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Bone Morphogenetic Proteins Shape T_{reg} Cells

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The transforming growth factor-β (TGF-β) family includes cytokines controlling cell behavior, differentiation and homeostasis of various tissues including components of the immune system. Despite well recognized importance of TGF-β in controlling T cell functions, the immunomodulatory roles of many other members of the TGF-β cytokine family, especially bone morphogenetic proteins (BMPs), start to emerge. Bone Morphogenic Protein Receptor 1α (BMPR1α) is upregulated by activated effector and Foxp3+ regulatory CD4+ T cells (Treg cells) and modulates functions of both of these cell types. BMPR1α inhibits generation of proinflammatory Th17 cells and sustains peripheral Treg cells. This finding underscores the importance of the BMPs in controlling Treg cell plasticity and transition between Treg and Th cells. BMPR1α deficiency in vitro induced and peripheral Treg cells led to upregulation of Kdm6b (Jmjd3) demethylase, an antagonist of polycomb repressive complex 2 (PRC2), and cell cycle inhibitor Cdkn1a (p21Cip1) promoting cell senescence. This indicates that BMPs and BMPR1α may represent regulatory modules shaping epigenetic landscape and controlling proinflammatory reprogramming of Th and Treg cells. Revealing functions of other BMP receptors and their crosstalk with receptors for TGF-β will contribute to our understanding of peripheral immunoregulation.

Keywords: Treg, Th17, BMP, BMPR1α, immunity, epigenetic, Kdm6b, Cdkn1a

INTRODUCTION

The major polarized Th subsets, Th1, Th2, Th9 and Th17 cells, are generated in response of CD4+ T cells to antigenic stimulation, co-stimulatory signals and cytokines and utilize specialized effector mechanisms to eliminate different types of pathogens (1–4). TGF-β has emerged as the cytokine controlling intrinsic activation of T cells and their antigenic responses (5, 6). In the presence of IL-4 or inflammatory cytokines, especially IL-6, TGF-β supports generation of Th9 or Th17 cells respectively (7, 8). Th cell functions are controlled by regulatory CD4+ T cells (T_{reg}), which express the transcription factor Foxp3 (9, 10). T_{reg} cells maintain immunological self-tolerance and homeostasis but also control clinical conditions including immunometabolic and degenerative diseases, and tissue regeneration (10–13). Population of thymus derived T_{reg} cells is complemented by peripheral T_{reg} cells generated from conventional CD4+ Th cells which upregulate Foxp3 in response to stimulation with antigen and TGF-β (14, 15). Peripheral T_{reg} cells exhibit considerable heterogeneity and utilize specialized mechanisms to constrain inflammatory reactions in response to self and exogenous antigens (16–19). Foxp3 is essential for T_{reg} cell function, especially for its...
Nevertheless, compromised function of Treg cells is not always
Foxp3 augmentation of anti-tumor immunity (44, 45). exTreg cells
reduced induction and homing of peripheral Treg cells, which proved essential to control abundance and
fitness of Treg cells (24–27). Treg-specific defects often correlate
with the development of several autoimmune disorders such as
type 1 diabetes, multiple sclerosis, psoriasis, rheumatoid
arthritis and Crohn’s disease (10, 28–31). This includes reduced induction and homing of peripheral Treg cells, alleviated or altered suppressor mechanisms and decreased
stability of Treg phenotype. Deficiency of Treg cells caused by
mutations of Foxp3 results in early onset autoimmune disease as
demonstrated in Foxp3 mutant scurfy mice and humans with
IPEX (immune dysregulation, polyendocrinopathy, enteropathy, X-linked) syndrome (32, 33). Deletion of multiple other genes
affecting Foxp3 protein stability or altered epigenetic status of
Foxp3 gene locus resulted in compromised function of Treg cells
and were associated with autoimmune pathology (34, 35). Nevertheless, compromised function of Treg cells is not always
associated with their reduced frequency (36, 37). For example,
signaling through the IL-27R or TGF-βRI, impacted Treg cell
function but was not accompanied by major phenotypic or
quantitative changes of Treg population resulting in systemic
autoimmunity (38, 39).

