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Meet the editor



Dr. Xuehui He received her Ph.D. at Tübingen University, Germany. After graduation, she moved to Radboud University Medical Center, Netherlands, to investigate the regulation of the human immune system in relation to immune-mediated diseases. Her research interests include the maintenance of human Treg stability and identity, developing novel small-molecule-inhibitors, and immune profiling of patients with distinct autoimmune diseases including psoriasis, psoriatic arthritis, and type 1 diabetes as well as cancer patients undergoing treatment with checkpoint inhibitors. With the advent of high-throughput techniques and the availability of multi-omics data generated from a large set of samples, Dr. Xuehui He is also specialized in applying various tools and methods for data integration, analysis and interpretation. She believes that combining multi-omics data to highlight the interrelationships of the involved biomolecules and their functions is crucial to fully understand human health and diseases.

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Preface

The immune system defends the body from invading microbes and protects against disease. When pathogens like bacteria or viruses pass through the skin or mucosal membranes the innate immune cells are initially triggered, inducing a quick but non-specific response. Thereafter, the adaptive immune system is activated, which is more powerful but takes a couple of days to be fully activated. The main carriers of the adaptive immune system are lymphocytes, also called white blood cells, which include B cells and T cells. Antibody response is mainly mediated by B cells, whereas T cells are involved in cell-mediated immune response. Both CD4 and CD8 T cells can be further grouped into distinct subsets based on their differentiated cell functions. Effector cell subsets induce a proinflammatory immune response, thus delaminating pathogens and antigens, while regulatory cell subsets induce an anti-inflammatory immune response that is crucial for immune homeostasis and preventing autoimmune disease. Various immune cells have been found to have a regulatory capacity, such as regulatory T cells (Treg), regulatory B cells (Breg), macrophages, myeloid-derived suppressor cells (MDSCs), and tolerogenic dendritic cells (tol-DCs, tDCs). This book focuses on regulatory T cells, including CD4+CD25+Foxp3 Treg cells and interleukin 10 (IL-10)-producing type 1 regulatory T (Tr1) cells.

Tr1 cells are currently identified by the unique cytokine profile of high levels of IL-10 and transforming growth factor beta (TGF β), low levels of IL-2, and the absence of IL-4 after stimulation [1]. The specific cell surface markers used for identification of Tr1 cells include CD49b and LAG-3. Tr1 cells do not constitutively express Foxp3. Foxp3 is required neither for Tr1 cell induction nor suppressive function since it can be isolated from peripheral blood of patients with immune dysregulation polyendocrinopathy enteropathy X-linked (IPEX) syndrome, a disease condition due to *FOXP3* gene mutations [2]. Tr1 cells are multifaceted suppressors that use several immune regulation mechanisms to achieve tolerance. Tr1 cells can inhibit T-cell responses via cell-cell contact, metabolic disruption, and cytolysis. Chapter 1 discusses the potential applications of Tr1 cells in cell-based therapy.

Sakaguchi introduced the concept of T-cell-mediated suppression by describing a subset of CD4+ T cells with co-expression of interleukin-2 receptor (IL-2R) alpha-chain (CD25), which were found to be anergic and to suppress autoimmune disease in thymecotimized mice [3]. Later, Foxp3 was identified as a master regulator gene for Treg development and function. CD4+CD25^{high}CD127^{low} T cells in human peripheral blood can identify a population with high Foxp3 expression. Several other markers were also described for the identification of Treg cells in humans, such as CTLA-4, GITR, TIGIT, and CD49d [4, 5]. To keep the Treg cell lineage stability and identity, epigenetic mechanisms including DNA methylation histone modifications and nucleosome positioning are essential for controlling Treg signature gene expression and thus maintaining suppressive function [6]. It is known that Foxp3 plays a critical role as a transcriptional activator and repressor. Foxp3 can bind to more

than 700 genes involved in various cellular programs including TCR signaling, cell communication, and transcriptional regulation [7]. Due to Treg cells' crucial role in immune homeostasis and tolerance, therapeutic strategies for autoimmune disease and transplantation patients have been developed that target Treg cells directly or indirectly. Chapters 2–4 present the state of the art in therapeutic interventions of Treg cells in immune regulation, application of immune checkpoint inhibitors in cancer treatment, and pattern recognition receptor-mediated regulatory T-cell functions.

The potential therapeutic use of Treg cells for the treatment of autoimmune diseases, transplant rejection, and graft-versus-host disease is currently being investigated in clinical trials. Treg cells might also help to control the autoinflammatory adverse events that are often associated with checkpoint inhibitor treatment for cancer patients. However, engineering Treg cells to enhance specificity, stability, functional activity and delivery, and efficiency is challenging. We anticipate that the new multi-omics tools and CRISPR-Cas9-mediated technology will allow for the rapid growth of Treg-based immunotherapies.

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Chapter 1

Type 1 Regulatory T Cells and Their Application in Cell Therapy

Chao Gu and SangKon Oh

Abstract

Critical roles of regulatory T cells (Tregs) in the maintenance of immune homeostasis by controlling unwanted types of immune responses have been well documented. Therefore, Treg-based therapeutic strategies for inflammatory diseases have long been investigated. Type 1 regulatory T (Tr1) cells and Foxp3⁺ Tregs are two major subsets of regulatory CD4⁺ T cells. In contrast to Foxp3⁺ Tregs, the master transcription regulator for Tr1 cells still remains elusive. Nevertheless, Tr1 cells are generally defined as a specialized subset of CD4⁺ T cells, which are induced in the periphery during antigen exposure in tolerogenic condition. As one of their key features, Tr1 cells express immunosuppressive cytokine IL-10, which can repress the function of effector immune cells independently of Foxp3 expression. In this book chapter, we discuss the recent developments in the field of Tr1 cells, including major characteristics of Tr1 cells, methods for Tr1 induction as well as their therapeutic potentials in immune-mediated diseases.

Keywords: Tr1 cells, Tregs, IL-10, Foxp3, CD49b, LAG-3, cell therapy, immune regulation

1. Introduction

The immune system is a delicate network consisting of a variety of cellular and molecular components that are designed to protect the host by clearing invading foreign pathogens as well as altered self antigens [1]. In addition, immune system is also equipped with a fine-tuned regulatory machinery that can maintain the balance between activation and suppression of immune responses to achieve immune homeostasis and tolerance.

Studies on the mechanisms of immune regulation have revealed multiple different cell types, including subsets of T cells [2, 3], B cells [4, 5], NK cells [6, 7], and myeloid-derived suppressor cells (MDSCs) [8, 9], with immune regulatory function. Among them, two types of regulatory CD4⁺ T cells, namely type 1 regulatory T (Tr1) cells and Forkhead box protein P3⁺ regulatory T cells (Foxp3⁺ Tregs) are best studied so far. These two types of Tregs have, to some extent, overlapping functions in immune regulation. For example, they both can downregulate unwanted types of immune responses and play important roles in the maintenance of immune tolerance in general. However, mounting evidence suggests that Tr1 cells and Foxp3⁺ Tregs are distinct populations of regulatory CD4⁺ T cells [10] and more importantly, they can also display different immune regulatory properties [11–13]. For example, human Tr1 cells, but not Foxp3⁺ Tregs, have been reported to secrete IL-22 and protect gut epithelial cells from TNF α -induced damage [14, 15].

Foxp3 is known to be the master transcription regulator for Foxp3⁺ Tregs [16–18]. Both naïve and memory CD4⁺ T cells are known to differentiate into Tregs with induced Foxp3 expression [19]. Mutation in the *FOXP3/Foxp3* gene gives rise to hyperactive T cell responses [16, 20]. In contrast, though many transcription factors have been reported to transactivate *IL10/Il10* gene, which plays an important role in the differentiation of Tr1 cells, the master transcription regulator for Tr1 cells is still under investigation. Therefore, several key features have been proposed to identify Tr1 cells. First, Tr1 cells produce predominantly IL-10 and TGFβ. However, Tr1 cells can also express different amounts of other cytokines, including IFNγ [21, 22], depending on the microenvironments where Tr1 cells localize. Second, Tr1 cells exhibit suppressive functions without constitutive Foxp3 expression. IL-10 expressed by Tr1 cells plays a major role in Tr1 cell-mediated immune suppression. Third, CD49b and Lymphocyte-activation gene 3 (LAG-3) have been proposed as surface markers for both human and mouse Tr1 cells [10]. However, whether they contribute to the immunosuppressive functions of Tr1 cells remains elusive so far. In addition, CD49b and LAG-3 are also expressed by other cell types, including CD8⁺ T cells and B cells, which can also express IL-10. In addition to CD49b and LAG-3, Tr1 cells can express other surface proteins, including CTLA-4, PD-1, T cell immunoglobulin and mucin domain-containing protein 3 (TIM-3), T cell immunoreceptor with Ig and ITIM domains (TIGIT), CD226, inducible T cell costimulator (ICOS), and CCR5. Of note, these surface molecules can be expressed not only by Tr1 cells, but also by Foxp3⁺ Tregs and non-Treg populations, depending on the immune context [23].

Herein, we review the major characteristics of Tr1 cells and different experimental methods to induce Tr1 cells both *in vitro* and *in vivo*. We also summarize animal models and human diseases in which Tr1 cells are indispensable in controlling inflammatory immune responses. In addition, we recapitulate clinical trials using Tr1 cells as immunotherapeutics. Lastly, we discuss the future perspectives and major questions to be addressed in the field of Tr1 cells.

2. Tr1 cells and Foxp3⁺ Tregs are distinct populations of regulatory T cells

Chronic stimulation of naïve CD4⁺ T cells from both human and mouse in the presence of IL-10 has been reported to induce IL-10-producing antigen-specific immunosuppressive T cells *in vitro* [24]. More importantly, this induced CD4⁺ T cell population can prevent the development of colitis *in vivo* induced by pathogenic CD4⁺CD45RB^{hi} splenic T cells in mice [24]. Based on these findings, such antigen-specific IL-10-producing immunoregulatory CD4⁺ T cells are therefore designated Tr1 cells [24]. Of note, the term “Tr1 cells” was coined several years before the initial studies reporting Foxp3⁺ Tregs [16, 17], therefore, the question whether Tr1 cells and Foxp3⁺ Tregs could be distinct populations of regulatory T cells remained unsolved at that time.

By utilizing the IL-10 reporter mice, in which the cellular source of IL-10 can be detected, the presence of Tr1 cells is further investigated *in vivo* [25, 26]. In a steady state, Tr1 cells have been found in multiple tissues of mice, including small intestine and spleen [10, 26]. More importantly, in the IL-10 and Foxp3 dual-reporter mice, the presence of Foxp3⁺IL-10⁺ Tr1 cells and Foxp3⁺IL-10^{+/-} Tregs, as well as their different distributions in tissues and developmental origins under steady state condition have been observed *in vivo*, suggesting that Tr1 cells and Foxp3⁺ Tregs are different subsets [10, 26]. Of note, there is only low and transient Foxp3 expression upon activation of Tr1 cells, and functional Tr1 cells have been generated *in vitro* from Foxp3-mutated

CD4⁺ T cells of immunodysregulation polyendocrinopathy enteropathy X-linked syndrome (IPEX) patients [13], indicating that in contrast to Foxp3⁺ Tregs [16, 17], Tr1 cells do not require Foxp3 for their development or suppressive function [13].

Taken together, all these findings have identified that immunosuppressive Tr1 cells are different T cell population from Foxp3⁺ Tregs. More importantly, Tr1 cells also play important roles in the induction and maintenance of immune homeostasis.

3. Experimental induction of Tr1 cells in animal models *in vivo* and in humans *in vitro*

So far, multiple methods have been reported to induce Tr1 cells (Table 1). Different microbial components have been shown to induce and further promote Tr1

Reagent and Method	Mouse	References	Human	References
Heat-killed <i>Mycobacterium vaccae</i> suspension	+	[27]		
<i>Bordetella pertussis</i> filamentous hemagglutinin	+	[28]		
Cholera toxin	+	[29, 30]		
<i>V. filiformis</i> lysate	+	[31]		
<i>Lactobacillus pentosus</i> KF340	+	[32]		
<i>B. breve</i>	+	[33]		
Microbiota-derived short-chain fatty acids	+	[34]		
PEGylated G-CSF	+	[35]		
Bowman-Birk inhibitor	+	[36, 37]		
Rapamycin + IL-10	+	[38]		
Rapamycin + G-CSF	+	[39, 40]		
Vitamin D3 + dexamethasone	+	[41]	+	[41]
IL-10	+	[24]	+	[24]
TGFβ	+	[26, 42]		
IL-27	+	[43–49]	?	[50, 51]
IFNα			+	[52, 53]
IL-6			+	[54]
DC-ASGPR agonist			+	[22, 55]
ICOS–ICOSL ligation	+	[56]	+	[57]
Indoleamine-2,3-dioxygenase (IDO)			+	[58]
Activin-A	+	[59]	+	[60]
Retinoic acid (RA)	+	[61]	+	[62]
CD2–CD58 ligation			+	[63]
Co-stimulation of CD46			+	[64]
Co-stimulation of CD55			+	[65]
Artificial APCs			+	[66, 67]

Table 1.
 Factors that promote the generation of Tr1 cells in mice and humans.

cell differentiation in mice *in vivo*. For example, subcutaneous injection of heat-killed *Mycobacterium vaccae* suspension induces allergen-specific IL-10-producing Tr1-like cells that can protect mice against airway inflammation [27]; treatment with filamentous hemagglutinin from *Bordetella pertussis* inhibits IL-12, but induces IL-10 expression by dendritic cells (DCs), which in turn direct naïve CD4⁺ T cell differentiation into Tr1 cells in the respiratory tract [28]; immunization of mice with antigen in the presence of cholera toxin gives rise to antigen-specific Tr1 cells [29, 30]; *Vitreoscilla filiformis* lysate can induce tolerogenic DCs and further drive the differentiation of murine Tr1 cells to suppress effector T cells and inflammation *in vivo* [31]; *Lactobacillus pentosus* KF340 can modulate DCs to promote Tr1 cell response, which can prevent systemic inflammation in a mouse model of atopic dermatitis [32]; oral administration of *Bifidobacterium breve* has been reported to mitigate intestinal inflammation in mice via the induction of Tr1 cells [33]; gut microbiota-derived short-chain fatty acids can enhance microbiota antigen-specific Tr1-like cell induction and inhibit murine colitis induced by dextran sulfate sodium [34].

In addition, pharmacological approaches, including PEGylated G-CSF [35], Bowman-Birk inhibitor, which is a soybean-derived serine protease inhibitor [36, 37], rapamycin combined with IL-10 [38] or G-CSF [39, 40], and a combination of immunosuppressive drugs vitamin D3 and dexamethasone [41], have been reported to induce Tr1 cells, therefore promote transplantation tolerance or suppress autoimmunity in mice *in vivo*.

IL-10 is known to be the primary cytokine that can drive the generation of both mouse and human Tr1 cells [24]. In addition, TGFβ secreted by CD4⁺CD8⁻CD11c⁺ splenic DCs has been reported to induce the development of mouse Tr1 cells, which can mediate immune suppression *in vivo* [42]. In contrast, IFNα, but not TGFβ, can act synergistically with IL-10 to induce the generation of human Tr1 cells from naïve CD4⁺ T cells *in vitro* [52].

Of note, IL-10 administration alone failed to induce T cell tolerance in animal models of transplantation [68, 69] and autoimmune diseases [70, 71]. Results from these studies suggest that the induction of immune tolerance *in vivo* via Tr1 cell differentiation might require chronic antigen-specific stimulation in the presence of IL-10. Therefore, systemic administration of IL-10 alone may not be sufficient to control inflammatory immune response, and therefore fail to establish immune tolerance *in vivo* [24].

IL-10-producing macrophages with M2 phenotype have recently been reported to play an important role in immune tolerance via induction of Tr1 cells in the mouse model of allogeneic pancreatic islet transplantation [72]. In addition, multiple studies have suggested that IL-10 expressed by DCs plays a critical role in Tr1 cell induction. For example, IL-10-producing CD11c^{lo}CD45RB^{hi} plasmacytoid-like DCs in mouse lymph nodes and spleens have been reported to induce immune tolerance through the enhancement of Tr1 cell differentiation *in vivo* [73]. Repetitive stimulation of human naïve T cells with immature or mature DCs differentiated in the presence of exogenous IL-10 has also been reported to promote the differentiation of Tr1 cells *in vitro* [74, 75]. In addition, targeting self- and foreign antigens to myeloid DCs via C-type lectin receptor DC-ASGPR using antigen-antibody fusion proteins, which can stimulate IL-10 expression by DCs, has been shown to elicit antigen-specific immunosuppressive Tr1 cells from naïve and memory human CD4⁺ T cells *in vitro* as well as in non-human primates *in vivo* [22, 55]. Furthermore, a subset of IL-10-producing human DCs, namely DC-10, has been discovered in the peripheral blood *in vivo* [75]. In addition, DC-10 can also be generated from monocytes *in vitro* in the presence of

IL-10 [75]. More importantly, DC-10 isolated from either peripheral blood or generated *in vitro* can induce antigen-specific Tr1 cells via an IL-10-dependent manner, which further supports the importance of DC-derived IL-10 in the induction of Tr1 cells [75–77].

