelial cells. Biopsy specimens were digested in a 37°C CO2 incubator with a cocktail of enzymes containing 1 mg/mL each of collagenase, DNase, and trypsin inhibitor for 1–2 hours. Digested tissue was filtered through a 70-μm cell strainer to obtain single cells, centrifuged at 1200 rpm for 10 minutes. The pellet was suspended in commercially available beads for human CD4+ T cell isolation according to the manufacturer’s instructions (cat. 130-096-533; lot 5180406200; Miltenyi Biotec, San Diego, CA). Isolated CD4+ T cells subsequently were subjected to in situ PLA and fluorescence-activated cell sorting.

Isolation of Tregs From Human PBMCs

The CD4+CD25+ regulatory T-cell isolation kit (cat. 130-091-301, lot 5180316290; Miltenyi Biotec) was used for isolating Tregs from human PBMCs according to the manufacturer’s instructions. Briefly, a specified volume of isolated platelet was diluted in phosphate-buffered saline (PBS) and then added to Ficoll Paque Plus (Pittsburgh, PA). This mixture then was centrifuged at 1500 rpm for...
30 minutes at 12°C in a swinging bucket rotor without brakes. The lymphocyte layer was removed and washed with PBS followed by centrifugation at 1200 rpm for 10 minutes at 12°C. Lysis buffer was added to the cells, incubated for 5 minutes at room temperature, and spun down at 800 rpm for 10 minutes to remove platelets.

Lymphocytes were suspended in RPMI + 10% FCS (Gibco, Carlsbad, CA) for 30 minutes to obtain the desired nonadherent lymphocytes. These freshly prepared nonadherent lymphocytes or PBMCs then were subjected to CD4⁺CD25⁺⁺ Treg isolation to obtain super pure Tregs. Isolated CD4⁺CD25⁺ T cells were kept and used as negative controls in relevant experiments as indicated.

**Cells, Cell Culture, Differentiation of CD4⁺ T Cells, Stimulation Conditions, and Statistical Analysis**

Jurkat T cells were maintained in medium A (RPMI 1640 supplemented with 10% FCS, 10 mmol/L HEPES, pH 7.4, and 2 mmol/L L-glutamine) at less than 10⁶ cells/mL. HEK293T cells were maintained in medium supplemented with 10% FCS, 4.5 g/L D-glucose, and L-glutamine. Jurkat cells were activated with plate-bound anti-human CD3 (5 μg/mL, clone OKT3, cat. 16-0037-85, lot 7347573; Affymetrix eBioscience, Santa Clara, CA) and anti-human CD28 (2 μg/mL, clone CD28.2, cat. 555735, lot 7340520; BD Biosciences, San Jose, CA) or cell activation cocktail (cat. 423302, lot B248900; BioLegend, San Diego, CA) containing 0.081 μmol/L PMA and 1.34 μmol/L ionomycin. Naïve CD4⁺ T cells were isolated from mice spleen using the CD4⁺ T-cell isolation kit according to the manufacturer’s instructions (cat. 130-104-454, lot 5171103089; Miltenyi Biotec). For PLA studies, Th17 cells were obtained by culturing CD4⁺ T cells for 3 days in the presence of anti-mouse CD3 (2 μg/mL, clone 145-2C11, cat. 555307, lot 7241732; BD Biosciences), anti-mouse CD28 (2 μg/mL, clone 37.51, cat. 535324, lot 7066810; BD Biosciences), recombinant murine IL6 (50 ng/mL, cat. 216-16, lot 11145012916; Peprotech, Rocky Hill, NJ), recombinant human transforming growth factor-β1 (1 ng/mL, cat. 100-21C, lot 0915354; Peprotech), anti-mouse IL4 (10 μg/mL, lot 504108, lot B201326; BioLegend), anti-mouse interferon-γ (10 μg/mL, lot 505812, lot B213311; BioLegend), and IL23 (5 μg/mL, cat. 1887-ML-010, lot MLE2613091; R&D Systems, Minneapolis, MN).

Mouse-induced Tregs were obtained by culturing naive CD4⁺ T cells for 3 days in the presence of anti-mouse CD3 (2 μg/mL), anti-mouse CD28 (2 μg/mL), human IL2 (100 U/μL; Peprotech), and transforming growth factor-β1 (5 ng/mL); naïve mouse CD4⁺ T cells expanded for 3 days in the presence of anti-CD3 (2 μg/mL), anti-mouse CD28 (2 μg/mL), and human IL2 (100 U/μL; Peprotech). Primary human Tregs were cultured overnight with anti-human CD3 (10 μg/mL, clone UCHT1, cat. 555329, lot 7347573; BD Biosciences), human IL2 (100 U/μL, Peprotech), and anti-human CD28 (2 μg/mL, clone CD28.2, cat. 555725, lot 8060981; BD Biosciences). Human Tregs were treated with human IL6 (50 ng/mL, cat. 200-06, lot 071316; Peprotech) and dimethyl sulfoxide or the JAK1/2 inhibitor ruxolitinib (cat. S1378; Selleckchem, Houston, TX) for the indicated time points.