Uncovering what mechanisms control Treg cell homeostasis
become even more important when it was discovered that Treg
 cells which lost Foxp3 expression (exTreg cells) may produce
inflammatory cytokines, IFN-γ and IL-17 (40, 41). While
downregulation of Foxp3 may be required to alleviate suppressive effect of Treg cells, allowing for effective immune
responses to pathogens, in other cases Treg cell instability
exacerbated tissue damage and contributed to immune
pathology (42, 43). Treg instability also contributes to the
augmentation of anti-tumor immunity (44, 45). exTreg cells
promoted destruction of pancreatic islets and accelerated onset
of diabetes (41). In rheumatoid arthritis and EAE, pathogenic
Th17 cells were shown to arise from Treg cells (46, 47). In
contrast, resolution of inflammation may depend on the
opposite process of trans differentiation of Th17 cells into Treg
cells (47, 48). Thus, regulation of the Th cell lineage plasticity is
critical for understanding of immune regulation and pathogenesis of autoimmune diseases (49, 50).

**GENERATION AND MAINTENANCE OF TREG POPULATION**

Multiple reports identified membrane and soluble molecules
which proved essential to control abundance and fitness of Treg
cell population in peripheral organs and promote their
suppressor function. This includes signaling through the TCR,
costimulatory molecules (CD28 and CTLA-4) and cytokines
receptors (18, 43, 51–56). IL-2 and TGF-β were the most
studied cytokines in the context of Treg cell biology. IL-2 is a
key cytokine required for induction of Foxp3 in thymic Treg
precursors and in peripheral CD4+ T cells (14, 57–59).
Mechanistically, Stat5 in response to IL-2 signaling binds enhancer in the Foxp3 gene inducing its expression in the
thymus (60). In peripheral Treg cells IL-2 induced transcriptional program controls metabolic fitness of Treg cells,
sustains their survival and suppressor function and prevents
autoimmunity (61, 62). Foxp3 CNS2 (conserved noncoding
sequence) enhancer element acts as an IL-2 sensor by binding
Stat5 and conferring stable inheritance of Foxp3 expression (63).
IL-2 induced genetic program of Treg cell differentiation and
peripheral maintenance depend on activation of Smad3 and the
presence of TGF-β (59, 64–66). While both IL-2 and TGF-β
promote generation and sustain Treg cells, IL-2 inhibits and TGF-β
enhances generation of effector Th17 cells underscoring the
importance of context dependent signaling for Th lineage
ontogeny (67, 68).