In addition to DC-derived IL-10, inducible T cell costimulator ligand (ICOSL) expression by mouse pulmonary DCs plays an important role in the induction of IL-10-producing Tr1-like cells, as interruption of the ICOS–ICOSL signaling suppresses Tr1-like cell induction and blocks the development of tolerance to allergen in mouse *in vivo* [56]. Human plasmacytoid DCs (pDCs) express enhanced level of ICOSL upon maturation, which is known to promote the differentiation of IL-10-producing Tr1-like cells [57]. Furthermore, mature pDCs isolated from the peripheral blood of rheumatoid arthritis patients have high levels of indoleamine-2,3-dioxygenase (IDO), which can promote Tr1 cell differentiation [58]. However, whether ICOSL and IDO expression by pDCs is associated with IL-10 requires further investigation.

Of note, Tr1 cell development in the gut-associated lymphoid tissues in mice does not require IL-10 but mainly depends on TGF β for their induction and/or maintenance, suggesting that other cytokine(s) could compensate for the absence of IL-10 to induce Tr1 cells [26]. Subsequent studies have further reported that IL-27 plays a critical role in inducing mouse Tr1 cells. Indeed, short-term activation of murine T cells in the presence of IL-27 results in the induction of Tr1 cells *in vitro* and *in vivo* [43–49]. In comparison, the role of IL-27 in inducing human Tr1 cells has been less studied. In humans, plasma IL-27 has been found to be correlated with peripheral CD4⁺IL-10⁺ T cells in Sjögren Syndrome patients [78]. Positive correlation between serum IL-27 and frequency of CD4⁺CD45RA⁻CD49b⁺LAG-3⁺ Tr1 cells in the peripheral blood has been reported in the severe forms of paracoccidioidomycosis [79]. In addition, IL-27 has been reported to induce IL-10-producing Tr1-like cells from human naïve CD4⁺ T cells *in vitro* [50, 51], however, the suppressive function of these human Tr1-like cells requires further investigation.

In addition to cytokines mentioned above, retinoic acid (RA) has been reported to induce antigen-specific Tr1 cells in mouse *in vivo*, which is further enhanced by co-administration of IL-2 [61]. Immunization of mice with autoantigens in the presence of RA and IL-2 can suppress the development of autoimmunity in the mouse models of experimental autoimmune encephalomyelitis (EAE) and autoimmune uveitis [61]. In addition, RA by itself is sufficient to induce retinaldehyde dehydrogenase (RALDH) expression and endow human DCs with tolerogenic properties to elicit Tr1-like cells *in vitro* [62]. Aerobic glycolysis has also been reported to support Tr1 cell differentiation through a metabolic program controlled by hypoxia-inducible factor 1 alpha (HIF-1 α) and aryl hydrocarbon receptor (AHR) [80], suggesting that both immunological and metabolic signals in a specific microenvironment can play pivotal roles in regulating Tr1 cell induction.

Furthermore, activation of human T cells via CD2 results in human Tr1 cell induction [63]. IL-10 is reported to downregulate the expression of costimulatory molecules CD80 and CD86 without affecting CD58/LFA-3 expression on antigen-presenting cells (APCs) [81]. Costimulation of human CD4⁺ T cells via CD2 by its ligand CD58 induces the differentiation of Tr1 cells independently of IL-10 [63], suggesting that CD2 costimulation triggers an intrinsic signaling pathway resulting in Tr1 cell differentiation. In addition, costimulation of human naïve CD4⁺ cells through CD46 [64] or CD55 [65] can induce CD4⁺ T cells to display a Tr1 cell phenotype. However, the precise mechanisms in which signals via CD46 and CD55 contribute to the induction of Tr1 cells remain to be determined.

4. Enigmatic lineage-defining transcription factor for Tr1 cells

So far, there is no master transcription regulator confirmed for either human or mouse Tr1 cells. Current understanding of mechanisms underlying the induction of Tr1 cells is mainly limited to IL-10 gene transactivation, and a number of transcription factors have been reported in this process (**Table 2**).

In mouse, IL-27 can promote IL-10 production by CD4⁺ T cells through activation of STAT1 and STAT3 and drive the differentiation of Tr1 cells [44, 48, 82, 97]. Similarly, other cytokines that can activate STAT3, including IFN α and IL-6, have also been reported to promote Tr1 cells [52–54, 83].

In addition, IL-27-mediated signaling cascade through early growth response 2 (Egr-2) and B lymphocyte induced maturation protein-1 (Blimp-1) has been reported to play an important role in inducing mouse Tr1 cells. Retroviral gene transfer of Egr-2 can convert mouse naïve CD4⁺ T cells into IL-10-producing and LAG-3-expressing antigen-specific immunosuppressive T cells *in vivo* [84]. Subsequent study has further revealed that IL-27 is sufficient to induce Egr-2, IL-10, and LAG-3 expression in mouse naïve CD4⁺ T cells, whereas induction of IL-10 and Blimp-1 by

Markers	Mouse	References	Human	References
CD49b	+	[10]	+	[10]
LAG-3	+	[10]	+	[10]
CD226	+	[10]	+	[10]
Kinases and Transcription Factors				
STAT1	+	[48, 82]	+	[51]
STAT3	+	[44, 54]	+	[51, 83]
Egr-2	+	[47, 84]		
Blimp-1	+	[47, 85, 86]		
c-Maf	+	[45, 46, 86]	+	[60]
AHR	+	[45, 46]	+	[60]
IRF4	+	[87]	+	[60]
ITK	+	[87]	+	[87, 88]
Eomes	+	[89]	+	[89, 90]
ROR- α	+	[91]	+	[91]
IRF1	+	[92]		
BATF	+	[92]		
HIF-1 α	+	[80]		
Mechanisms of Suppression				
Cytokines (IL-10 and TGF β)	+	[24, 41]	+	[24, 74]
Killing of APCs (GzmB and perforin)			+	[93]
Cell-cell contact (CTLA-4 and PD-1)			+	[94, 95]
Metabolic disruption (CD39 and CD73)	+	[80]	+	[96]

Table 2.

Cellular and molecular features of mouse and human Tr1 Cells and their mechanisms of action.

IL-27 is dependent on Egr-2 [47]. Deficiency of Blimp-1 in mouse CD4⁺ T cells results in impaired IL-10 production, whereas Blimp-1 overexpression has been reported to promote the Tr1 cell phenotype in effector T cells [98]. Blimp-1 is also found to promote IL-10 production by Tr1 cells in mouse models of malaria and visceral leishmaniasis [85]. A recent study has examined the transcriptional network driven by IL-27 across different mouse T cell subsets and identified multiple regulators of IL-10 expression [86]. Two central regulators, *Prdm1* (Blimp-1) and *Maf* (musculoaponeurotic fibrosarcoma, c-Maf) are found to cooperatively drive the expression of signature genes induced by IL-27 in Tr1 cells and mediate IL-10 expression in all T helper cells [86]. More importantly, genetic depletion of *Prdm1* and *Maf* in T cells, but not either alone, results in the development of spontaneous colitis in mice, which underscores the importance of the crosstalk between *Prdm1* and *Maf* in the maintenance of immune homeostasis *in vivo* [86].

In addition, IL-27 is also reported to induce the expression of c-Maf, which acts in synergy with AHR, to promote IL-10 expression and differentiation of mouse Tr1 cells [45, 46]. Mice with impaired AHR signaling in CD4⁺ T cells show lower IL-10 production and resistance to IL-27-mediated mitigation of EAE [46]. Furthermore, IL-27-driven c-Maf expression has been reported to transactivate IL-21 production [45, 46]. IL-21 by itself fails to induce Tr1 cells from native CD4⁺ T cell, but it serves as an autocrine growth factor for the expansion as well as maintenance of Tr1 cells induced by IL-27, which is evidenced by the observation that loss of IL-21 signaling in CD4⁺ T cells results in the inhibition of IL-27-driven generation of IL-10-producing T cells *in vitro* and in IL-21R-deficient mice *in vivo* [45]. Nonetheless, the detailed roles of IL-27 in the induction and activation of Tr1 cells in humans remain to be investigated.

Treatment of human naive T cells with activin-A, a member of the TGF β superfamily, has been reported to induce the activation of interferon regulatory factor 4 (IRF4) [60]. IRF4, along with AHR and its binding partner, AHR nuclear translocator (ARNT), forms a tripartite transcription factor complex that is necessary for the differentiation and effector functions of human Tr1 cells [60]. In addition, IRF4 is also involved in the functional development of mouse Tr1 cells [87]. IL-2-inducible T-cell kinase (ITK) downstream of T cell receptor is found to serve a critical role for the activation of Ras/MAPK/IRF4 signal cascade, which further enables the functional development of Tr1 cells [87, 88]. Furthermore, adoptive transfer of human Tr1 cells induced by activin-A to a humanized mouse model of allergic asthma has been shown to provide the protection against major disease manifestations [60]. Activin-A is also reported to induce a population of antigen-specific IL-10-producing regulatory CD4⁺ T cells, possibly representing Tr1 cells, which can protect against Th2-associated airway hyperresponsiveness and allergic airway disease in mice [59].

Other transcription factors, including Eomesodermin (Eomes) [89, 90], retinoic acid-related orphan receptor α (ROR- α) [91], have also been proposed to transactivate IL-10 expression in CD4⁺ T cells and promote Tr1 cell differentiation. Furthermore, it has been reported that interferon regulatory factor 1 (IRF1) and basic leucine zipper ATF-like transcription factor (BATF) are induced early on during IL-27-induced Tr1 differentiation and act as pioneering factors for the differentiation of Tr1 cells in mouse [92]. BATF prepares the genomic landscape for the binding of additional transcription factors necessary for the development of Tr1 cells, and IRF1 specifically transactivates of the *Il10* gene for Tr1 cell differentiation in mice [92].

With the findings of these transcription factors in IL-10 gene transactivation, however, the lineage-defining transcription factor for mouse and human Tr1 cells is still elusive, which remains a key question to be answered in the study of Tr1 cells.

5. Phenotype of Tr1 cells

Though the immunosuppressive functions of Tr1 cells have been reported both *in vitro* and *in vivo*, their phenotype, in contrast, remains poorly defined. Coexpression of CD49b and LAG-3 has been proposed as the surface markers for both human and mouse Tr1 cells [10]. It has been known that CD49b is expressed on memory T cells [99], while LAG-3 is expressed on activated CD4⁺ and CD8⁺ T cells. In addition, high level of LAG-3 is also expressed by other immune cells, such as Foxp3⁺ Tregs and IL-10-producing B cells [100, 101]. Therefore, the single use of CD49b or LAG-3 is not sufficient to define a pure population of functional Tr1 cells or separate these cells from other T helper cells or Treg cells. Of note, coexpression of CD49b and LAG-3 is found not limited to the Foxp3⁺ Tr1 cells but is also observed in Foxp3⁺ Tregs and CD8⁺ T cells that produce IL-10 [102]. Indeed, IL-10-producing Tr1 cells, Foxp3⁺ Tregs and CD8⁺ T cells are all capable of co-expressing CD49b and LAG-3 *in vitro* when differentiated under IL-10-inducing conditions, and *in vivo* upon pathogenic encounter or infection in the pulmonary mucosa [102]. Therefore, it is highly recommended that a deliberate and precise gating strategy will need to be made to isolate CD49b⁺LAG-3⁺ memory Tr1 cells with the exclusion of B cells, CD8⁺ and Foxp3⁺ cells.

In addition to CD49b and LAG-3, Tr1 cells can express many other surface molecules, including PD-1, CTLA-4, TIGIT, TIM3, ICOS and CD226, as well as ectoenzymes CD39 and CD73, depending on the immune context [103, 104]. Although expression of such additional inhibitory receptors by Tr1 cells is generally in line with their immunosuppressive function, it is also necessary to realize that their expression is not specific to Tr1 cells.

6. Mechanism of Tr1 cells in immune suppression

The regulatory function of Tr1 cells requires their activation via TCR by cognate antigen recognition. In addition, Tr1 cells can also display bystander immunosuppressive activity to proximal T cells regardless of their antigen specificity. This indicates that activated Tr1 cells can regulate immune responses via both antigen-specific and non-specific manners (**Figure 1** and **Table 2**). Upon activation, human and mouse Tr1 cells secrete IL-10 and TGFβ [24, 41, 74], which suppress T cell responses directly and indirectly. IL-10 can limit the magnitude of immune responses by reducing the surface expression of MHC class II molecules [105–107], co-stimulatory molecules [108, 109], as well as the secretion of pro-inflammatory cytokines by APCs, followed by the suppression of effector T cell responses [104]. TGFβ expressed by Tr1 cells can also repress APC functions and inhibit T cell proliferation and cytokine production [52]. Granzyme B (GzmB) and perforin expressed by Tr1 cells can selectively kill APCs via both cognate and non-cognate mechanisms [93]. Cytolysis of the APCs can consequently suppress antigen-specific T cells and bystander T cells [110].

In addition to secretion of soluble factors including cytokines and enzymes, expression of inhibitory molecules PD-1 and CTLA-4 by Tr1 cells can repress effector T cells via cell contact-dependent manner, which is evidenced by that finding that blockade of CTLA-4 or PD-1 can decrease the suppressor activity of human Tr1 cells [94, 95]. Expression of ectoenzymes CD39 and CD73 [23, 103], though not exclusive to Tr1 cells as mentioned earlier, can facilitate Tr1-mediated suppression of effector T cells via metabolic disruption [80, 96]. In addition, IL-10-producing Foxp3⁺ Tr1-like cells have also been reported to downregulate B cell antibody production due to low or no expression

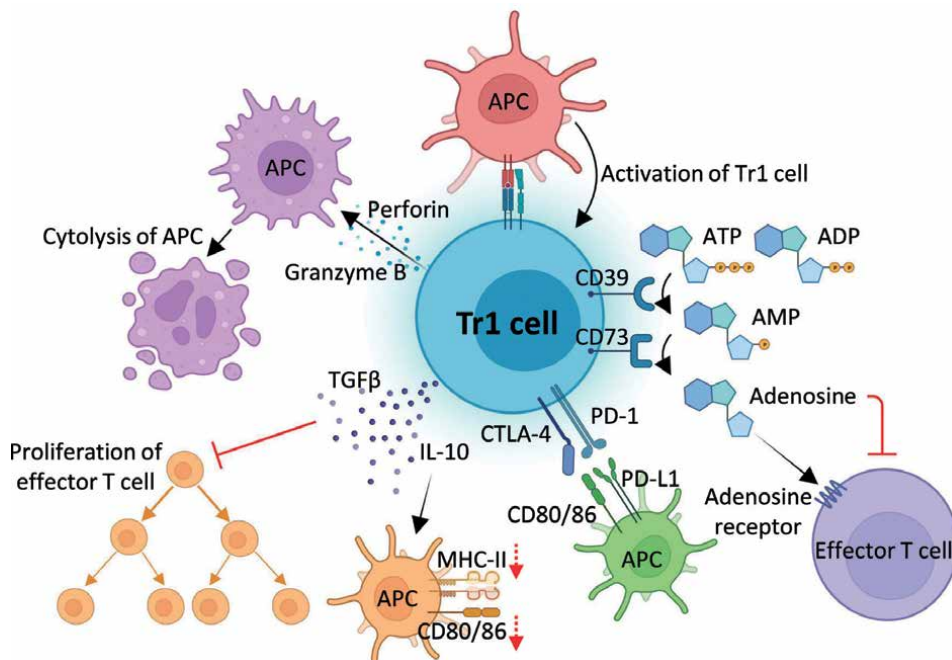


Figure 1. *Suppressive mechanisms of Tr1 cells. Upon activation, Tr1 cells suppress immune responses both directly and indirectly. The secretion of granzyme B and perforin can induce cytolysis of APCs, resulting in inhibition of both antigenspecific T cells and bystander T cells. TGFβ secreted by activated Tr1 cells can inhibit T cell proliferation and cytokine production while IL-10 can downregulate expression of MHC-II molecules, co-stimulatory molecules and production of pro-inflammatory cytokines by APCs. Tr1 cells can also inhibit APC-induced effector T cell activation via cell-cell contact involving CTLA-4 and PD-1. Ectoenzymes CD39 and CD73 expressed by Tr1 cells can mediate the suppression of effector T cells via metabolic disruption.*

of CD40L [111]. Taken together, Tr1 cells can exhibit their immunosuppressive function through multiple mechanisms. In future studies, it would be of significance to investigate whether the suppressive mechanisms of Tr1 cells in different clinical settings are associated with the stage of disease progression and pathological microenvironment.