**Statistical Analysis**

Data are expressed as the means ± SEM or ± SD as indicated. Differences between groups were compared using 1-way analysis of variance followed by the Bonferroni post hoc test in which P < .05 was the minimum requirement for a statistically significant difference using GraphPad Prism 5.0 software (San Diego, CA). Differences between 2 groups were compared using the Student t test.

**PLA and Confocal Microscopy of Fixed Cells**

The proximity ligation method relies on dual proximal binding by pairs of detection probes to protein molecules to generate amenable DNA strands. The oligonucleotides on the probes, when brought in close proximity of <30 nm by adjacent proteins, are enzymatically ligated to generate circularized DNA bound to the probe-antibody/protein complex. The circularized DNA then is amplified with one of the oligonucleotides serving as the primer. Fluorescently labeled product covalently linked to the antibody–protein complex then was imaged by confocal microscopy. To begin, cells were harvested and plated on 8-well Lab-Tek chamber slides (Thermo Fisher Scientific, Waltham, MA) coated with fibronectin (Corning, Corning, NY) for 3 hours to allow cell attachment, and then treated as indicated. Cells then were fixed with 4% paraformaldehyde, permeabilized with 0.15% Triton X-100 (Invitrogen, Carlsbad, CA), and then washed with PBS. Cells were blocked for 1 hour with 5% bovine serum albumin containing 0.1% glycine and then incubated with the indicated primary antibodies. Protein–protein interactions and post-translational modifications were measured by Duolink (Sigma, St. Louis, MO) in situ fluorescence PLA probes (cat. DUO92004, lot SLBV2508; cat. DUO092002, lot SLBT9623; cat. DUO92006, lot SLBT4800) and detection reagents (cat. DUO92008, lot SLBV3043) in accordance with the manufacturer’s instructions. Cells were mounted with Duolink 4’6-diamidino-2-phenylindole–containing mounting medium (cat. 82040, lot A61722/1; Sigma-Aldrich). Images of cells were captured by using a C-Apochromat 40× objective/1.20 W korrM27 of a fluorescent confocal microscope (LSM 780 AxiosObserver; Carl Zeiss, Jena, Germany). Images were processed using the Zen lite 2012 software (Carl Zeiss). Quantitation of nuclear PLA signals from cell images were performed as follows: percentage of cells positive for nuclear PLA dots, number of nuclear PLA signals per cell, or nuclear PLA fluorescent intensity. To quantitate the percentage of cells positive for PLA signals, cells that displayed no PLA dot were considered to be negative and those with more than 1 PLA dot were considered PLA positive and then expressed as a percentage of total cells that were imaged. To quantitate the number of PLA signals per cell, the number of PLA dots per cell was counted. To quantitate PLA fluorescent intensity, a line was drawn around the nuclei and fluorescence values were generated using ImageJ (National Institute of Health, Bethesda, MD) and plotted using Prism (GraphPad Software, San Diego, CA).
**Antibodies for PLA**

Primary antibodies used were rabbit monoclonal anti-FOXP3 (1:500, cat. ab54501, lot GR285227-2; Abcam, Cambridge, MA), mouse monoclonal anti-EZH2 (1:100, cat. 3147; Cell Signaling, Beverly, MA), mouse monoclonal anti-myc (1:500, cat. 2276, lot 24; Cell Signaling), rabbit monoclonal anti-His (1:500, cat. sc-499, lot 11214; Santa Cruz Biotechnology, Santa Cruz, CA), mouse monoclonal anti-phospho (p)-tyrosine (1:100, cat. sc-7020, lot L2916; Santa Cruz Biotechnology), mouse monoclonal anti-STAT3 (1:1000, cat. 9139, lot 7; Cell Signaling), rabbit monoclonal anti-pSTAT3-Y705 (1:100, cat. 9131, lot 30; Cell Signaling), rabbit monoclonal anti-pSTAT3-S727 (1:100, cat. 9134, lot 20; Cell Signaling).