Immunoregulatory role of TGF-β has been known before the
discovery of Treg cells (69). TGF-β provides vital signals that
limit immune activation so deletion of the TGF-β1 gene in
experimental mice, which abrogated TGF-β signaling in
multiple T cell subsets, induced severe autoimmune
inflammatory disease (5, 70). T cell specific inhibition of TGF-
βRII signaling had similar outcome and precipitated systemic
autoimmune disease characterized by massive activation and
expansion of T cells (71, 72). Co-transfer of naïve CD4+ T cells
expressing dominant negative TGF-βRII, and Treg cells, into
recipient mice demonstrated that effector cells need to respond
to TGF-β for the Treg cells to control their activation (73). T cell
specific deletion of TGF-βRII revealed that TGF-β signaling is
not required for thymic development of Treg cells but supports
Foxp3 expression, suppressor function and sustains peripheral
population of Treg cells (74, 75). In summary, earlier reports
supported conclusions that while Treg thymic development is
not affected, both T cell autonomous and Treg dependent
tolerance mechanisms are abrogated by elimination of TGF-β
signaling in effector Th and in Treg cells (75–77). The caveat of
these experiments is that they relied on inhibition of TGF-β
signaling in multiple T cell subsets and examined Treg cells in
the context of induced severe autoimmune inflammatory
disease, complicating interpretation of the role of TGF-β in
Treg cells (6). In contrast, analysis of newborn mice with T cell
specific TGF-βRII gene deletion and, inhibition of TGF-β
signaling in thymic organ cultures identified TGF-β, in
connection with IL-2, as cytokines essential for inducing
Foxp3 expression and thymocyte commitment to Treg cell
differentiation in the thymus (78). However, another report
defined TGF-β role in Treg development to be limited to
enhancing survival and protection from negative selection of
thyocytes committed to become Treg cells (79). This report of
limited impact of TGF-β in inducing Treg cell generation was
questioned by demonstrating that intrathymic transfer of early
thyocytes, where TGF-βRII gene deletion is induced at the
double positive stage, failed to produce any Treg cells,
corroborating reports that TGF-β signaling is indispensable for
intrinsic properties of target cells (91). Endocrine fashion determined by tissue environment and pleiotropic cytokines which act in autocrine, paracrine and cytokines sustaining tissue homeostasis. BMPs are highly BMP precursors. Proteases involved in producing active, mature controlling BMP gene expression, secretion and maturation of homeostasis of tissues and organs, and is achieved by adding inducing differentiation of osteoblasts, bone-forming cells, BMPs control multiple cellular processes including differentiation of various cell types, adhesion, migration and proliferation and apoptosis (83, 84). They have prominent role in regulating body axes formation during embryonal development, regulate epithelial - mesenchymal transition in cancer and wound healing (83, 85-87). BMPs sustain stem cell renewal and differentiation, including tissue specific and cancer stem cells (88-90). Individual BMPs often have overlapping functions, but they can be highly specific when function as morphogens or cytokines sustaining tissue homeostasis. BMPs are highly pleiotropic cytokines which act in autocrine, paracrine and endocrine fashion determined by tissue environment and intrinsic properties of target cells (91).

Tight regulation of BMP signaling is crucial to maintain homeostasis of tissues and organs, and is achieved by controlling BMP gene expression, secretion and maturation of BMP precursors. Proteases involved in producing active, mature BMPs include furin, which is induced in activated T cells and essential for Treg cell suppressor function (92). Mature BMPs are bound and sequestered by soluble (e.g. chordin, noggin, gremlin) or membrane/matrix proteins (e.g. fibrin, small leucine-rich proteins) or pseudoreceptors like BAMBI (BMP and Activin Membrane-Bound Inhibitor) (93, 94). This complex system regulates BMPs bioavailability by controlling their secretion, proteolytic maturation of BMP precursors, degradation and sequestration.

TGF-β family cytokines, including BMPs, signal through heteromeric complexes of type I and type II receptors, which have activity of serine/threonine kinases (Figure 1). Cytokine ligand binds to a type II receptor and the ligand-receptor complex binds to a type I receptor. Formation of a ternary complex activates receptor kinase activity and induces phosphorylation of transcription factors, Smads, which activates canonical signal transduction pathway (84). TGF-β itself binds TGF-βRII and TGF-βRII (Alk-5) and induces phosphorylation of Smad2/3. BMPs bind one of type II receptors, BMPR2, activin receptor type 2A (ACVR2A) or activin receptor type 2B (ACVR2B). Ligand binding to type II receptor induces recruitment of one of type I receptors, activin receptor-like kinase 1 (Alk-1, ACVRLI1), activin A receptor type 1 (Alk-2, ACVR1), activin receptor type 1B (Alk-4, ACVR1B), BMPRIα (Alk-3) or BMPR1β (Alk-6, not expressed by CD4 cells) and leads to conformational change of the heteromeric receptor to induce kinase activity of type I receptor and phosphorylation of Smad1/5/8. Promiscuity of ligand receptor interactions contributes to redundant functions of BMPs but also underlies signaling crosstalk between TGF-β and BMPs. TGF-β bound to TGF-βRII may recruit and transphosphorylate ACVR1I or BMPRIα with subsequent phosphorylation and activation of Smad1/5/8 (95). Type II receptors ACVR2A or ACVR2B may also bind TGF-βRI with resulting phosphorylation of Smad2/3. Thus, combinatorial activation of both Smad pathways could be essential for signaling crosstalk of TGF-β and BMPs (96). Smad transcription factors phosphorylated by TGF-β or by BMP receptors (R-Smads) form trimeric complexes with Smad4 and translocate into nucleus. They interact with multiple co-activators, including genes controlling Treg phenotype, and bind specific motifs present in regulatory regions of Smad inducible genes, including Foxp3 (83, 84). Besides activating Smads, BMPs signal through multiple Smad-independent (non-canonical) pathways (99). This involves activation of Tak-1 (TGF-β activated kinase 1) and downstream activation of NF-κB (100-104). Smad independent signaling also includes activation of PI3K-Akt pathway (105). Finally, BMPs activate p38/JNK kinases which engages TRAF4 or TRAF6 and activates Tak1 (106-108).