7. Therapeutic potentials of Tr1 cells

The immunoregulatory capacity of Tr1 cells has been tested in multiple different murine models of inflammatory diseases. Foxp3⁺ Tr1 cells isolated from the intestine of *Il10^{eGFP}Foxp3^{RFP}* double reporter mice have been shown to suppress colitis caused by the transfer of pathogenic Th17 cells in an IL-10-dependent manner *in vivo* [112]. In a mouse model of multiple sclerosis, transfer of OVA-specific Tr1 cells can prevent EAE development when antigen-specific Tr1 cells are activated by intracranial injection of OVA [41]. In a mouse GVHD model, Tr1 cells have been reported to constitute the most abundant regulatory population after allogeneic bone marrow transplantation [89]. More importantly, transfer of purified populations of Tr1 cells can significantly suppress GVHD and contribute significantly to transplant survival [89]. In acute and chronic collagen-induced arthritis mouse models, transfer of collagen type II-specific Tr1 cells can reduce the incidence and clinical symptoms of arthritis in both preventive and therapeutic settings, with a significant impact on collagen type

II-specific antibodies. Importantly, injection of collagen-specific Tr1 cells can significantly decrease the proliferation of antigen-specific effector T cells *in vivo* [113].

Human gliadin-specific Tr1 cell clones generated *in vitro* from the intestinal mucosa of celiac patients in remission have been shown to inhibit pathogenic T cell response to dietary gliadin [114]. With good manufacturing practice (GMP)-compatible protocols to differentiate and expand human Tr1 cells *in vitro*, Tr1 cells are also being used as a therapeutic product in clinical applications. IL-10-aneergized donor T cells which contain Tr1 cells specific for recipient alloantigens generated *in vitro* have been tested in controlling GVHD in a clinical trial in which patients with high-risk/advanced stage hematologic malignancies received haplo-identical HSCT [115]. Patients had mild to moderate GVHD and showed rapid immune reconstitution [115]. Donor-derived T cells remained hyporesponsive to recipient alloantigens *in vitro* and an increase in cells with Tr1 cell signatures has been observed over time in recipients. Results from this study give the first indication of the feasibility of Tr1 cell-based immune therapy and show promise for the future use of Tr1 cells as treatment for hematologic malignancies and immune-related diseases [115]. T-allo10, as an improved cell product generated by stimulation of donor T cells with host-derived DC-10 in the presence of IL-10, contains a higher percentage of Tr1 cells (up to 15% of CD49b⁺ LAG-3⁺ Tr1 cells) [23], when compared with the previous generation of IL-10-aneergized T cells (containing <5% Tr1 cells) used in the clinical trial mentioned above. The overall immunological outcome of T-allo10 in controlling GVHD in patients who received mismatched HSCT for the treatment of hematologic malignancies is still under investigation in an ongoing Phase I trial (ClinicalTrials.gov Identifier: NCT03198234).

In addition to GVHD in HSCT, the therapeutic effect of Tr1 cells in controlling graft rejection in solid organ transplantation is also being investigated. The protocol for generation of recipient-derived donor-specific Tr1 cells for kidney transplantation has been developed [116]. In addition, *Drosophila*-derived artificial APCs have been developed to induce antigen-specific Tr1 cells [66]. Schneider *Drosophila* cells transfected with a transmembrane form of a murine anti-human CD3 monoclonal antibody, together with human CD80 and CD58, as well as human IL-2 and IL-4, have been shown to expand a large number of antigen-specific Tr1 cells [66]. Using this method, Tr1 cells have also been tested to treat inflammatory disease in a phase I/IIa clinical study, in which OVA-specific Tr1 cell clones generated *in vitro* using artificial APCs have been adoptively transferred to patients with refractory Crohn's disease [67]. Patients were fed with OVA-enriched diet to ensure activation of OVA-specific Tr1 cells migrating to the gut. Administration of these OVA-specific Tr1 cells to patients with refractory Crohn's disease was well tolerated and had dose-related efficacy. Though the clinical effect was limited, reaching the maximum at 5 weeks after treatment and declining thereafter, the OVA-specific immune response correlated with clinical outcomes, supporting immunosuppressive function of OVA-specific Tr1 cells [67].

Induction of stable and sustained expression of IL-10 by conventional CD4⁺ T cells has been developed as an alternative strategy to generate a large number of Tr1 cells. The lentiviral vectors encoding both human IL-10 gene and a marker GFP gene of selection have been tested to induce Tr1 cells [117]. It has been reported that lentiviral vector-mediated human IL-10 gene transfer converts conventional human CD4⁺ T cells into Tr1-like cells, namely CD4^{IL-10} cells. These cells resemble Tr1 cells phenotypically and functionally as they express large amount of IL-10, repress T cell responses *in vitro*, and more importantly, prevent xenogeneic GVHD development and progression *in vivo* [117]. Subsequent study has further reported that in addition to suppress T cell responses both *in vitro* and *in vivo*, CD4^{IL-10} cells were also capable

of killing myeloid leukemia cells in an HLA class I-dependent but Ag-independent manner [118]. This new generation of Tr1 cell product paves the way for adoptive cell therapy with Tr1 cells in patients undergoing allogeneic organ transplantation and HSCT [15, 119, 120].

Furthermore, utilization of artificial chimeric antigen receptors (CARs) to redirect regulatory T cell specificity towards pathogenic cell populations and antigens has also provided new insights in designing and implementing the next generation of Tr1 cells, CAR-Tr1 cells, for the treatment of transplantation rejection, autoimmunity, and leukemia [121–123]. In addition, genome editing techniques (including the application of CRISPR–Cas9) are under investigation to further enhance the specificity and immune regulatory functions of Tregs [122]. Together, all these progresses will certainly further increase the therapeutic value of Tr1 cells.

8. Conclusion

In the last two decades, the immune suppressive functions of Tr1 cells have been demonstrated both *in vitro* and *in vivo*. Studies from different groups have shown that Tr1 cells are able to prevent and constrain undesirable immune responses in different disease contexts, and therefore promote immune tolerance. These important discoveries have led to the idea that Tr1 cells could serve as a therapeutic product to promote and restore immune tolerance in transplantation, as well as in inflammatory and autoimmune diseases. The completed clinical trials have shown, to some extent, the safety of Tr1 cell-based therapy and further indicated the therapeutic potentials. Different methods are being developed to generate better Tr1 cell products. However, with all these advances, questions on Tr1 cells including whether they represent an established T cell lineage and whether Tr1 cells induced *in vitro* can maintain long-term immunoregulatory functions due to possible plasticity and repolarization *in vivo* remain unanswered. In addition, there is controversy over how well CD49b/LAG-3 surface co-expression signature defines circulating Tr1 cells in healthy individuals as many labs, including ours, struggle to use CD49b and LAG-3 to isolate Tr1 cells from bulk culture and it may not be the best approach when compared to the clinically applicable IL-10 cytokine capture method [14]. Future studies will need to elucidate the key molecules, including better and more stringent cell surface marker(s) as well as lineage-defining transcription factor(s) of Tr1 cells. In addition, a deeper and more comprehensive understanding on the biology of Tr1 cells is also necessary to deliver safer and more effective Tr1 cells that can be used to treat different diseases which require long-term regulation of inflammatory immune responses.

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Conflict of interest


The authors declare no conflict of interest.

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Chapter 2

Function and Therapeutic Intervention of Regulatory T Cells in Immune Regulation

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Abstract

Although the detailed mechanisms of regulatory T cells (Tregs) in regulating immune responses have not been completely clarified yet, Tregs therapy on autoimmune diseases and organ transplantation is making robust progress, along with the gradually enhancing knowledge of the Tregs function. In this chapter, on the basis of summarizing the immunomodulatory functions of Tregs, we reviewed the latest scientific progress and status of our understanding, as well as the prospect of stimulation and expansion of Tregs *in vivo* and *in vitro* followed by adoptive transfer or autologous cell therapy in animal models and clinical trials, respectively. Moreover, we also assessed the current technological limitation and potential side effects of polyclonal and antigen-specific Tregs-based approaches and techniques, to promote the development of rescue, revive, or rejuvenate Tregs in the therapeutic intervention to treat autoimmune diseases and transplantation.

Keywords: regulatory T cell, polyclonal Treg, antigen-specific Treg, therapeutic intervention, transplantation, autoimmune disease

1. Introduction

Regulatory T cells (Tregs), as a subgroup of T cells with immunosuppressive function, were first reported in 1970s by Gershon and Kondo [1]. According to the developmental origin, Tregs can be broadly classified into two groups. Tregs that grow in the thymus are called natural (nTregs) or thymic (tTregs) Tregs, and that develop at the periphery by specific stimuli of conventional CD4⁺ T cells are termed peripheral Treg (pTregs). When Tregs are induced by specific factors, such as interleukin-2 (IL-2) and transforming growth factor (TGF)- β , *in vitro* are called induced Tregs (iTregs) [2]. At present, Tregs have emerged as a vital part in understanding the immune response to pathogens, controlling the development of allergies, transplantation, and autoimmune diseases, as well as in the application of treating tumors, since their “re-discovery” more than 20 years before [3]. However, the detailed mechanisms of Tregs in regulating both innate and adaptive immune responses are still not completely understood. In this chapter, we will review the latest scientific progress and status on our understanding and prospect of stimulation and expansion of Tregs *in vivo* and *in vitro* followed by adoptive transfer or autologous cell therapy in animal models and clinical trials.

We will also assess the current technological limitation and potential side effects of polyclonal and antigen-specific Tregs-cell-based approaches and techniques.

2. Tregs function

2.1 Loss of Tregs and development of autoimmune diseases

Every manifestation stemming from Tregs paucity highlights a vital function of Tregs in preventing fatal autoimmune inflammation. The immunosuppressive function of Tregs is mainly dependent on continuous expression of the transcription factor forkhead box protein 3 (Foxp3), which is a critical regulator of CD4⁺CD25⁺ Tregs development and function. Loss function of Foxp3 results in a fatal autoimmune disease featuring all known types of inflammatory responses. Studies have demonstrated that the typical or fatal autoimmune responses that occurred in the Foxp3-mutant scurfy mice or Foxp3-null mice are related to the deficiency of CD4⁺CD25⁺ Tregs, but not to the cell-intrinsic dysfunction of CD4⁺CD25⁻ T cells. When being transferred into the neonatal Foxp3-deficient mice, Tregs can preferentially expand and control the development of autoimmune disease. Furthermore, ectopic expression of Foxp3 can confer suppressor function on peripheral CD4⁺CD25⁻ T cells [4]. Even in severely diseased mice, by reinstating Foxp3 protein expression and suppressor function in cells expressing a reversible Foxp3 null allele, the rescued Tregs normalized immune activation, quelled severe tissue inflammation, reversed fatal autoimmune disease, and provided long-term protection against them. It is indicated that Tregs are capable of resetting the immune homeostasis in broad-spectrum systemic inflammation and autoimmune diseases [5].

X-linked autoimmunity-allergic dysregulation syndrome (XLAAD), which has been renamed as Immunodysregulation, polyendocrinopathy, enteropathy, and X-linked syndrome (IPEX), was a rare inborn error of immune regulation and autoimmune lymphoproliferative illness in humans [6]. As one of the most well-known Mendelian disorders, IPEX is characterized by a loss of immunological tolerance caused by a lack of functioning Tregs and was discovered to be associated with the mutations in Foxp3 [7, 8]. In the absence of Tregs, activated CD4⁺ T cells instigate multi-organ damage resulting in type 1 diabetes (T1D), enteropathy, eczema, hypothyroidism, and other autoimmune disorders.

Moreover, studies on Tregs depletion by cytotoxic T-lymphocyte antigen (CTLA)-4 Ab (e.g., ipilimumab) in tumor patients have shown a strong correlation between the induction of tumor regression and autoimmunity [9]. Ipilimumab acts not only on effector T cells (Teffs) but also on Tregs because the latter ones in both mouse systems and humans can be directly targeted by ipilimumab due to the constitutive expression of CTLA-4 on their cell surface [10, 11]. Except for a decreased frequency of circulating CD25⁺CD4⁺ Tregs can be observed upon ipilimumab, CTLA-4 blockade renders Teffs resistant to the inhibitory activity of Tregs, rather than modulating the immunosuppressive effects of Tregs on T cells and NK cells [12]. It is indicated that loss of Tregs has a close relationship with the development of autoimmune diseases from another perspective.

2.2 Immune tolerance and prevention of autoimmunity

Our body's immune system has evolved to perform self-tolerance to resist the autoimmune reactions directed against our own cells via sophisticated mechanisms. On the T

cell level, self-tolerance is executed by deletion of T cells with self-reactive T cell receptor (TCR) in the thymus (central tolerance) or maintained by specialized cells, including Tregs, outside of the thymus (peripheral tolerance). The importance of Tregs for the maintenance of immune tolerance has also been illustrated to have a close relationship with the expression of the Foxp3 gene, both in humans and mice [13, 14]. Foxp3, together with other transcription factors and coactivators/corepressors, represses the transcription of IL-2 in Tregs, rendering them highly dependent on exogenous IL-2 (mainly produced by activated non-Tregs) for their maintenance and function. Tregs constitutively express the high-affinity IL-2 receptor (α chain), which serves as a sink for IL-2 that controls the expansion of T effs. The development of autoimmune/inflammatory disease can be promoted if disrupting this IL-2-mediated feedback loop at any step. Further, manipulation of this feedback loop is instrumental in tuning the intensity of Tregs-mediated suppression, hence the strength of a variety of immune responses [15]. Foxp3 also activates the genes encoding Tregs-associated molecules, including CD25, CTLA-4, and Glucocorticoid induces tumor necrosis factor receptor (GITR) and confers suppressive activity to Tregs, which directly suppress non-Tregs or modulate the function of antigen-presenting cells (APCs) to activate non-Tregs [16].

2.3 Mechanisms of immune suppression

The Tregs-mediated immune suppression may be related to three mechanisms, including secretion of immunosuppressive cytokines [17], cell-contact-dependent suppression [18], and functional modification or killing of APCs [19]. More than one mechanism may operate for controlling the particular immune response in a synergistic and sequential manner.

IL-10 and TGF- β may act as the main immunosuppressive cytokines contributing to control the autoimmune disorders or inflammatory diseases secreted by Tregs [17]. IL-10 indirectly prevents antigen-specific T cell activation, which is associated with downregulation of the antigen presentation and accessory cell functions of monocytes, macrophages, and dendritic cells (DCs), as well as inhibits T-cell expansion by directly inhibiting IL-2 production by these cells. The pivotal function of TGF- β is to maintain tolerance via the regulation of lymphocyte proliferation, differentiation, and survival. TGF- β can block the proliferation of T lymphocytes by suppressing the expression of IL-2 (via Smad3 signaling pathway), cyclins (including cyclin D2 and cyclin E), cyclin-dependent kinase (CDK)-4, and c-myc. TGF- β also can inhibit the differentiation of Th1 and Th2 cells by blocking the T-bet/STAT4 and GATA-3/NFAT signaling transduction pathway, and down-regulating the differentiation of cytotoxic T lymphocyte (CTL) via regulating the expression of c-myc and T-bet [20]. TGF- β can also induce the expression of Foxp3 and the generation of Tregs. In addition, nTregs can also predominantly produce IL-35, a new member of the IL-12 family, to perform the suppressive function [21]. IL-35 is a novel Epstein-Barr-virus-induced gene (Ebi) 3-IL-12 α heterodimeric cytokine, and Ebi3, which encodes IL-27 β , is a downstream target of Foxp3. Ebi3^{-/-} and IL12 α ^{-/-} Tregs have significantly reduced regulatory activity *in vitro* and fail to control homeostatic proliferation and cure inflammatory bowel disease (IBD) *in vivo*.

Antigen-activated Tregs, which are highly mobile, are swiftly recruited to APCs (especially DCs), upon being stimulated by the specific antigen. The recruitment of Tregs to APCs is in chemokines or adhesion molecules depended on manner. Once the Tregs aggregate around the APCs, they will outcompete antigen-specific naïve T cells regarding interaction with DCs, mainly because of the high expression of adhesion molecules on Tregs, such as lymphocyte function-associated antigen (LFA)-1 [22].