**Transient Transfections**

Jurkat T cells were transiently transfected with indicated plasmids by electroporation at 315 mV for 10 ms and harvested 36–48 hours later. HEK293T cells were transiently transfected by Lipofectamine 2000 according to the manufacturer's instructions (cat. 11668-19, lot 1924211; Invitrogen, Carlsbad, CA) for 48–72 hours.

**Co-IP Assay and Immunoblotting Analysis**

HEK293T cells treated with human IL6 (50 ng/mL, cat. 200-06, lot 071316; Peprotech) and naïve/differentiated CD4+ T cells were harvested, washed with cold PBS, and lysed with RIPA lysis buffer containing 50 mmol/L Tris-HCl, pH 7.4, 1% NP-40, 150 mmol/L NaCl, and 2 mmol/L EDTA. Lysates were precleared with protein A (cat. 1134515001, lot 01001330; Roche, Indianapolis, IN) or protein G (cat. 11243233001, lot 10232222; Roche) beads for 1 hour and spun down. Supernatant was incubated with protein A or G beads plus the indicated primary antibody to immunoprecipitate the protein of interest. Co-immunoprecipitated and immunoprecipitated proteins were detected by Western blot using the indicated primary antibodies and horseradish-peroxidase–conjugated secondary antibodies.

**Antibodies for Immunoblotting Analysis**

Primary antibodies used were rabbit monoclonal anti-FOXP3 (3 µg/mL, cat. A301-900A; Bethyl Laboratories, Montgomery, TX), rat monoclonal anti-FOXP3 (2 µg/mL, cat. 14-4776-82, lot 4325553; eBioscience), rabbit monoclonal anti-EZH2 (1:1000, cat. 5246, lot 7; Cell Signaling), mouse monoclonal anti-myc (1:1000, cat. 2276, lot 24; Cell Signaling), rabbit monoclonal anti-SUZ12 (1:1000, cat. 14269, lot 1; Cell Signaling), and anti-EED (1:1000, cat. CS200603; Millipore, St. Louis, MO), rabbit monoclonal anti-H3K27me3 (1:1000, cat. CS204393; Millipore), mouse monoclonal anti-H3 (1:1000, cat. 14269, lot 1; Cell Signaling), mouse monoclonal anti-STAT3 (1:1000, cat. 9139, lot 10; Cell Signaling), and rabbit monoclonal anti-pSTAT3 (1:100, cat. 9131, lot 30; Cell Signaling).

**Plasmids**

**WT FOXP3** coding DNA exons (1293 base pairs) were amplified from PBMC-derived human Tregs using primers for BamH1 and Xho1 restriction sites. Digested (Nucleospin Gel and polymerase chain reaction clean-up, Takara, Palo Alto, CA) FOXP3 DNA then was cloned into pCDNA3.1–His-tagged vector plasmid to generate a fusion of His-tagged FOXP3 (pCDNA3.1–His–FOXP3). Fusion plasmid myc–DDK–tagged human EZH2 was obtained from Origene (cat. RC202054, Rockville, MD), whereas myc–His–tagged human EZH2 was a kind gift from Mien-Chie Hung. The human IL2 luciferase reporter was purchased from Affymetrix (cat. LR1014).

**Flow Cytometry**

For cell-surface staining, cells were directly stained with the indicated antibodies in stain buffer (BioLegend). For intracellular staining, cells were treated as indicated with or without brefeldin A (cat. 420601, lot B211242; BioLegend), fixed and permeabilized with buffer (cat. 51-2090KZ, lot 7180887; BD Biosciences) and then stained with relevant primary antibodies and fluorochrome-conjugated secondary antibodies, alternatively, cells were stained with fluorochrome-conjugated primary antibodies. The antibodies used were mouse monoclonal anti-EZH2 (1:100, lot 3174, lot 4; Cell Signaling), goat anti-mouse IgG (H + L) (1:1000, A21235, lot 1704598; Life Technologies), anti-rat IgG–Alexa Flour 647 (1:1000, cat. 400526, lot B22506; Invitrogen), anti-human FOXP3–Alexa Flour 488 (cat. 320212, lot B231491; BioLegend), mouse monoclonal anti-His–Alexa Flour 488 (cat. A01800, lot 15L000966; GentScript, Piscataway, NJ), anti-human IL2–Alexa Flour 647 (cat. 500315, lot B264459; Biolegend). Cells were washed with staining buffer (cat. 420201, lot B247190; BioLegend) or perm/wash buffer (cat. 51-2091KZ, lot 7311596; BD Biosciences), respectively, to remove unbound antibodies. Cells subsequently were subjected to flow cytometry for fluorescence-activated cell sorting and electronically gated on live cells for analysis.