**BONE MORPHOGENETIC PROTEINS, THEIR RECEPTORS AND SIGNALING PATHWAYS**

Bone Morphogenetic Proteins (BMPs) are the largest subfamily of the TGF-β cytokine superfamily which also includes TGF-β, a founding member of the family, activins, nodal and growth and differentiation factors. BMPs were identified by their ability to induce bone differentiation (82). It is now well known that in addition of inducing differentiation of osteoblasts, bone-forming cells, BMPs control multiple cellular processes including differentiation of various cell types, adhesion, migration and proliferation and apoptosis (83, 84). They have prominent role in regulating body axes formation during embryonal development, regulate epithelial - mesenchymal transition in cancer and wound healing (83, 85-87). BMPs sustain stem cell renewal and differentiation, including tissue specific and cancer stem cells (88-90). Individual BMPs often have overlapping functions, but they can be highly specific when function as morphogens or cytokines sustaining tissue homeostasis. BMPs are highly pleiotropic cytokines which act in autocrine, paracrine and endocrine fashion determined by tissue environment and intrinsic properties of target cells (91).

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**BONE MORPHOGENETIC PROTEINS CONTROL OF T<sub>REG</sub> LINEAGE**

While TGF-β mediated regulation of Th lineage differentiation and immune system homeostasis have been extensively studied, the role of other members of the TGF-β family, including BMPs is only starting to emerge (109). Recent reports demonstrate that BMPs, similar to TGF-β, are immunomodulatory cytokines which control differentiation and functions of immune cells impacting immune tolerance, inflammation and lineage specification of effector Th cells (110). BMPs regulate thymic development of T cells, but published results remain controversial (111-115). Both thymocytes and thymic stromal cells produce
BMPs and express BMP receptors. Fetal thymic cultures and signaling inhibitor studies showed that BMPs are required for early thymocyte progenitor homeostasis but block transition from double negative to double positive thymocytes (112, 116). In contrast, analysis of conditional knockout mice where BMPR1α gene was deleted in hematopoietic cells (by crossing to vav-cre mice) did not reveal changes in thymus cellularity and subset proportions (114). Analysis of mice where BMPR1α gene was deleted in double positive thymocytes showed normal development of T cells with the exception of a population of Foxp3+ Treg cells which was severely decreased suggesting a unique role of this receptor in Treg specification (117). However, thymic but not peripheral Treg population was normal when BMPR1α gene was deleted at the later stage, in thymocytes expressing Foxp3 (118).