Tregs can modulate the function of APCs. Activated Tregs promote the downregulation of CD80 and CD86 on APCs or stimulate DCs to form the enzyme indoleamine 2, 3-dioxygenase both by a CTLA-4-dependent mechanism [23, 24]. Indoleamine 2, 3-dioxygenase is capable of catabolizing the essential amino acid tryptophan to kynurenines, which are toxic to T cells. Alternatively, Tregs can induce the apoptosis of responder T cells or APCs by secreting granzyme/perforin or immunosuppressive cytokines (such as IL-10), or through the delivery of a negative signal (possible including intracellular cyclic AMP) to inactivate the responder T cells [19]. The upregulation of intracellular cyclic AMP will lead to the inhibition of T cell proliferation and IL-2 production, as well as the generation of pericellular adenosine catalyzed by CD39 and CD73 by Tregs.

3. Tregs and autoimmune and autoinflammatory diseases

3.1 Tregs and type 1 diabetes

Type 1 diabetes (T1D) is a typical kind of autoimmune disease affecting millions of people worldwide with a steadily rising incidence, and islet infiltrating self-reactive T cells mediated β -cell destruction is considered to be primary pathogenesis of this disease. The initiation of the autoimmune process is related to the recognition of self-antigens by the autoreactive subsets of CD4⁺ T-helper lymphocytes, which can preferentially produce the Th1 cytokine spectrum after activation. The presence of autoreactive CD8⁺ cytotoxic T lymphocytes is necessary for the further development of T1D as well. It has been demonstrated that CD4⁺CD25⁺FoxP3⁺ Tregs also play an indispensable role in the development of T1D by preventing destructive autoimmunity [25]. Although the application of immunosuppressive reagents is one of the available therapies, it can have severe side effects. Optimal immune-based therapies for T1D should restore self-tolerance without inducing chronic immunosuppression. Thus, efforts to repair or replace Tregs in T1D probably can reverse autoimmune response and protect the remaining insulin-producing β cells. There is a large body of evidence to suggest that Foxp3⁺ Tregs function is altered in patients with T1D, though the overall frequency of Foxp3⁺ Tregs may be unaltered in these individuals [26, 27]. Data from the non-obese diabetic (NOD) mouse model of autoimmune diabetes and human with T1D suggest that increasing resistance of T cells to Tregs regulation may be the primary cause for reduced suppression, and it can be explained by the inability of T cells to provide an environment conducive to Tregs fitness and function, including the reduced IL-2 production or downregulation of the IL-2 signaling pathway by T cells [28, 29].

Apart from their canonical function of immune suppression, it is now well accepted that Tregs can likewise be induced in the periphery in an antigen-specific manner and take residence in tissues to play important roles in maintaining tissue homeostasis. So, antigen-specific induction of disease-relevant Tregs will offer the opportunity to treat or prevent the T1D for a long-standing goal. It has been demonstrated that in the peripheral blood of children who are at risk to develop T1D, the proportion of insulin-specific Tregs reduced during the onset of islet autoimmunity, while the higher reduction was related to a rapid progression to clinically overt T1D [30]. This finding suggested that inducing these insulin-specific Tregs may delay the progression to clinically symptomatic T1D. Nevertheless, very little is known about pancreas residing Tregs, and all studies conducted so far on these tissue-specific Tregs

focused solely on NOD mice with ongoing insulinitis. A recent study found that a combinatorial regimen involving the anti-CD3, cyclophosphamide (CyP), and IAC (IL-2/JES6-1) antibody complex can promote the engraftment of antigen-specific donor Tregs through ablating host conditioning and control islet autoimmunity without long-term immunosuppression [31].

3.2 Tregs and rheumatoid arthritis

Rheumatoid arthritis (RA) is one kind of common systemic inflammatory autoimmune disease, and its typical clinical symptoms are musculoskeletal pain, joint swelling, and stiffness, which can seriously damage body function and reduce the quality of life of patients. Patients with RA are more likely to develop osteoporosis, infection, cardiovascular diseases, respiratory diseases, cancer, and other diseases than the general population. Similar to other autoimmune diseases, Tregs also play a vital role in the pathogenetic process in RA. When the number and/or function of Tregs are decreased or inhibited, autoantigen or ligand death receptors (DRs) related immune cascade can be amplified, and the levels of various cytokines, such as IL-2, will be rapidly increased, leading to the activation of macrophages in the synovium of bones and joints to produce many inflammatory cytokines including IL-1, IL-6, and IL-8 [32, 33]. These inflammatory reactions destroy articular cartilage and eventually lead to joint deformities.

However, contradictory results on the number (increased [34], unchanged [35], or decreased [36]) and functional characteristics (enhancement [32] or attenuation [33]) of Tregs in the peripheral blood of patients with RA have been reported in different studies, and this discrepancy can be explained by the ongoing difficulties in the recognition of Tregs. In most studies, the high-level expression of Foxp3, CD25, and low-level expression of CD127 (the α -chain of the IL-7 receptor) are used to define Tregs, and the CD3⁺CD4⁺CD25^{high}CD127^{low} phenotype is most commonly isolated from Tregs population. However, Foxp3 requires intracellular staining and the expression levels in Tregs in the resting state and activated state are different, and conventional T cells (Tconvs) also express a low levels of Foxp3 and CD25 upon TCR stimulation and low levels of CD127 [37]. Thus, some other supplementary cell surface markers, such as CD62 ligand, integrin Ea (CD103), GITR (TNFRSF18), CTLA-4 (CD152), CD45RO, and neuropilin, have been also used to identify Tregs in clinical practice [38]. CD45RA and CD45RO can be used to distinguish immature Tregs (CD45RA⁺Foxp3^{low}) from activated memory Tregs (CD45RA⁻Foxp3^{high}) cells [39]. A more stringent method to define Tregs has revealed the number of Tregs decreased in peripheral blood and increased in synovial fluid by performing a meta-analysis [40].

However, although the Tregs isolated from RA patients can show normal inhibitory activity *in vitro*, they function abnormally when circulating in the synovial fluid, which is caused by the overexpression of IL-6 induced inflammatory environment [41, 42]. Tregs in this inflammatory environment are resistant to Tregs-mediated repression, and the sensitivity of APCs to the inhibition of Tregs also decreased [43, 44]. Moreover, the arthritic synovial fibroblasts can promote the transformation of CD25^{low}Foxp3⁺CD4⁺ T cells into Th17 cells in the oxygen deficiency synovial microenvironment, and the latter one shows a stronger ability to induce osteoclast production [45]. The process of transformation is closely related to the activation of the hypoxia-inducible factor-1 α (HIF-1 α) pathway.

3.3 Tregs and autoimmune hepatitis

Autoimmune hepatitis (AIH) is a severe hepatopathy that occurs globally in all ethnicities and affects children and adults of all ages. It is with a female predominance and characterized by hypergammaglobulinemia, interface hepatitis on histology, and seropositivity for disease-defining autoantibodies. In AIH, the autoimmune reaction resulting in liver injury initiates with the presentation of liver autoantigen by APCs to an uncommitted T lymphocyte. Following antigen encounter, Th0 becomes activated and differentiates into Th1, Th2, and Th17. Th1 cells secrete interferon (IFN)- γ and IL-2, which can lead to the activation of macrophages and upregulation of major histocompatibility complex (MHC) class I and II by hepatocytes [46]. Th2 lymphocytes secrete IL-4 and IL-10, which can promote the B cell activation and maturation into plasma cells. Plasma cells then produce autoantibodies and mediate cell cytotoxicity in turn [47]. Activation of Th17 cells, which can secrete IL-17 proinflammatory cytokines, has been associated with the induction of pro-fibrotic events [48]. The autoimmune attack will continue perpetrating and favoring the progression of tissue damage if these events are not opposed by effective immunoregulation.

It has been demonstrated that the impairment of Tregs plays an important role in the initiation and progression of AIH. A numerical and functional defect in CD4⁺CD25^{+/high}Foxp3⁺ cells was reported in patients with AIH compared with the healthy subjects [49]. Before immunosuppressive treatment is instituted, Tregs isolated from AIH patients are also impaired in their ability to expand, and unable to regulate CD4⁺ and CD8⁺ T cells proliferation and modify CD4⁺ and CD8⁺ T cells cytokine profile as in the case of healthy controls [50, 51].

This deficiency of Tregs in AIH patients might be linked to increased expression of the cell surface marker CD127 [52] and defects in the expression of the ectonucleotidase CD39 [53]. CD127 is also known as the α -chain of the IL-7 receptor (IL-7R α), while CD39⁺ Tregs decrease in frequency in AIH patients leading to the failure to control the production of IL-17 by Th17. So, Tregs in AIH subjects are more prone to acquire features of effectors than their counterparts when exposed to a proinflammatory challenge, which suggests the defective immunoregulation of Tregs in AIH might have some relationship with the increased conversion of Tregs into effector lymphocytes [53]. A recent study confirmed that impaired CD39 levels derive from alterations of aryl hydrocarbon receptor (AhR) signaling [54]. AhR is a mediator of toxin responses and adaptive immunity. Upon binding to endogenous or exogenous ligands, AhR undergoes activation, which will bring about the upregulation of CD39.

However, aberrantly high levels of aryl hydrocarbon receptor repressor and estrogen receptor alpha (Er α) can be detected in AIH. AhR binds Er α with higher affinity than aryl hydrocarbon receptor nuclear translocator (ARNT), the classical AhR binding partner. These non-conventional binding give rise to impaired CD39 upregulation.

Impaired Tregs function in AIH is also linked to defective levels of Galectin-9 (Gal-9). Gal-9, a member of the galectin family, is one kind of β galactoside binding protein expressed on Tregs. It can bind to the mucin domain 3 (Tim-3) on CD4⁺CD25⁻ Tregs. Upon Gal-9 binding to Tim-3, apoptosis in CD4⁺CD25⁻ Tregs will be induced. Thus, reduced expression of Gal-9 in Tregs in AIH contributes to the less suppressing ability of Tregs and rendering CD4⁺CD25⁻ Tregs less prone to the control of Tregs [55].

In addition, defective Tregs function in AIH is linked with reduced ability to produce IL-10 as well. It is resulting from poor response to IL-2 as reflected by

impaired ability to upregulate the phosphor signal transducer and activator of transcription 5 (pSTAT-5) [56].

3.4 Tregs and inflammatory bowel disease

Inflammatory bowel disease (IBD) is a chronic, inflammatory, and autoimmune disorder. The types of IBD include ulcerative colitis (UC) and Crohn's disease. The etiology of IBD is possibly linked to the dissonance of the host immune system, genetic variability as well as an environmental factor, and the pathogenesis of this disorder has not been fully elucidated [57]. In recent years, it has been found that the abnormal intestinal mucosal immune system plays a crucial role in the occurrence, development, and prognosis of IBD, involving the imbalance in Th17 and Tregs [58]. The differentiation of Th17 cells goes through three stages—initiated by IL-6 and TGF- β , expanded by IL-21, and IL-23 maintains the stable maturation of Th17 cells during the later stage of differentiation [59]. Except for protecting the intestinal mucosa via keeping the balance of the immune microenvironment, Th17 cells also can exacerbate the intestinal inflammatory response through secreting proinflammatory cytokines, such as IL-17. Compared with the healthy controls, Th17 cells infiltrate the intestinal mucosa of IBD patients and the amount of IL-17 increases [60]. Tregs and Th17 cells are related through differentiation and share a common signal pathway mediated by TGF- β . In the UC mouse model, Th17 cells in the peripheral blood of mice increased, yet Tregs decreased [61]. Therefore, Tregs deficiency may be the central link in the pathogenesis of IBD and the regulation of Th17/Tregs balance is prospective to be a new target for the treatment of IBD. The immunological factors affecting the Th17/Tregs balance in IBD consist of both TCR and costimulatory signals and cytokines. IL-2 inducible T cell kinase (ITK), a critical regulator of intracellular signaling downstream of the TCR, positively regulates the differentiation of Th17 and negatively regulates the differentiation of Tregs [62]. The T cell costimulatory molecule OX40 and its cognate ligand OX40L collectively play an essential role in keeping the growth of Th17 and Tregs, that is, activation of OX40 enhanced Th17 function while blocking OX40L decreased Tregs proliferation [63].

4. Tregs and transplantation

While organ transplantation is one of the greatest achievements in modern medicine, rejection is still the major barrier to successful transplantation. The immune response to an allograft is an ongoing dialog between the innate and adaptive immune systems. One of the reasons that transplantation induces such a dynamic immune response is the high precursor frequency of T cells capable of responding to mismatched MHC molecules. Although immunosuppression regimens are effectively able to control the acute rejection and decrease graft loss in the first year after transplantation, it is difficult to get a durable effect on long-term graft survival with these modern regimens, owing to a combination of drug toxicities, the emergence of chronic alloimmune responses and the serious complications, such as chronic infections or malignancies. Studies on experimental transplant models have suggested a role for Tregs in protecting allografts by suppressing both autoimmune and alloimmune responses [64, 65]. Further, Tregs-based therapies do not require harsh conditioning and have a risk of graft-versus-host disease.

4.1 Tregs and solid organ transplantation

The first step in the adaptive immune response to a transplant in a solid organ transplantation recipient is T-cell recognition of alloantigen or allorecognition. Graft-specific Tconvs, which are capable of direct recognition of alloantigen, are present at a very high frequency so that they can respond to the transplant without first clonally expanding in lymph nodes. When graft-specific Tconvs are recruited to the graft, they will lead to inflammation and tissue damage. Increasing graft-specific Tregs combined with the reduction of graft-specific Tconvs allow the former one to dominate in the graft and prevent recruitment and activation of the later one. Moreover, once entering the draining lymph node, inflammatory APCs can activate more graft-specific Tconvs, while tolerogenic APCs are able to expand graft-specific Tregs and prevent the expansion of graft-specific Tconvs to maintain tolerance [66].

Moreover, Tregs with direct alloantigen specificity, which are also present at high frequency, play important role in the induction of tolerance, whereas Tregs with indirect alloantigen specificity are important for the maintenance of tolerance [67]. Tregs control transplant rejection by first migrating to the organ to prevent graft damage and then retreating to draining lymph nodes to maintain tolerance [65]. During an active alloimmune response, Tregs with both direct and indirect specificities expand and infiltrate the organs, but the homeostatic function of Tregs is insufficient to prevent rejection from occurring due to the potency of alloimmune responses until the organs have suffered substantial damage [67]. That is because Teffs arrive at the graft site first and expand in number before the arrival of Tregs so that the grafts are dominated by Teffs [64], and at the peak of alloimmune responses, a high antigen load, vigorous co-stimulation, and high concentrations of cytokines, such as IL-1 and IL-6, override Tregs suppression so that effective immune functions can be carried out to induce rejection quickly. Thus, prevention of rejection and establishment of tolerance by Tregs require attenuation of Teffs responses and inflammation control.

4.2 Tregs and allogeneic hematopoietic cell and bone marrow transplantation

Currently, allogeneic hematopoietic cells transplantation (HCT) or bone marrow transplantation (BMT) in humans is widely used in the treatment of tumors of the hematopoietic and immune systems, including leukemia, lymphoma, and myeloma. However, they are usually complicated by serious and potentially lethal side effects, such as immunodeficiency and graft-versus-host disease (GVHD). GVHD represents a dysregulated immune response and has been assessed across both major and minor histocompatibility barriers, and the pace of these reactions is much more accelerated across major histocompatibility barriers. The onset and course of GVHD depend on the degree of major and minor MHC disparity and the T-cell dose. It has been demonstrated by using animal models that T cells rapidly migrate to nodal sites, spleen, and mesenteric lymph nodes and begin to dramatically expand by 3–4 days following adoptive transfer, and within 7–10 days, they infiltrate the major sites of GVHD pathophysiology, such as lymph nodes, spleen, gastric intestinal tract (GI tract), liver, and skin [68]. Depletion of CD4⁺CD25⁺ T cells from the donor graft accelerated the GVHD course and increased lethality, which provided evidence for the role of Tregs in mediating GVHD [69]. Tregs also expand dramatically upon adoptive transfer and traffic to nodal sites to promote immune reconstitution and suppress GVHD across both major and minor histocompatibility barriers, while interestingly allowing for the maintenance of graft-versus-tumor (GVT) responses [70–72]. Tregs proliferate

in the same way as Tconvs with similar kinetics and tend to fade out over time. Upon the adoptive transfer, the dramatic expansion of Tconvs can be detected, whereas when the same numbers of Tregs were adopted along with the Tconvs, this dramatic proliferation of Tconvs is significantly reduced, yet the homing and activation of Tconvs are not impacted [73]. It is indicated that the adopted Tconvs are still able to be activated and home to specific sites within the body, yet this drastic T-cell expansion required for GVHD is diminished. Thus, clinical strategies to enhance the function of Tregs hold great promise to improve outcomes following allogeneic HCT and BMT.