**ChIP Assays**

ChIP assays were performed in Jurkat cells (4 × 10^6) by cross-linking with 1% formaldehyde for 10 minutes at room temperature and then washed with ice-cold PBS supplemented with protease inhibitors. Cells were resuspended in sodium dodecyl sulfate lysis buffer (50 mmol/L Tris–HCl, pH 8.1, 10 mmol/L EDTA, 1% sodium dodecyl sulfate, and protease inhibitors). Lysates were sonicated (40–45 W for 10-second bursts, 8 times on ice) to yield 100–500 bp of chromatin fragments and diluted 10-fold with ChIP dilution buffer (20 mmol/L Tris–HCl, pH 8.1, 1 mmol/L EDTA, 150 mmol/L NaCl, 0.3% Triton X-100, and protease inhibitors). Lysates were precleared with protein A agarose/salmon sperm DNA (cat. 16-157, lot 2798592; Millipore) for 2 hours and then incubated with rabbit monoclonal anti-H3K27me3 (1:1000, cat. 17-622; Millipore) or relevant IgG control overnight, followed by incubation with protein A agarose/salmon sperm DNA for 3 hours at 4°C. Protein A agarose–bound complexes were washed simultaneously with low salt, high salt, and LiCl immune complex wash buffers as well as Tris–EDTA buffer. Antibody/protein/DNA complexes were eluted. Quantitative polymerase chain
reaction was performed for the IFN\(\gamma\) promoter (forward primer: 5’-CTGATGAAAGCATCCTCTCACC-3’; reverse primer: 5’-CGATGAGACGACCCATTATGCC-3’).

**Site-Directed Mutagenesis**

DNA base substitutions and deletions were performed using the Q5 site-directed mutagenesis kit (New England Biolabs, Ipswich, MA) according to the manufacturer’s instructions. Forward and reverse primer sequences required for specific site mutagenesis were generated using the NEBase Changer tool (Ipswich, MA). Primers used were as follows: FOX3P-C232G (TGT mutation to GGT: forward-CAGGGCACAAGGTC and reverse-CCCTTCTCATCCAGAAGATGG; FOX3P-L242P (CTG mutation to CCT: leucine 242 to proline): forward-GGTACAGTCTCCTGAGCAGCAGC, reverse-ATCTCTCCAGGAGAGAGATGG, reverse-TTGTGCCCTGCCCTTCTC; FOX3P-D250A (AGGAGGAGAC; and FOX3P-K250D (CTG mutation to CCTAGAGAAGCTGAGTGCCATGC, reverse-CATGCTG-3’). Constructs (control renilla luciferase and luciferase reporter plasmids) were generated using the Q5 site-directed mutagenesis kit (New England Biolabs, Ipswich, MA) according to the manufacturer’s instructions. Forward and reverse primer sequences required for specific site mutagenesis were generated using the NEBase Changer tool (Ipswich, MA). Primers used were as follows: FOX3P-C232G (TGT mutation to GGT: forward-CAGGGCACAAGGTC and reverse-CCCTTCTCATCCAGAAGATGG; FOX3P-L242P (CTG mutation to CCT: leucine 242 to proline): forward-CAGGGCACAAGGTC and reverse-CCCTTCTCATCCAGAAGATGG; FOX3P-L242P (CTG mutation to CCT: leucine 242 to proline): forward-CTGCTG-3’).

**Luciferase Reporter Assays**

Jurkat T cells were transfected with the indicated constructs (control renilla luciferase and IL2 firefly luciferase) for 48–72 hours. Cells were treated as indicated, anti-human CD3 (OKT3, 10 μg/mL) and anti-human CD28 (2 μg/mL) or cell activation cocktail containing 0.081 μmol/L PMA and 1.34 μmol/L ionomycin for 12 hours or overnight. Cells also were treated with the EZH2 inhibitor GSK126 (cat. S7061; Selleckchem) as indicated. Cells were harvested and luciferase activity was detected and measured by using the Dual-Luciferase Assay Reporter System kit (E1960, lot 000021191; Promega, Madison, WI) and a Synergy H1-Multi Mode plate reader (BioTek, Winooski, VT) according to the manufacturer’s instructions.

**References**


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Author contributions
Adebowale O. Bamidele was responsible for the study concept and design, data acquisition, data analysis and interpretation, and manuscript preparation; Phyllis A. Svingen was responsible for data acquisition and manuscript preparation and revision; Michelle Gonzalez, Mary R. Sagstetter, Olga F. Sarmento, and Manuel B. Regen T-bet. Nature 2017;550:142.

Conflicts of interest
The authors disclose no conflicts.

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