BMPR1α is expressed in mature CD4+ T cells in lymph nodes, spleen and peripheral organs (118). It is expressed at low level in naive CD4+ T cells and at higher levels in activated Th and Treg cells. It is upregulated following T cell activation within hours. Since expression of BMPR2 is not affected by T cells activation, it is upregulation of BMPR1α which renders activated CD4+ T cell sensitive to BMPs (119). In vitro studies using signaling inhibitors have shown that BMPs regulate proliferation and activation of CD4+ T cells but the role of BMPs in controlling peripheral Treg cells was not addressed (120, 121). Blockade of BMP signaling in rheumatoid arthritis patients augmented inflammation induced by IL-17 and BMPs ameliorated intestinal inflammation suggesting that cellular targets of BMP signaling may include effector Th17 and Treg cells (122–125). BMP2/4 or activin A synergized with the TGF-β to generate inducible Treg (iTreg) cells but were not able to completely replace TGF-β and induce Foxp3 expression (126, 127). Foxp3 enhancer, CNS1, contains canonical Smad1/5/8 binding site that partially overlaps Smad2/3 site. T cells activated in the presence of BMPs differentiated into Th1 or Th2 but Th17 differentiation was inhibited. BMP signaling resulted in inhibition of Rorc and IL-17 upregulation (119). These results were complemented by analysis of CD4+ T cells deficient in BMPR1α (117, 119). Generation of Th17 cells in vitro, induced by IL-6 and TGF-β, is greatly enhanced by abrogation of the BMPR1α signaling but it still requires presence of TGF-β. At the same time, in vitro generation of iTreg cells is impaired, not improved, by BMPR1α deficiency, suggesting complex interaction between BMPR1α and TGF-β.

**FIGURE 1** | Schematic overview of the canonical, SMAD-dependent BMP and TGF-β signaling pathway. Signaling is initiated by binding to a heteromeric complex of type I receptors, e.g. BMPR1α, TGF-βR1, ACVRL1 or ACVR1, associated with type II receptors, e.g. BMPR2, TGF-βR2, ACVR2A/2B. Intracellular, BMP or TGF-β responsive transcription factors, Smads become phosphorylated and associate with co-Smad4 and translocate into nucleus. This signaling pathway is controlled by inhibitory Smad6. Once in the nucleus Smad complexes associate with transcription factors e.g. Runx2, Id1/2 or NFAT, bind regulatory regions of Smad dependent genes and regulate transcription. The figure shows interdependence of BMP and TGF-β signaling at the level of receptor binding and Smad phosphorylation.
signaling pathways (117). Deletion of BMPR1α gene does not affect phosphorylation of Smad2/3 in CD4+ T cells activated for 1 hour in the presence of TGF-β, however genes mediating responses to TGF-β signaling, including Smad3, Tsc22D1, Skil, were differentially expressed when analyzed after 4 days (128, 129). Transcriptome analyses using RNA-seq revealed that of 72 transcription factors identified as differentially expressed between wild type and BMPR1α deficient iTreg cells, 39 included genes identified in previous reports to support Th17 cell differentiation and 17 to support iTreg cell generation (130–135). Transcription factors Rorc, Rxra, Batf, Maf, Ikaros2 and Ikaros4 were overexpressed in BMPR1α deficient iTreg cells, while Hoxp and Foxp3 had lower expression compared to wild type iTreg cells (118). BMPR1α deficient iTreg cells also had lower expression of Crem, Pde3b and Gpr83, genes associated with iTreg phenotype (21, 118, 136, 137). Thus, BMPR1α signaling in naive cells affects developmental programme controlling lineage choice of iTreg cells and, likely, balance between these two cell subsets.

**ALTERED ONTOGENESIS AND PHENOTYPIC STABILITY OF BMPR1α DEFICIENT T_{REG} CELLS**

Abrogation of BMPR1α signaling in mature T_{reg} cells resulted in increased proportion of T_{reg} cells expressing low levels of Foxp3, as mice aged, and significantly altered proportions of T_{reg} cells expressing naive (CD44^{low}CD62L^{+}) and mature (CD44^{hi}CD62L^{low}) phenotype. T_{reg} cells still expressing high levels of Foxp3, and naive phenotype, were replaced by cells with low expression of Foxp3, and mature phenotype, and these cells dominated peripheral T_{reg} population in aged mice. Acquisition of mature phenotype is associated with T_{reg} activation, or is evidence of cellular senescence indicating disruption of peripheral homeostasis (138, 139). Analysis of cell surface markers showed that BMPR1α-deficient T_{reg} cells expressed lower levels of CD39 and Klrk1, indicating that their suppressor function and terminal maturation are impaired (140, 141). Phenotypic changes of the T_{reg} population were accompanied by gradual upregulation of CD44, and downregulation of CD62L, on conventional CD4+ T cells in aging mice. Progressive loss of Foxp3 expression, associated with senescent phenotype, and increased presence of activated, conventional T cells, are consistent with compromised T_{reg} cell suppressor function and unstable T_{reg} phenotype (118).