5. Tregs therapy

The ability of Tregs to maintain self-tolerance means they are critical for the control and prevention of autoimmune diseases. Currently, a large body of data in the literature has provided evidence on the possible Tregs therapy for various immune-mediated diseases. Restoring immune homeostasis and tolerance through the promotion, activation, or delivery of Tregs has emerged as a focus for therapies aimed at curing or controlling autoimmune diseases. A variety of Tregs-based therapies are being explored in the treatment and prevention of autoimmune diseases, such as *ex vivo*-expanded polyclonal Tregs or Tregs transduced with an autoantigen-specific TCR, chimeric antigen receptor (CAR). In addition, some other non-cell-based therapies related to Tregs, including low-dose IL-2 and heat shock protein (HSP), may also be beneficial.

5.1 Polyclonal Tregs therapy

Polyclonal Tregs therapy uses autologous *ex vivo*-expanded Tregs to restore tolerance and is considered a next-generation cellular therapy for several autoimmune diseases and inflammatory immune disorders. Tregs isolated from peripheral blood are stimulated and expanded *in vitro* by using anti-CD3/CD28 antibody-coated beads and high dose IL-2, or anti-CD28 super agonists [74, 75]. The first preclinical proof of concept for use of polyclonal Tregs was demonstrated in 1995 that CD4⁺CD25⁺ T cells could be used to transfer tolerance in athymic nude mice by suppressing self-reactive lymphocytes [76]. Then, expanded Tregs with a polyclonal specificity are reportedly more efficient in suppressive function and have demonstrated potential in various preclinical models of GVHD [77], solid organ transplantation [78], and autoimmune diseases [79]. Several clinical trials have been carried out to examine the safety and feasibility of polyclonal Tregs for T1D [80], transplantation [81], and GVHD [82], and the use of polyclonal Tregs in these diseases have shown significant therapeutic potential. For example, one robust clinical trial on T1D with polyclonal Tregs demonstrated that the expanded autologous Tregs retained their T cell receptor diversity and owned enhanced functional activity. Fourteen adult subjects with T1D received *ex vivo*-expanded autologous CD4⁺CD127^{low/-}CD25⁺ polyclonal Tregs (0.05×10^8 to 26×10^8 cells). A transient increase in Tregs, which retained a broad CD4⁺Foxp3⁺CD25^{hi}CD127^{low} phenotype long-term, was detected in recipients. There were no infusion reactions or cell therapy-related high-grade adverse events [80]. Besides, some other clinical trials for polyclonal Tregs therapy in autoimmune hepatitis (NCT02704338), Crohn's disease (NCT03185000), Pemphigus (NCT03239470), and Alzheimer's disease (NCT03865017) are also under investigation. Positive results from these clinical trials have allayed the concerns that polyclonal Tregs therapy would promote

generalized immune suppression, leading to an increased risk of infection and cancer, which has not been found.

However, the therapeutic effect of this clinical trial correlated with increased Tregs post-infusion, and only persisted for a short time. The subsequent trials confirmed the limited persistence of expanded Tregs even after a second infusion [83], and obtaining sufficient cell numbers can be challenging in many disease scenarios [84], although polyclonal Tregs therapy is generally considered safe and efficacious. Perhaps the use of other Tregs-promoting therapies in combination with polyclonal Tregs therapy would prolong the suppressive effect and increase the number of Tregs with improved patient outcomes.

5.1.1 Low-dose IL-2 in combination with polyclonal Tregs therapy

As mentioned earlier, it has been widely accepted that IL-2 plays a critical role mainly in Tregs fitness and homeostasis, thus low-dose IL-2 therapy alone has the effect of expanding *in vivo* Tregs. Co-administration of polyclonal Tregs and low-dose IL-2 has been considered as an additional strategy to restore the defective Treg pool and is expected to boost Tregs number and function after administration. Recent work has reported the possibility to expand Tregs using low-dose IL-2 *in vivo* [85]. In this phase I-II clinical trial on 46 individuals with mild to moderate forms of various autoimmune diseases, including RA, ankylosing spondylitis, systemic lupus erythematosus, psoriasis, Bechet's disease, granulomatosis with polyangiitis, Takayasu's disease, IBD, AIH and sclerosing cholangitis, all the patients received low-dose IL-2 (1 million IU/day) for 5 days, followed by fortnightly injections for 6 months. Low-dose IL-2 can be well tolerated whatever the disease and the concomitant treatments, and specific Tregs expansion and activation can be detected in all patients, without effector T cell activation. The increase in Tregs percentage was mainly evident on day 8 and was then contained thereafter, despite the levels remaining slightly higher compared to baseline. However, specific data on AIH patients ($n = 2$) were not presented, which indicated the effects of low-dose IL-2 in AIH patients remain unclear. In another study on two AIH patients with persistent disease activity [86], low-dose IL-2 was administered at 1 million IU for 5 days monthly for a total of 6 months. The proportion of circulating Tregs increased in both cases with a peak observed on day 9 and returning to baseline levels on day 28. This suggests that the effect of low-dose IL-2 on Tregs frequency is transient. Given the small number of cases enrolled, further studies in larger numbers of subjects should be performed to assess the efficacy as well as the long-term effects of this treatment on Tregs, particularly on their suppressive function, expansion, and plasticity.

Furthermore, an advantage of low-dose IL-2 therapy is that recombinant human IL-2 is already available as a therapeutic drug called Aldesleukin or Proleukin for the treatment of malignant melanoma and renal cell carcinoma in the clinic [87].

5.1.2 HSP in integrating Tregs expansion and activation

HSPs are highly conserved proteins present in all kingdoms of organisms, and expressed under stress conditions to protect the cells from injuries. They are classified into five families according to their molecular weight, including HSPH, HSPC, HSPA, HSPD, and DNAJ. Intracellular HSPs play an essential role in physiological processes, involving of folding of nascent and stress-accumulated protein-substrate assembly and preventing the aggregation of these proteins, transporting across membranes

and degrading other proteins. While extracellular or receptor-bound HSPs mediate immunological functions and immunomodulatory activity, including the induction, proliferation, suppressive function, and cytokine production of Tregs [88]. In patients with juvenile idiopathic arthritis (JIA), DNAJ was found to improve the suppressive function of Tregs in culture and stimulate T cells for the production of IL-10, and high serum levels of DNAJ correspond with a milder course of the disease, indicating epitopes derived from human DNAJ can induce differentiation and/or stimulate cell proliferation of Tregs [89]. Acting as co-stimulators of human Tregs, HSPD can enhance the suppression and proliferation of Tregs via binding of Toll-like receptor (TLR) 2 on the Tregs surface to inhibit target T cell proliferation, IFN- γ and tumor necrosis factor (TNF)- α secretion, as well as upregulate the expression of IL-10 [90]. HSPD can enhance the differentiation of cord blood mononuclear cell (CBMC) into CD4⁺IL-10⁺Foxp3⁺ Tregs as well [91]. HSPA can stimulate the suppressive activity of Tregs, increase the production of IL-10, and downregulate the production of inflammatory cytokines via the TLR4-signaling pathway, which may be important for Foxp3 induction [92]. Animal studies have shown that oral, nasal, intraperitoneal, or intradermal administration of HSPA significantly inhibits the development of the autoimmune arthritic model, which suggested that suppression of autoimmune response in experimental animals was mediated by increased expansion of Tregs specific for HSPA, and the secretion of anti-inflammatory IL-10 [93–95]. Moreover, HSPC can promote Tregs-dependent suppression as well [96]. HSP gp96, the endoplasmic reticulum form of HSPC, is required for Tregs maintenance and function, as loss of GP96 resulted in instability of the Tregs lineage and impairment of suppressive functions *in vivo*. In the absence of HSP gp96, Tregs are unable to maintain Foxp3 expression levels and can lead to systemic accumulation of IFN- γ -producing and IL-17-producing T cells, because HSP gp96 is an essential chaperone for the cell-surface protein glycoprotein A repetitions predominant (GARP). GARP is a docking receptor for latent membrane-associated TGF- β (mLTGF- β). The HSP gp96-deficient Tregs prevent the expression of mLTGF- β and resulted in inefficient production of active TGF- β [97]. Meanwhile, immunization of HSP gp96 can increase Tregs frequency, expansion, and suppressive function, which shows obvious therapeutic effects in a *Lyn*^{-/-} mouse model of systemic lupus erythematosus and myelin oligodendrocyte glycoprotein (MOG)-induced experimental autoimmune encephalomyelitis (EAE) [98].

5.1.3 Foxp3-transduced T cells

Tregs constitutively express the transcription factor Foxp3, which is critical for their immunosuppressive function. Several studies have provided evidence that ectopic expression of Foxp3 can confer a suppressive phenotype to naïve or memory CD4⁺ T cells, so it is probably a way to circumvent the requirement of a large number of polyclonal Tregs for therapy [99]. Lentiviral delivery of the Foxp3 gene into IPEX patient-derived CD4⁺ T cells can acquire the characteristic features, such as decreased proliferation, hyporesponsiveness, reduced cytokine release, and suppressive activity, which are able to mirror the Tregs population from healthy donors, and these induced Tregs were demonstrated to be stable in inflammatory conditions not only *in vitro* but also *in vivo* in a xenograft mouse model of GVHD [100]. Several other studies have also shown the efficiency of Foxp3-transduced Tregs in combating autoimmune diseases, such as allergy [101] and collagen-induced arthritis [102]. Recently, the CRISPR/Cas9 system has been applied to the domain for stable and high-level

expression of Foxp3 in Tconvs, and these edited Tregs-like cells were able to suppress the immune response in a xeno-GVHD mouse model [103]. These studies demonstrate the applicability of gene correction in the treatment of autoimmune diseases.

Cell permeable form of Foxp3 is another approach to enforce Tregs differentiation. This protein form can link to the protein transduction domain (PTD) from the HIV transactivator of transcription and allow Foxp3 to be delivered to the cytoplasm and nucleus, which has been shown to induce a Tregs phenotype in both human and mouse T cells [104]. However, a major limitation of this approach is the high cost for human patients.

5.2 Antigen-specific Tregs

While the initially limited success of polyclonal Tregs is encouraging, the amounts of cells needed for infusions are quite large and the risk of nonspecific immunosuppression should be considered. Tregs developed in the thymus (i.e., nTregs) harbor a TCR repertoire that is skewed toward self-antigens, while Tregs induced in the periphery in an antigen-specific manner (i.e., pTregs) can be characterized with a TCR repertoire different from their nTregs counterparts [105]. So, it is a good strategy to induce disease-relevant antigen-specific Tregs with the goal to interfere with the unwanted immune reactions in allergies and autoimmunity and to restore the self-tolerance, and it has been verified through considerate research in humans or mice [106, 107]. Compared with the polyclonal Tregs therapy, growing evidence from animal models indicates that antigen-specific Tregs may be more efficient in controlling pathological immune responses in a disease-specific manner. It is possible because infused Tregs migrating toward the tissues of cognate antigen exposure will lead to more effective and localized control of inflammation, along with risk reduction of broad immunosuppression and its related adverse events [108, 109]. Moreover, the enhanced migration ability of antigen-specific Tregs to target tissues can probably lead to a lower administration number of Tregs than the polyclonal approach, and facilitate the obtainment of Tregs via standard *in vitro* expansion protocols.

5.2.1 TCR-Tregs therapy

Tregs therapy can be enhanced by the introduction of an autoantigen-specific TCR (TCR-Tregs), which have the ability to redirect their response toward the desired autoantigen specificity. Tregs can be *ex vivo*-transduced to express a high-affinity and autoantigen-specific TCR by way of retroviral or lentiviral transduction and subsequently expanded to treat a specific autoimmune disease. For instance, a low number of autoantigen-specific Tregs were needed to sufficiently prevent or even reverse T1D in a NOD mice model, which was engineered to express a diabetogenic TCR [108]. Another group showed that as few as 2000 antigen-specific Tregs were all that was required to prevent T1D in mice [110]. Preclinical studies in mouse models have also shown that TCR-engineered Tregs are more effective in suppressing the Teffs responses against specific antigens in autoimmune diseases, such as colitis, multiple sclerosis, and arthritis [111–113], even in tolerance induction to MHC mismatched heart grafts [114].

Compared to polyclonal Tregs, fewer antigen-specific Tregs may be needed to alleviate autoimmune disease; however, the challenge of the identification of an appropriate, high-affinity, autoantigen-specific TCR for transduction onto Tregs still remains, due to some autoimmune diseases being with poorly defined dominant

epitopes. It is hard to isolate and identify antigen-specific Tregs due to both the great diversity in TCRs and very low count of them naturally circulating in the peripheral blood. The majority of antigen-specific Tregs were generated using TCRs isolated from Tconvs, which would influence the stability, avidity, and migration to specific parts of the engineered Tregs, for the reason that the intrinsic affinity and specificity of TCRs isolated from Tregs are distinct from Tconvs. Moreover, there are some other limitations of this approach, such as the requirement for MHC restriction and the risk of mispairing with endogenous TCR.

Single-cell sequencing is required for TCR identification since each T cell clone expresses a different TCR sequence from the others, and the successful sequencing of both the α and β chain TCR is required to successfully identify one TCR [115]. In a recent study, single-cell TCR analyses of islet Tregs revealed their specificity for insulin and other islet derived antigen, and these antigen-specific Tregs were reported to be efficient in protecting NOD mice from diabetes [116].

5.2.2 CAR-Tregs therapy

Although Tregs engineered with TCRs (TCR-Tregs) seem to be promising, they are still MHC-restricted and their modular application in individual patients is constrained. Engineer with genes encoding chimeric antigen receptors (CARs), which typically consist of a single-chain variable fragment (scFv) for binding to a monoclonal antibody, an extracellular hinge, a transmembrane region, and intracellular signaling domains, is an MHC-independent strategy of generating antigen specificity for Tregs [117]. In animal models, CAR-Tregs have shown great potential for treating different diseases, especially allograft rejection and various autoimmune diseases.

HLA-A mismatching is often associated with poor outcomes after transplantation, so, HLA-A is a potential target antigen to generate antigen-specific Tregs for inducing transplantation tolerance. One kind of HLA-A2-specific CAR (A2-CAR) Tregs was created in a peptide-independent manner, and not only can maintain high expression of canonical Tregs markers, including Foxp3, CD25, Helios, CTLA-4, and a high degree of demethylation of the Treg-specific demethylated region (TSDR) of the FOXP3 locus but also can enable stronger antigen-specific activation than did an endogenous TCR [118]. Further, CAR-stimulated Tregs had a higher surface expression of CTLA-4, latency-associated peptide (LAP), and the inactive precursor of TGF- β than TCR-Tregs. Unlike TCR-Tregs, CARs could also stimulate IL-2-independent Tregs proliferation in the short term [118]. Thus, CAR-Tregs may be superior to TCR-Tregs.

CAR Tregs isolated from transgenic BALB/c mice with a CAR specific for 2,4,6-trinitrophenol (TNP), an antigen commonly used in a mouse model of colitis, were reported to capable of suppressing the proliferation of TefFs *in vitro* even in the absence of B7-CD28 co-stimulation, and the mortality rate of TNP-CAR-tg mice significantly decreased in comparison with WT mice [119]. In situ fluorescent micro endoscopic evaluation verified that TNP-CAR Tregs localized to the inflamed colonic mucosa. Thereafter, a novel protocol that enabled efficient and reproducible retroviral transduction and expansion of murine nTregs was developed in a non-transgenic mouse model, bringing about a highly enriched population of TNP-specific Tregs. The TNP-CAR Tregs show suppressive capabilities to TefFs both *in vitro* and *in vivo*, and TNP-CAR Tregs-mediated suppression *in vitro* was partially dependent on cell-cell contact but not on IL-10 or TGF- β 1 [120]. Moreover, based on the previously engineered Tregs to express a TCR specific for a myelin basic protein (MBP) peptide,

which can suppress the proliferation of MBP-reactive T_H17s and ameliorated MOG-induced EAE, the approach by creating human Tregs expressing functional single-chain CAR (scFv CAR), targeting either MBP or MOG was extended. These scFv CAR-transduced Tregs retained Foxp3 and Helios after long-term expansion *in vitro*. Importantly, these engineered CAR-Tregs were able to suppress autoimmune pathology in EAE, demonstrating that these Tregs have the potential to be used as a cellular therapy for multiple sclerosis (MS) patients [121].

5.3 Taking Tregs into medicine

5.3.1 Comparison table showing different approaches, techniques, and stages among studies

Different approaches that involve boosting Tregs have been tested in several disease settings so far. Polyclonal Tregs and antigen-specific Tregs therapy have demonstrated their efficacy in immunotherapy in various clinical trials or preclinical models (**Table 1**).

5.3.2 Challenge and bottleneck of Tregs therapy

To sum up, Tregs are crucial in maintaining tolerance. Hence, Treg immunotherapy is an attractive therapeutic option in autoimmune diseases and organ transplantations. However, there are still many challenges and bottlenecks in implementing Treg therapy.

At first, the cellular variability of Tregs is wide. It is important to characterize the phenotype and suppressor function of each subtype of Tregs present in the periphery or the thymus. The success of Treg therapy depends initially on the isolation and characterization of cells, while current research does not use a universally applicable standard for Treg identification. This gap in identification leads to conflicting and doubtful research results. Meanwhile, one of the drawbacks of this cell therapy is the time delay to administer Tregs from taking peripheral blood to obtaining sufficient numbers of cells, and antigen-specific Treg technology may presumably need administration of lower Treg numbers than polyclonal approaches. Secondly, to improve the efficacy of Treg immunotherapy, it is necessary that Tregs can migrate, survive, and function in the specific target tissue. The plasticity of polyclonal or CAR-Tregs in an inflamed microenvironment is still an unknown factor. The inflamed microenvironment enriched with pro-inflammatory cytokines can either lead to a reduction in the potency of Tregs or resistance of T_H17s to Treg suppression, or even converting Tregs into pathogenic T_H17s. There are also questions to be addressed regarding the long-term proliferative potential and survival of polyclonal or antigen-specific Tregs in the tissue microenvironment, which is enriched with cytokines, metabolites, low oxygen levels, and microbial peptides.

Thirdly, the application of CAR-Tregs is an exciting option in both transplantation and autoimmune diseases, when the antigen is known. Nevertheless, before CAR-Tregs can be put into practice in the clinic, there are still obstacles required to be overcome, because antibodies specific for self- or alloantigen must be characterized to construct antigen-specific CAR-Tregs. For the reason that autoimmune diseases always have a large autoantigenic repertoire of T or B cells, or spreading epitope, it will be not adequate to focus Treg therapy on one specific epitope for an autoantigen. Although CAR-Tregs own a greater affinity to the cognate antigen than TCR-Tregs,

Approach	Technique	Indication	Stage of study	Study ID or references
Polyclonal Tregs therapy	Autologous polyclonally expanded Tregs	T1D	Clinical trials phase 1 (completed)	NCT01210664
Polyclonal Tregs therapy	<i>Ex-vivo</i> expanded donor regulatory T cells	GVHD	Clinical trials phase I (active)	NCT01795573
Polyclonal Tregs therapy	Autologous polyclonally expanded Tregs	Kidney transplant	Clinical trials phase I/II (Active)	NCT02129881
Polyclonal Tregs therapy	Donor alloantigen reactive Tregs	Liver transplant	Clinical trials phase I (recruiting)	NCT02188719
Polyclonal Tregs therapy	Autologous polyclonal expanded nTregs	AIH	Clinical trials phase I/II (unknown)	NCT02704338
Antigen-specific Tregs therapy	CD4 ⁺ CD25 ⁺ T cells from TCR-transgenic BDC2.5 mice expanded <i>in vitro</i> with BDC peptide and NOD DCs	T1D	Preclinical studies (NOD model)	[122]
Antigen-specific Tregs therapy	CD4 ⁺ T cells transduced with Foxp3 and a TCR of a CIA-associated T cell clone	RA	Preclinical studies (DBA1 mice)	[123]
Antigen-specific Tregs therapy	CD4 ⁺ CD25 ⁺ T cells from TCR-transgenic Tg4 mice expanded <i>in vitro</i> with anti-CD3/CD28 beads	MS	Preclinical studies (B10.PL mice)	[124]
Antigen-specific Tregs therapy	CAR-engineered CD4 ⁺ CD25 ⁺ Tregs specific for CEA	Colitis	Preclinical studies (CEABAC mice)	[111]
Antigen-specific Tregs therapy	CAR-engineered human CD4 ⁺ CD25 ⁺ Tregs specific for HLA-A2	Skin transplantation	Preclinical studies (CEABAC mice)	[125]
Antigen-specific Tregs therapy	TGF- β -induced iTregs generated from CD4 ⁺ T cells of TxA23 mice	Autoimmune gastritis	Preclinical studies (BALB/c mice)	[126]
Antigen-specific Tregs therapy	TGF- β -induced OVA-specific iTregs generated from CD4 ⁺ T cells of OT-II mice	GVHD	Preclinical studies (C57Bl/6 mice)	[127]

Table 1. Clinical trials or preclinical models with polyclonal Tregs or antigen-specific Tregs in different diseases.

the former requires the target cells to have at least 100 target autoantigens for successful recognition and Tregs stimulation. Moreover, it has not been confirmed yet whether CAR-Tregs would also lead to adverse reactions, such as cytokine storm and neuronal cytotoxicity, as the treatments with anti-tumor CAR-T cells.

Besides, it is still a hard nut to crack to access the localization of infused Tregs to the exact target site, and exhaustion of Tregs may limit their efficacy in immunosuppression. Meanwhile, the choice of immunosuppression in patients with Tregs therapy is crucial, for example, rapamycin has been shown to enhance Tregs

frequency. To achieve efficacious and successful Tregs therapy, it is necessary to continue on immunosuppression that is favorable to Tregs survival and proliferation.

Therefore, more work is required to administer Tregs therapy effectively and safely to restore tolerance in transplantations and autoimmune diseases.

6. Prospect (perils and promises)

Tregs have proved to be a major breakthrough as an exciting immunotherapy option in the last two decades. Early phase clinical trials demonstrated safety, feasibility, and early efficacy with Tregs therapy in both autoimmune diseases and organ transplantation. The development of antigen-specific Tregs and CAR-Tregs would lead to exciting new frontiers in the cell therapy field as these cells are more efficacious and lesser numbers are required due to their target tissue homing affinity. It is crucial to obtain tissue biopsies following Tregs infusion to access the localization of infused cells. Optimizing the manufacturing processes and culture media will support infused Tregs survival in future clinical trials. In addition, improving our understanding on the patient's omics profile with new technology will also allow us to put the personalized Tregs immunotherapy into effect.

In a word, although challenges still remain, the prospect of Tregs immunotherapy is exciting if the cell therapy community can maintain the collaboration closely. The immunosuppression-free period for patients with autoimmune disease and transplantation is in front of us.

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Chapter 3

The Role of Immune Checkpoints in Cancer Progression

Rahmad Aji Prasetya and Devyani Diah Wulansari

Abstract

Immune checkpoint proteins are like two-faced swords that first act as gatekeepers of the immune system to protect the host from tissue damage. In contrast, these proteins can corroborate cancer progression by inhibiting tumor-specific immune responses. Here, we summarized the regulation and signaling cascade of immune checkpoint molecules (PD-1/PD-L1, CTLA-4, TIM3, TIGIT, LAG3, and BTLA), including their role in providing co-inhibitory signals for regulating T-cell response. The involvement of immune checkpoint molecules to drive cancer growth is elaborated with explanations about various anticancer strategies, such as (1) the overexpression of immune checkpoints in cancer cells, immune cells, or the surrounding environment leading to incapacities of the tumor-specific immune response, (2) immune checkpoints interference to metabolic pathways then deplete nutrients needed by immune cells, (3) the interaction between immune checkpoints and regulatory T cells. Lastly, future challenges of immune checkpoint inhibitors are discussed briefly to get insight into their applicability in the clinical setting.

Keywords: immune checkpoint proteins, cancer development, anti-tumor, metabolic reprogramming, regulatory T cells

1. Introduction

Cancer or tumor cells express neoantigens that the immune system can identify from healthy neighboring cells due to genetic mutations. These changes typically result in a tumor-reactive T cell response, most notably CD8⁺ T cells. However, this mechanism is frequently ineffective at eradicating cancer cells [1]. One cause for this failure is the suppression of invading T cells by a wide range of immunosuppressive mechanisms found in the tumor microenvironment (TME), such as regulatory T cells (Tregs) or immunosuppressive cytokines [2, 3].

Furthermore, binding of the T cell receptor (TCR) to the antigenic peptide bound to the major histocompatibility complex (MHC) of the antigen-presenting cell (APC) is not adequate to yield an immune response, particularly to eradicate cancer cells. Thus, the additional stimulatory co-signal produced by co-receptors is required. These co-receptors play an essential role in modulating T cell responsiveness and balancing co-stimulatory and inhibitory (i.e., immune checkpoint) signals [4]. Extended TCR signals generated from T cells exposure to their cognate antigen result in enhanced and persistent expression of inhibitory co-receptors like cytotoxic T-lymphocyte-associated

antigen 4 (CTLA-4), programmed death protein 1 (PD-1), or many other immune checkpoints. At this moment, T cells enter a state of dysfunction or exhaustion, allowing cancer cells to grow unchecked [5, 6]. Therefore, blockage to these immune checkpoints can reinvigorate the anti-tumor function of immune cells. This chapter aimed to elaborate on the involvement of immune checkpoints in cancer development. It includes the explanation of the normal trafficking and inhibitory signaling of each checkpoint, followed by discussions about how immune checkpoint contributes to cancer growth.

2. Regulation and signaling of immune checkpoints

Immune checkpoints serve as the immune system's gatekeepers and are required for sustaining self-tolerance, thus protecting the host from tissue damage. These immunological checkpoint molecules have modulated T cell responses to self-proteins, persistent infections, and tumor antigens. A few of them, including but are not limited to PD-1, CTLA-4, Lymphocyte activation gene 3 (LAG3; or known as cluster of differentiation 223 [CD223]), T cell immunoglobulin and mucin-domain containing-3 (TIM-3), T cell immunoreceptor with immunoglobulin and ITIM—immunoreceptor tyrosine-based inhibitory motif—domain (TIGIT), and B and T lymphocyte attenuator (BTLA; or known as CD272), have been discovered and investigated as targets in cancer immunotherapy. In general, immune checkpoints are membrane proteins expressed in the endoplasmic reticulum (ER) and subsequently transported to the cell surface to perform their inhibitory roles, which requires the protein sorting system to transport them sequentially through the Golgi apparatus secretory vesicles. Glycosylation acts as quality control during surface delivery, ensuring that only mature and functional immunological checkpoints reach the cell surface. Immune checkpoints are internalized and recycled when they reach the cell surface, providing a quick regulatory pathway to control their surface levels. Immune checkpoints can be ubiquitinated and sorted to the proteasome or lysosome for destruction, another critical method for controlling protein levels. The surface level of immunological checkpoints is determined by several biological mechanisms, which affect cell signaling [7]. This section elaborates on the normal regulations and signaling of each immune checkpoints molecules before discussing its involvement in cancer development.

2.1 PD-1/PD-L1 regulations and signaling

PD-1 trafficking in the membrane is regulated by the core fucosyltransferase 8 (fut8) in ER. Upon Tcell activation, PD-1 is internalized, then ubiquitinated by F-box protein 38 (FBXO38) for proteasome degradation or recycled back to the surface with the help of thymocyte selection-associated high mobility group box protein (Tox), thus prolonged PD-1 activity. Additionally, Tox expression induces Tcell depletion in hepatocellular cancer [7, 8]. Besides, another extension of PD-1 activity is caused by FBXO38's low transcriptional level in the TME. Hence, the FBXO38-mediated PD-1 degradation pathway is defective. TCR signaling was the source of FBXO38 downregulation in the absence of concurrent CD28-CD80/86 signaling. CD28-CD80/86 binding provides critical signals for T cell activation in the presence of TCR stimulation. Persistent tumor antigen binding and low CD80/86 expression on cancerous cells might explain the lower FBXO38 expression in tumor-infiltrating lymphocytes (TILs) [7, 9].

Similar to PD-1, its first functionally identified ligand of PD-L1 (also known as B7 homolog 1 [B7-H1] or CD274) is constantly internalized, recycled, or degraded.

Regulation of PD-L1 recycling is managed by CKLF-like MARVEL transmembrane domain containing 6 (CMTM6). Meanwhile, ubiquitination and degradation are regulated by multiple proteins such as cyclin D–CDK4 and the cullin 3–SPOP [10], β -TrCP [11], COP9 signalosome 5 (CSN5) [12], Huntingtin-interacting protein 1-related (HIP1R) [13], and others. Each protein is a druggable target to inhibit PD-L1 accumulation, thereby increasing T cell-mediated cytotoxicity.

Regarding the inhibitory signals following the binding of PD1 to PD-L1 or other ligands, it blocks kinases that play a role in activating T cells through the phosphatase SHP2. Besides, since PD1 inhibition blocks the TCR 'stop signal', this pathway can alter the length of T cell–APC or T cell–target cell interaction [14]. In detail, PD-1 is phosphorylated through immune receptor tyrosine-based switch motif (ITSM) and ITIM. Then, PD-1 binds the Src homology 2 (SH2) domains of SH2-containing phosphatase 2 (SHP2) or SHP1, which initiate its inhibitory effect by suppressing both TCR and CD28 co-stimulatory signaling [7, 15–17]. Moreover, PD-1 signaling also reduces cytokine production (interleukin [IL]-2, interferon [IFN]- α , tumor necrosis factor [TNF]- α), cell cycle progression, and pro-survival Bcl-xL gene expression by interfering with early TCR/CD28 signaling. PD-1/PD-L1 interaction is associated with IL-2-dependent positive feedback and transcription factors involved in effector functions such as GATA-3, T-bet, and Eomes. As signal transduction can only occur during TCR-dependent signaling, PD-1 activity is thus only relevant during simultaneous T cell activation. Mice without the receptor appear healthy at first. Still, they acquire autoimmune disorders such as lupus-like proliferative glomerulonephritis and arthritis, as well as enhanced inflammation after infections at a later age. In humans, genetic variations in the PD-1 region are more likely to suffer autoimmune disorders [18, 19].

2.2 CTLA-4 regulations and signaling

Unlike PD-1/PD-L1, which is constitutively expressed on the membrane, CTLA-4 is primarily stored inside the cytoplasm of resting naïve T lymphocytes. The T cell receptor-interacting molecule (TRIM)/LAX/Rab8 complex and phospholipase D (PLD)/ADP ribosylation factor-1 (ARF1)-dependent exocytosis are required for CTLA-4 trafficking from trans Golgi network (TGN) to the cell surface [20]. Exocytosis of CTLA-4-containing vesicles causes upregulation of CTLA-4 on the cell surface due to stimulatory signals originating from TCR and CD28-B7 interaction. More robust TCR signaling causes more CTLA-4 to be translocated to the cell surface, and this process works in a graded feedback loop. CTLA-4 on the surface is rapidly internalized during normal physiologic conditions, resulting in relatively low expression. The clathrin-associated adaptor complex (AP-2) interaction to the unphosphorylated YVKM motif promotes rapid CTLA-4 internalization, which is then either destroyed in the lysosome or returned to the cell surface through LPS responsive beige-like anchor protein (LRBA). Besides, CTLA-4 in TGN may also be transported to the lysosome for destruction through AP-1 binding [7, 21, 22].

The intrinsic signaling of CTLA-4 that dampens T cell immune response has been widely contested with no agreement [23]. However, both CTLA-4 and CD28 interact with the identical ligands, CD80 (B7-1) and CD86 (B7-2). Because CTLA-4 has a 20-fold higher binding affinity than CD28, the intrinsic inhibitory signal rises once CTLA-4 outcompetes CD28, even if CTLA-4 is activated later [24, 25]. In addition to T cell response intrinsic inhibition, CTLA-4 is hypothesized to decrease extrinsic T cell signaling. For example, CTLA-4 suppresses CD80/86 expression on APCs via trans-endocytosis or by increasing tumor growth factor β (TGF β), which in turn

suppresses CD80/86 expression [26]. CTLA-4 is phosphorylated when it binds to its ligands, activating phosphoinositide 3-kinase (PI3K) pathways leading to dephosphorylation of the CD3 chain, decreasing the TCR's signaling potential. CTLA-4 also prevents T cells from proliferating by inhibiting IL-2 transcription. Additionally, CTLA-4 stimulates the production of indoleamine 2,3-dioxygenase (IDO) in dendritic cells via CD80/86 ligation, resulting in T cell suppression [27].