When wild type or BMPR1α-deficient T_{reg} cells, expressing high levels of Foxp3, were co-transferred to lymphopenic mice, with naive conventional CD4+ T cells, only wild type T_{reg} cells retained Foxp3 expression, and were able to protect recipient mice from inflammatory bowel disease. BMPR1α-deficient T_{reg} cells had high expression of CCR6 and IL-23R, receptors regulating homing and promoting differentiation of Th17 cells or their precursors. This was associated with increased levels of Rorc, IFN-γ and IL-17 in donor BMPR1α-deficient cells (41).

Immunization of mice with BMPR1α-deficient T_{reg} cells led to robust activation of conventional CD4+ T cells, which expressed higher levels of activation markers, and inflammatory cytokines IFN-γ and IL-17. BMPR1α deficient T_{reg} cells in immunized mice had lower expression of Foxp3, CD39, 4-1BB, and Klrk1. CD39 is an ectonuclease directly involved in T_{reg} suppressor function, and 4-1BB binding of galectin-9 augments T_{reg} function (140, 142–144). Klrk1 is upregulated on antigen activated, highly suppressive T_{reg} cells (141). Similarly, exacerbated inflammatory response was observed in mice infected with Citrobacter rodentium, a mouse model of bacterial colitis (145). These findings indicate unstable phenotype, and decreased ability of BMPR1α-deficient T_{reg} cells, to control inflammation and point to the importance of BMPs signaling to control immune homeostasis in situ and in inflammation.

**SIGNALING CIRCUITS CONTROLLED BY BMPR1α SIGNALING**

Transcriptome analyses of T_{reg} and iT_{reg} cells revealed that BMPR1α gene deletion results in elevated levels of genes promoting phenotypic plasticity and functional adaptation of T_{reg} lineage cells including Rorc, IRF4, Hif1α, Batf3 (Figure 2) (118, 146, 147). This finding is consistent with observed downregulation of Foxp3 and enhanced production of Th1/Th17 cells in inflammatory conditions by BMPR1α-deficient T_{reg} cells (46, 148–150). In addition, a set of genes differentially expressed between BMPR1α-sufficient and deficient T_{reg} and iT_{reg} cells included Cdkn1a (p21^{Cip1}) and Kdm6b (Jump3). Higher levels of these genes in BMPR1α-deficient cells provided cues how BMP signaling shapes T_{reg} population (Figure 2).

Cdkn1a is a cell cycle inhibitor associated with cell maturation and senescence (151). Higher expression of Cdkn1a in peripheral BMPR1α-deficient T_{reg} cells correlates with decreased proliferation and renewal of this subset while promoting maturation and senescence. Cdkn1a also controls CD4+ T cell responses to antigen and generation of memory or anergic cells (152). Kdm6b demethylase is an antagonist of polycomb repressive complex 2 (PRC2) which sustains repressive trimethylation of H3K27. Differentiation of wild type, naive CD4+ T cells into iT_{reg} cells is associated with downregulation of Kdm6b. In contrast, Kdm6b expression remains elevated when BMPR1α-deficient CD4+ T cells when they differentiate into iT_{reg} cells. Kdm6b is also elevated in T_{reg} cells directly isolated from mutant experimental mice (118). In CD4+ T cells Kdm6b promoted proinflammatory immune responses and enhanced cellular senescence (153). Upregulation of Cdkn1a and Cdkn2a (p16^{ink4a}), controlled by Kdm6b, regulated cell cycle and inhibited reprogramming into self-renewing pluripotent stem cells supported by BMP signaling (88, 154, 155). Consistent with these reports, Cdkn1a expression in T cells was found to depend on epigenetic status of DNA and was upregulated by histone deacetylase inhibitors (156).

Mechanistic control of T_{reg} cells by Kdm6b and BMPR1α signaling is consistent with reports demonstrating that inhibition of EzH2, a H3K27 methyltransferase of the PRC2, compromised T_{reg} cell function in tumors and autoimmune diseases (157, 158).
Ezh2 is induced in T<sub>reg</sub> cells upon activation, and sustains T<sub>reg</sub> cell stability and function in inflammation (159–161). Deletion of Ezh2 gene in T<sub>reg</sub> cells increased production of exT<sub>reg</sub> cells, infiltration of CD8<sup>+</sup> and effector CD4<sup>+</sup>/T<sub>reg</sub> ratio in tumors, production of TNF-α and IFN-γ (157). Altogether, BMPR1α signaling in T<sub>reg</sub> cells modulates expression of Kdm6b, an antagonist of Ezh2, and epigenetic landscape controlling T<sub>reg</sub> cell plasticity.

**DISCUSSION**

Dysfunction of T<sub>reg</sub> cells, resulting in altered balance between effector and T<sub>reg</sub> cells, is considered a main underlying cause of most autoimmune diseases (162). Acquisition of effector Th cell functions, rather than decreased proportions of T<sub>reg</sub> cells, are the main cause of autoimmune pathologies but little is understood how this process is controlled (163). Heterogeneity of the T<sub>reg</sub> cell population may account for effector like properties of T<sub>reg</sub> cells, while Foxp3 expression is retained (43, 164). In addition, genetic cell fate mapping, suggested that phenotypic plasticity of the T<sub>reg</sub> cell lineage, especially in inflammatory environment, results in the presence of different proportions of effector CD4<sup>+</sup> T cells that downregulate Foxp3 expression (41, 165). Finally, the functions of T<sub>reg</sub> cells are shaped by tissue specific environmental factors, leading to the development of specialized subsets of T<sub>reg</sub> cells controlling tissue homeostasis and regeneration (11–13, 166).

Foxp3 expression and development of a specific epigenetic signature are required to sustain T<sub>reg</sub> functions (167, 168). Abrogation of BMPR1α signaling in T<sub>reg</sub> cells led to a gradual loss of Foxp3 expression, and was associated with upregulation of transcription factors specific for effector Th lineages, Th1 and Th17 cells. Molecular changes were accompanied by decreased suppressor functions in situ and enhanced responses to immunization or bacterial infections. These findings are consistent with reports demonstrating that inhibition of the BMP signaling exacerbated rheumatoid arthritis, and BMPs treatment ameliorated renal inflammation (122, 125). Altered transcriptional landscape in BMPR1α-deficient T<sub>reg</sub> cells was...
associated with epigenetic changes, mediated by overexpression of the Kdm6b demethylase (118, 153). Overexpression of Kdm6b impaired generation of iT<sub>reg</sub> cells, and promoted inflammation by enhanced generation of Th17 cells (169, 170). Overexpression of Cdkn1a in BMPR1<sub>α</sub>-deficient T<sub>reg</sub> cells led to acquisition of mature, senescent phenotype and decreased proliferation of T<sub>reg</sub> cells. This result is consistent with earlier reports of BMPs regulating renewal and differentiation of embryonic and tissue specific stem cells including T cell progenitors (88, 115, 155). T<sub>reg</sub> cell senescence may be a factor in progression of chronic autoimmune diseases (171). In summary, BMPs and BMPR1<sub>α</sub> signaling controls critical molecular circuits, impacting both Foxp3 expression and epigenetic landscape of T<sub>reg</sub> cells. While little is known how BMPs may affect tissue resident T<sub>reg</sub> cells, one could speculate that tight control of BMP secretion, maturation and stability predisposes them to perform immunoregulatory functions and contribute to the acquisition of organ specific features.

**AUTHOR CONTRIBUTIONS**

PK conceived the idea for the review, outlined, and wrote the manuscript.

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