2.3 TIM-3 regulations and signaling

TIM-3 is expressed on both T cells and innate immune cells. Four ligands have been identified: carcinoembryonic antigen cell adhesion molecule 1 (Ceacam1), C-type lectin galectin9 (Galectin9), high-mobility group box 1 (HMGB1), and non-protein ligand phosphatidylserine (PtdSer). Ceacam1 is a transmembrane protein that interacts in *cis* and *trans* directions. Ceacam1-TIM-3 *cis* binding induces TIM3 surface expression in T cells while *trans* binding inhibits the effector T cell causing exhaustion and maintaining T cell tolerance [28]. TIM-3 binding to both Ceacam1 and galectin-9 results in the release of Bat3, a TIM-3 signaling pathway inhibitory regulator, from its binding location on the Tim-3 cytoplasmic tail [29]. The other ligands, HMGB1, primarily modulate innate immunity like dendritic cells (DC). In DCs, HMGB1 is required for nucleic acid trafficking into endosomal vesicles, a fundamental step in sensing tumor-derived stressors or pathogen-associated molecular patterns and initiating host defenses against malignancies or pathogen infections [30].

TIM-3 is more related to co-stimulatory proteins induced in activated T cells than to a dominant inhibitory protein like PD-1; thus, TIM-3 signaling remains a matter of debate. As checkpoint proteins, TIM-3 is a repressor of IFN- γ -secreting CD4⁺ Th1 and CD8⁺ T cells. These findings confirmed that inhibiting TIM-3 might correct the defective phenotype of T cells in vivo. In contrast, TIM-3 lacks a conventional ITIM or ITSM in its intracellular domain and lacks structural features that facilitate the recruitment of inhibitory phosphatases. Rather than that, both murine and human TIM-3 cytoplasmic tails include five conserved tyrosine residues, two of which, Y₂₅₆ and Y₂₆₃ in mice (Y₂₆₅, Y₂₇₂ in humans), have been demonstrated to be crucial for coupling to downstream signaling pathways. Y₂₅₆ and Y₂₆₃ in TIM-3's C-terminal tail interact with Bat3 in the absence of ligand-mediated TIM-3 signaling. Bat3 binds the catalytically active form of Lck in this state, resulting in the formation of an intracellular molecular complex with TIM-3 that retains and maybe enhances T cell signaling while repressing TIM-3-mediated cell death and exhaustion [31, 32]. TIM-3 activation on exhausted effector T cells is closely attributed to PD-1 expression, confirming the functional relationship between TIM-3 and PD-1 throughout the development of T cell exhaustion [33]. Concomitant therapy of anti-TIM-3 and anti-PD-1 is significantly more successful in these models, resulting in more significant tumor regression than either TIM-3 or PD-1 inhibition alone. TIM-3 inhibition in the setting of adaptive resistance to PD-1 treatment may be a useful way to treat individuals who develop resistance to anti-PD-1 therapy. This therapy regimen may be particularly beneficial for malignancies with resistance and immune escape from PD-1 inhibition [34, 35].

2.4 TIGIT regulations and signaling

Like CTLA-4 and CD28, TIGIT and CD226 can interact with identical ligands, CD112 and CD155. TIGIT is a co-inhibitory receptor, while CD226 is a co-stimulatory

receptor. Nevertheless, TIGIT possesses a higher affinity to its ligands than CD226; thus, TIGIT can inhibit co-stimulation signals by outcompeting CD226 ligands binding. TIGIT can bind directly to CD226 *in cis*, disrupting its homodimer formation and co-stimulatory activity [36, 37].

TIGIT's signaling is mostly studied in natural killer (NK) cells and activated CD4 and CD8 T cells. The cytoplasmic region of TIGIT comprises an ITIM motif and an immunoglobulin tail tyrosine (ITT)-like motif. Several studies demonstrate that tyrosine (Tyr₂₂₅) phosphorylation in either the ITIM or ITT-like motif is required for TIGIT's inhibitory action in human NK cells. According to Liu et al. (2013), the ITT-like motif recruits Src homology domain-containing inositol phosphatases (SHIP1) via cytosolic adaptor proteins Grb2. Recruited SHIP1 then suppresses phosphatidylinositol 3-kinase (PI3K) and mitogen-activated protein kinase (MAPK) signal to abolish NK cell function. Furthermore, TIGIT signaling can modulate the IFN- γ production of NK cells via the NF- κ B pathway. In this context, β -arrestin 2, another TIGIT adaptor, is involved in phosphorylating TIGIT and then inhibits TNF receptor-associated factor 6 (TRAF6) autoubiquitination, hence inhibiting NF- κ B activation and suppressing IFN- γ production [38–40].

2.5 LAG3 regulations and signaling

LAG3 inhibits CD4-dependent T cell activity by binding to MHC-II due to being structurally homologous with four extracellular immunoglobulin superfamily-like domains. Other investigations demonstrated that LAG3's inhibitory activity is not dependent on CD4 competition, but rather LAG-3 inhibited T cells responding to stable peptide-MHC-II by transducing inhibitory signals via its intracellular domain. Thus, LAG-3 may act more selectively, allowing tolerance to dominant autoantigens to persist [41, 42]. Alternatively, LAG3 can interact with another ligand like Galectin3 in TME and mediate the suppression of CD8 T cells [43]. Besides, liver sinusoidal endothelial cell lectin (LSECtin) can bind to LAG3 in human melanoma, causing tumor growth by abolishing IFN- γ production and proliferation of tumor-specific T cells [44]. Lastly, fibrinogen-like protein 1 (FGL1) was recently discovered as a novel LAG3 ligand. FGL1 is typically produced in trace amounts into the bloodstream by the liver. However, overexpression of FGL1 has been observed in some human malignancies. Inhibiting the interaction between FGL1 and LAG3 by monoclonal antibodies improves T cells' anticancer activity [45].

The signal transduction mechanism of LAG3 is regulated by two transmembranes, a disintegrin and metalloproteinase domain-containing protein 10 and 17 (ADAM10 and ADAM17)-mediated cleavage. TCR signaling enhances ADAM10 and ADAM17 cleavage activity, releasing sLAG3. The function of sLAG3 remains controversial as some studies consider this does not have a biological process, while the others state that sLAG3 allows effective T cell proliferation and function [46]. Besides, sLAG3 affects monocyte differentiation into macrophages and DCs, which have decreased immunostimulatory capacity [47].

2.6 BTLA regulations and signaling

BTLA and CD160 inhibit T cell activity via the same ligand, herpesvirus entry mediator (HVEM). BTLA-HVEM is an example of crosstalk between two superfamilies in which the ligand is a member of the TNF/TNFR superfamily. However, HVEM interaction with members of the TNF superfamily LIGHT (Lymphotoxins, Inducible,

competes with herpes simplex virus (HSV) Glycoprotein D for HVEM, expressed by T cells) produces a co-stimulatory signal on B and T cells. Hence, HVEM may be considered as a molecular switch that enables co-signaling between stimulatory and inhibitory T cells. Additionally, signaling between HVEM and its ligands appears to interact bidirectionally. The cis interaction between BTLA and HVEM inhibits the trans-ligation of HVEM by LIGHT and thus inhibits HVEM stimulatory signaling triggered by LIGHT binding [7, 48, 49].

Regarding the inhibitory signaling of BTLA, it follows the mechanism of PD-1/PD-L1 involving ITIM and ITSM to recruit SHP1/SHP2 [50]. In B-chronic lymphocytic leukemia (B-CLL), both HVEM and BTLA are overexpressed. This co-expression of HVEM and BTLA in CLL cells implies that an unsuccessful autocrine inhibitory loop is triggered. In addition, BTLA is typically downregulated during the development of human CD8⁺ T cells to effector cells. However, BTLA expression was more significant in melanoma-specific CD8⁺ T lymphocytes specialized for tumor antigens (TA). Despite effector differentiation, BTLA expression remained persistent, confounding T cell proliferation and IFN- γ production. Thus, BTLA may function similarly to PD1 as a T-cell inhibitory receptor in TME [51].

3. Immune checkpoints dysregulation affecting cancer cells

Recent studies have established that immune checkpoint molecules drive cancer growth via various anticancer strategies. The first one is the overexpression of immune checkpoints in cancer cells, immune cells, or the surrounding environment leading to incapacities of the tumor-specific immune response. Subsequently, immune checkpoints can interfere with metabolic pathways and deplete nutrients needed by immune cells. Lastly, immune checkpoints cripple cancer-specific immune responses by collaborating with regulatory T cells. This section deliberates each strategy thoroughly to get insight into how to combat those actions.

3.1 Overexpression of immune checkpoints favoring tumor growth

Accumulating evidence showed that several immune checkpoint molecules are overexpressed not only on the surface of cancer cells but also in T cells, Tregs, or even in TME. Here, we thoroughly describe how the immune checkpoint is upregulated and then inhibits antitumor activity. PD-1/PD-L1 are overexpressed on the surface of many cancer cells. Several proinflammatory mediators, which are secreted by activated T cells (types I and II IFN- γ , TNF- α , IL-10, and IL-4) or produced in TME (GM-CSF and VEGF), upregulate PD-L1 expression in the cancer cells resulting in suppression of PD1⁺ T cells activity. Moreover, cancer cells commonly carry altered PTEN (phosphatase and tension homolog deleted on chromosome ten)—PD-L1 suppressor gene—which may activate the S6K1 gene, resulting in a significant increase in PD-L1 mRNA to polysomes, which promotes PD-L1 mRNA translation and plasma membrane expression [6]. In pancreatic cancer cells, PTEN gene deletion influences PD-L1 expression at the translational level by activating the PI3K/AKT downstream mTOR-S6K1 signaling pathway, thereby increasing PD-L1 production and T lymphocyte apoptosis [52, 53].

Furthermore, amplification and translocation of CD274 on chromosome 9p24.1 have been associated with elevated expression of PD-L1 in Hodgkin's lymphoma, small cell lung cancer (SCLC), non-small cell lung cancer (NSCLC), lymphoma,

Epstein-Barr virus (EBV)-positive gastric cancer, and oral squamous cell carcinoma (OSCC). In SCLC, chromosomal rearrangements produce CD274 amplification without changing the open reading frame. It is found in various organs, but it is most commonly found in activated T and B lymphocyte cells, dendritic cells, monocytes, and other types of TCs. The CD274/PD-L1 gene is highly conserved, with homologs discovered across the vertebrate lineage (from *Danio rerio* to Primates), implying its wide range of functions. The CD274/PD-L1 promoter retains CpG methylation sites in the 5' untranslated region (UTR) and exon 1, but translation begins in exon 2 [54, 55]. JAK2, which encodes Janus kinase 2, an upstream kinase that controls PD-L1 expression, is also present on chromosome 9p, with a high alternation rate. The JAK family has been shown to contribute to PD-L1 upregulation by raising PD-L1 RNA expression through amplification and mutation. Because of the increased activity of the Janus kinase2 (JAK2) signal transducers and activators of transcription (STAT) signaling pathway, PD-L1 expression rises. DNA double-strand breaks (DSBs) consistently activate STAT signaling via the ataxia-telangiectasia mutant (ATM)/ATM- and ataxia-telangiectasia-related (ATR)/checkpoint kinase 1 (Chk1) kinases, leading to PD-L1 expression increase. Moreover, structural changes in CD274's 30 UTR boost protein production and improve cancer-immune evasion in human malignancies [55].

PD-L1 induction has also been associated with inflammatory stimuli such as IL-1b, IL-4, IL-6, IL-10, IL-12, IL-17, IL-27, tumor necrosis factor- α (TNF- α), and transforming growth factor- β (TGF- β). Among the several soluble inflammatory agents, IFN- γ is the most important in promoting PD-L1 expression. IFN- γ is a proinflammatory cytokine primarily generated by T and NK cells. IFN- γ attaches to its receptor, the interferon-gamma receptor (IFNGR), activating the JAK-STAT signaling pathway via STAT1. As a result, it increases the expression of transcription factors, particularly interferon-responsive factors (IRFs). IRF1 is a critical downstream signaling molecule of STAT1 that causes IFN-induced PD-L1. Other proinflammatory agents, IL-4 and TNF- α , have a synergistic impact on the activation of PD-L1 in renal cell carcinoma (RCC) via activating signaling molecules such as NF- κ B, I κ B, and STAT6. In dendritic cells and monocytes, blocking PD-L1 was associated with decreased IL-10 levels. Furthermore, IL-10 levels on Tyro3, Axl, and Mer (TAM) were closely connected to PD-L1 expression. In monocyte-derived macrophages, IL-12 upregulates PD-L1 expression, but in THP-1-derived macrophages, it downregulates PD-L1 expression. In monocytes, IL-17 is involved in the induction of PD-L1. IL-17 and TNF- α activate NF- κ B signaling in prostate cancer and NF- κ B and ERK1/2 in colon cancer, respectively, and upregulate PD-L1 expression. PD-L1 expression in dendritic cells is upregulated by IL-1b and IL-27. Furthermore, IL-27 activates phospho-STAT1 and phospho-STAT3 to enhance PD-L1 expression [54, 56].

Meanwhile, CTLA-4 is often constitutively overexpressed on Tregs and has been demonstrated to alter Tregs-mediated immune control. In multiple myeloma patients, FOXP3 and CTLA-4 genes from bone marrow samples were considerably overexpressed [57]. Another sample from peripheral blood mononuclear cells (PBMC) of breast cancer patients showed significantly higher mRNA expression of FOXP3 and CTLA-4 than healthy individuals [58]. Taken together, these results indicated the pivotal role of CTLA-4 in the accumulation of immunosuppressive Tregs in TME, leading to repression of anti-tumor immunity.

Regarding TIM-3 overexpression, it is induced by cytokine stimulation, especially in NK cells. TIM-3 is also extensively expressed on tumor-infiltrating lymphocytes. Similar to its expression pattern during persistent viral infection, TIM-3 is generally co-expressed with PD-1 and represents the most dysfunctional T cell subgroup. TIM-3

overexpression in human malignancies, particularly on immune cells, might be a predictive biomarker for a range of cancers. TIM-3 expression on CD4⁺ and CD8⁺ T lymphocytes was enhanced in individuals with hepatitis B virus-related hepatocellular carcinoma (HCC). TIM-3⁺T cells were replicative senescent and exhibited senescence-related surface and genomic markers. Furthermore, the quantity of tumor-infiltrating cells in TIM-3⁺ was inversely linked with HCC patient survival [59].

Furthermore, LAG3 is mainly expressed in activated T and natural killer (NK) cells, and it has been identified as a marker for CD4⁺ and CD8⁺ T cell activation. Increased LAG3 expression on T cells was observed in combination with other inhibitory receptors such as PD-1, TIGIT, TIM-3, CD160, and 2B4 under pathological conditions such as chronic inflammation or in TME, resulting in T cell exhaustion and reduced cytokine release. In melanoma and colon cancer, LAG3 expression was identified in tissue-infiltrating lymphocytes and peripheral Tregs, tumor-involved lymph nodes, and inside the tumor tissue itself. LAG3 was found on tumor-infiltrating Tregs in patients with head and neck squamous cell carcinoma and non-small cell lung cancer [60].

Similar to other checkpoint molecules, TIGIT is also significantly expressed on Tregs taken from PBMC of cancer patients, and it is further elevated in the TME. Increased TIGIT expression in Tregs is coupled with hypomethylation and FOXP3 binding at the TIGIT gene, distinguishing Tregs from activated effector CD4⁺ T cells. Furthermore, the Fap2 protein from *Fusobacterium nucleatum*, an anaerobic Gram commensal bacteria linked to colorectal cancer, binds directly to TIGIT but not CD226 to suppress NK cells and T cell-mediated tumor response. These findings imply that the gut microbiota modulates innate immune responses via TIGIT [61].

3.2 Immune checkpoints mediating metabolic reprogramming in TME

Due to cancer cells' resource intake and vascularization defects, TME is typically deficient in nutrients and oxygen. Cancer cells' increased need for glucose promotes competition in the TME, which has a detrimental effect on surrounding cells, such as immune cells. Immune checkpoint proteins have been shown to modulate the metabolic energetics of tumor cells, TME, and the tumor-specific immune response, resulting in metabolic reprogramming of both cancerous and immune cells. For instance, CD80 (B7-1) activated the mTOR kinase in naïve CD8⁺ T cells via the PI3K and STAT4 pathways in solid tumors. mTOR signaling is required to promote glycolysis via hypoxia-inducible factor-1 α (HIF-1 α) and protein synthesis for supporting cancer cell growth. This activation shifts nutrition balance, and cancerous cells outcompete the immune cells, then evading immune surveillance [62, 63].

Because amino acids are the building blocks of proteins, their availability is critical for tumor development. At the same time, immune cells need amino acids to differentiate and perform their effector activities, hence regulating tumor formation. Given this, a greater knowledge of how each cell species use amino acids in the TME looks critical for successfully stimulating anti-tumor immunity. Tryptophan deficiency impairs CD8⁺ T cell functions and enhances CD4⁺ Tregs cell functions, resulting in immunosuppression mediated by the CTLA-4 and PD-1/PD-L1 pathways. The effects are achieved mechanistically by activating the stress response kinase GCN2, which inhibits mTORC2 and its downstream target AKT [64, 65]. The other amino acids, such as glutamine and arginine, are also extensively consumed by the tumors and directly impoverish T cells, leading to the development of immunosuppressive TME [66]. Additionally, tumors may

produce and accumulate toxic compounds like aerobic glycolysis byproduct (lactate) in TME, leading to local acidification. Lactate acidosis and hypoxia can activate HIF-1 α and then upregulate PD-L1, further inhibiting T-cell responses specific to tumors. Besides, an acidic condition in the surrounding tumors environment suppresses cytokine production (IFN- γ) and limits the activity of T cell cytotoxic, NK cells, and dendritic cells [66, 67].

In contrast to the effector T cells, glucose deprivation may exert a negligible effect on intratumoral Tregs and lactic acid found in the TME may offer nourishment, thus supporting the immunosuppressive function of Tregs [68]. In addition, Tregs differentiation and recruitment is also supported by kynurenine, a metabolite produced from tryptophan through indoleamine 2,3 dioxygenase (IDO)-catabolization in TME [69]. Furthermore, hypoxia and fatty acids production may facilitate Tregs accumulation, thereby favoring its suppressive function [70].

3.3 Interaction between immune checkpoints and Treg cells

Another immune checkpoint favoring cancer growth strategy is its interaction with Tregs cells either by the expression on Tregs surface or inducing Tregs population and function. Treg cells function in the immune system to regulate and suppress other effector T cells. These cells are responsible for the homeostatic process of the immune system to maintain its unresponsiveness to self-antigens and protect the body from autoimmune reactions or excessive inflammation [71]. However, in this context, the interaction of two immunosuppressive mechanisms is critical in cancer survival from immunosurveillance and progression.

Almost all of the immune checkpoint molecules discussed in this chapter, except BTLA, are expressed in Tregs [72]. CTLA-4 is expressed constitutively on Tregs and induced on effector T cells when activated. CTLA-4 deficiency in Tregs was shown to affect their suppressive effects in animal models. Upon TCR stimulation, CTLA-4 is constitutively recruited on the Tregs cell surface, allowing continuous transendocytosis signaling. Hence, Tregs (CD4⁺ Foxp3⁺) can outperform activated conventional T cells (CD4⁺ Foxp3⁻) [73]. Subsequently, downregulation of B7 ligands on APCs leading to diminished CD28 co-stimulation is another way by which Tregs are hypothesized to govern effector T cells [74, 75].

In tumor tissue of non-small cell lung cancer (NSCLC) patients, the PD-L1 expressing CD25⁺ CD4⁺ (PD-L1^{hi}Tregs) population is higher than in blood or normal tissue. Interestingly, PD-L1^{hi}Tregs also correlated with PD-1⁺ CD8 [76]. In another cancer, highly expressed PD-L1 glioblastoma cells can induce Tregs expansion and maintain its immunosuppressive through PD-1/PD-L1 stimulation. Disrupting the PD-L1/PD-1 axis could target two immunosuppressive mechanisms: inhibition of signaling due to PD-1/PD-L1 ligation and stimulatory proliferation of Tregs cells, which indirectly promotes immunoresistance of high PD-L1 cancers. Thus, Tregs abundance may be a predictive biomarker for patients likely to react to anti-PD-1/anti-PD-L1 therapy or monitor treatment response [77].

Multiple immune checkpoints protein can coexpress and accumulate on the T cell surface, thus increasing dysfunctionality. On CD8⁺ TILs, it is found that TIGIT is coexpressed with TIM-3, PD-1, and LAG-3 [78]. Although, further investigation is needed to show whether these pathways synergize and whether coblockade is becoming a more efficient immunotherapeutic approach.

4. Future challenges and applicability of immune checkpoint inhibitors

Immunological tolerance is normally maintained so that the immune system can recognize and distinguish between self and non-self antigens or neoantigens. Although the immune system is expected to protect the host from exposure to non-self antigens, its robust effector mechanism allows to reverse the attack and disrupt the homeostasis of the immune system. Immune checkpoints, which have gained notoriety as possible cancer therapy targets, are essential immunoregulatory processes found throughout the body. Dysregulation of immune checkpoints promotes tumor cell evasion and plays a significant role in cancer pathogenesis. Therefore, several monoclonal antibodies have been made to block the interaction between ligand and receptor of immune checkpoints, enhancing host immunologic competence against tumors. The list of immune checkpoints inhibitors (ICI), which gained Food and Drug Administration (FDA) approval or are in ongoing clinical trials, is comprehensively summarized in [79]. However, only a tiny proportion of patients respond meaningfully to these therapies due to the signaling complexity and overlapped pathways as mentioned above. Thus, new routes and compounds are being investigated to enhance therapeutic responsiveness and applicability. In clinical practice, the difficulties in treating cancer patients revolve on eliminating the tumor and alleviating symptoms such as pain, fatigue, nausea/vomiting, cough, and diarrhea. Then, concomitant use of medications is negligible and generates new threats for drug interaction such as analgesics [80], steroids [81], antibiotics [82], or many others. Moreover, the use of ICI is often associated with immune-related adverse effects (irAEs). A retrospective study reported that among 1091 patients receiving ICI therapy, 487 (44.63%) patients experienced adverse effects. The most common is fatigue (13.9%), then dermatologic irAEs (12%), endocrine-related irAEs (9.89%), gastrointestinal toxicities (8.4%) and hepatotoxicities (4.94%) [83].

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Conflict of interest

The authors declare no conflict of interest.

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Chapter 4

Pattern Recognition Receptor-Mediated Regulatory T Cell Functions in Diseases

Ece Oylumlu, Goksu Uzel, Lubeyne Durmus, Meric Tas, Damla Gunes and Ceren Ciraci

Abstract

The advent of new technologies in gene expression, immunology, molecular biology, and computational modeling studies has expedited the discovery process and provided us with a holistic view of host immune responses that are highly regulated. The regulatory mechanisms of the immune system lie not only in weakening the attacker directly but also in fortifying the defender for the development of an efficient adaptive immune response. This chapter reviews a comprehensive set of experimental and bioinformatic studies designed to deepen the current knowledge on the regulatory T cells (Tregs) in the context of Pattern Recognition Receptors (PRRs). Initially, we examined both membrane-bound Toll-like Receptors (TLRs) and C Type Lectin Receptors (CLRs); and cytosolic NOD-like Receptors (NLRs) and RIG-I like Receptors (RLRs) in Tregs. Then, we revisited the disease conditions associated with regulatory T cells by emphasizing the essential roles of PRRs. Expanding our knowledge and strategies on the regulatory mechanisms are likely to provide our best chances for long-term disease control and maintenance of homeostasis.

Keywords: pattern recognition receptors, regulatory T cells, NLRs, TLRs, CTLs, RLRs, disease

1. Introduction

Regulatory T cells (Tregs) are a subtype of T cells that are responsible for the maintenance of homeostasis and tolerance to self-molecules. They mediate their action by suppressing the T cell proliferation, and cytokine productions; thereby preventing autoimmunity [1]. In this sense, Tregs can be both helpful to the host by alleviating the immunopathology, and immune system related tissue damages and unfortunately can also be harmful to the host by sabotaging the properly induced immune responses against pathogens [2]. Therefore, harnessing Treg mechanisms could be an efficient therapeutic approach to treat some distinct diseases, including infectious diseases, asthma and allergies, and cancer [3].

It is established that immune cells rely on the germ-line encoded pattern recognition receptors (PRR) that recognize common structural motifs shared by pathogens

called pathogen-associated molecular patterns (PAMPs), and also recognize cellular stress and death via molecules known as damage-associated molecular patterns (DAMPs) to initiate inflammation and activate tissue repair mechanisms [4]. As much as the efficacy of PRRs in executing an immune response is critical for the host, it can also be the reason for unintended responses. Fortunately, understanding of how PRRs drive these responses has expanded enormously in the last few decades. In this chapter, we compile the available data using the open-source databases and the current knowledge in an attempt to discern the layers of complex mechanisms from a regulatory T cell standpoint.

2. The expression profiles of Pattern Recognition Receptors (PRRs) in regulatory T cells (Tregs)

2.1 Membrane-bound Toll-Like Receptors (TLRs)

Toll-like receptors (TLRs) have critical roles in the initial defense of innate and adaptive immunity [5]. TLRs which are type I integral membrane receptors have three domains: The N-terminal domain (NTD), which is located either on the outside of the cell membrane or in endosomes, a single helix transmembrane domain that is in the center, and the C-terminal domain (CTD), which is located in the cytoplasm. The N-terminal ectodomains contain a conserved 19–25 tandem leucine-rich repeat (LRR) region leading to the recognition of PAMPs and DAMPs. NTD also contains glycan moieties to bind ligands from different pathogens. On the other hand, the CTD contains the toll-IL-1 receptor (TIR) homologous domain, which enables the interaction with downstream adaptor proteins for signal transduction and thus, activation of the signaling pathway [6–8]. To date, 13 members of the mammalian TLRs have been identified. 10 members of this receptor family are expressed in humans (TLR1–10), while 12 members are expressed in mice (TLR1–9, TLR11–13). Each TLR can recognize different PAMPs from various pathogens. TLRs divided into two classes according to their localization: cell surface and intracellular [4, 5]. TLR1/TLR2 (triacyl lipopeptides), TLR4 (lipopolysaccharide), TLR5 (flagellin), TLR2/TLR6 (lipoproteins), TLR10 (bacterial 23S rRNA) are expressed in the cell membrane and TLR3 (dsRNA), TLR7/TLR8 (ssRNA), TLR9 (unmethylated CpG DNA), TLR11 (flagellin or profilin-like molecule from *T. gondii*), TLR12 (profilin from *T. gondii*), and TLR13 (bacterial 23S rRNA) are expressed in endosomal membranes [4]. TLRs are important for the proper functioning of Tregs because they directly mediate the pathogen sensing. Tregs have higher expression levels of TLR4, TLR5, TLR7, and TLR8 as compared to the effector T cells in humans; however, especially TLR2, TLR4, TLR5, and TLR8 activation has different effects on the differentiation, expansion, and proliferation of Tregs [9]. Although their numbers increased, Tregs lost their suppressive function when treated with PAM3Cys to activate TLR2 signaling, along with T cell receptor (TCR) and interleukin 2 (IL2) stimulation in order for Treg differentiation and function [10, 11]. In this study, the immune response was suppressed neither *in vitro* nor *in vivo* in mice who underwent acute infection, as Tregs were not activated by the induction of the TLR2 signaling pathway [9]. However, when the TLR2 ligand was removed, Tregs' suppressive functions were recovered [11]. MyD88 is an adaptor protein located downstream of TLR2 signaling. Additionally, the effects of TLR2-MyD88 signaling pathway were examined in Tregs isolated from MyD88 deficient mice, and a reduction in suppressive functions of Tregs in the absence of MyD88 was

reported [5, 9]. Suppressive functions of Tregs were induced by cell-contact mechanisms and secretion of TGF β and IL10, which are immunosuppressive cytokines, without an increase in the number of Tregs [11].

Unlike TLR2, LPS induced TLR4 enhanced the suppression effect owing to the increase in FOXP3 expression in both human and murine Tregs. In fact, LPS not only increased the number of Tregs, but also increased the expression of activation markers in cells [12]. As for TLR5, the suppression capacity of CD4 + CD25+ Tregs increased as a result of TLR5 activation by flagellin [13]. TLR8, on the other hand, has been shown to abundantly express in Tregs and upon stimulation with TLR8 ligand, the suppressive function of Tregs was abolished but it had no effect on the Tregs proliferation [14]. Lastly, studies have revealed that TLR9 ligand CpG oligodeoxynucleotide induced proliferation of both effector T cells (Teff) and Tregs and partly inhibits the suppressive activity of regulatory T cells in rats. This combined effect of TLR9 ligand is likely to reinforce the adaptive immunity by not only expanding effector cells but also by mitigating the suppressive activity of regulatory T cells [15]. Taken together, multiple studies suggest that the suppressive properties of regulatory T cells with respect to their proliferation and cytokine production capacities may differ depending on the induction and the differential expression of different TLRs in regulatory T cells (**Figure 1**).

By examining the open-source databases of immune cell-specific gene expression profiles, we evaluated the results from published literature for TLRs in Tregs and compared their expressions among all available immune cell types. TLRs did not display a Treg specific high expression across the datasets we examined [16–18]. The DICE database generated by Schmiedel *et al* contains *RNA-seq* data of 13 immune cells including naive and memory Tregs (and two ex vivo activated cell types) collected from peripheral blood mononuclear cell fraction of 91 healthy human donors. We used this dataset for a detailed search in Tregs. Expression patterns of TLRs in Tregs are shown as boxplots (**Figure 1A and B**). Although TLRs had relatively low expression profiles, TLR1, TLR2, TLR5, and TLR6 are the ones with the most prominent representation and differential expression in Tregs (**Figure 1C and Table 1**). Interestingly, TLR1, TLR2, and TLR5 had higher expression in naive Tregs than memory Tregs, whereas TLR6 expression was higher in memory Tregs than naive Tregs. Additionally, this dataset presents the sex-biased transcripts for immune cell types. For example, TLR1 in naive Tregs were revealed as one of genes having female bias [16].

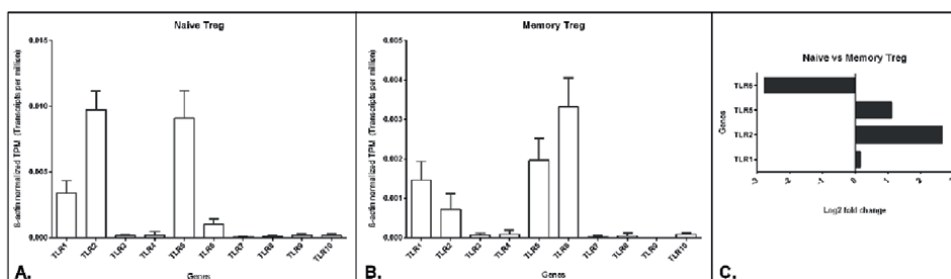


Figure 1. TLR expression profile in naive Tregs and memory Tregs: Expression of TLRs in A: naive (CD3+, CD4+, CD25 high, CD45RA+, CD127low); B: memory (CD3+, CD4+, CD25 high, CD45RA-, CD127low) regulatory T cells. C: Differentially expressed genes in between two Treg populations. Expression of genes reported as TPM was normalized to β -actin (TPMgene/TPM β -actin) for individual representation of naive and memory Tregs. Results are depicted as bar plots in GraphPad Prism.

	Biotype	Naive treg mean expression (TPM)	Memory treg mean expression (TPM)	Log 2 fold change	Adjusted p-value
TLR1	Protein coding	7.18	6.1	0.16	0.017
TLR2	Protein coding	14.71	2.27	2.66	6.90E–233
TLR5	Protein coding	15.46	6.59	1.12	6.90E–35
TLR6	Protein coding	1.08	6.31	–2.78	6.50E–251

Table 1.

Differentially expressed toll-like receptor family members in naïve and memory tregs, p-values (<https://dice-database.org/>).

2.2 Membrane-bound C-type lectin (CTLs) receptors in tregs

C-type lectin receptors (CLRs) also belong to the family of pattern recognition receptors (PRRs) which recognize PAMPs and induce innate immune responses [19]. CLRs comprise a variety of receptors including selectins, collectins, proteoglycans, and lymphocyte lectins. This receptor family possesses at least one structurally homologous carbohydrate recognition domain (CRD), also known as C-type lectin-like domain (CTLD), that determines the carbohydrate specificity [20]. Based on the protein location site on the cell membrane, CLRs are categorized as transmembrane receptors and secretory receptors [21]. Upon ligand recognition by CLRs, most of them are able to induce intracellular pathways and caspase-recruitment domain-containing domain protein 9 (CARD9) pathway, which are vital, and their dysregulation or malfunctioning may result in critical infections in humans and mice [22, 23].

CLRs are expressed on antigen presenting cells (APCs), such as dendritic cells (DCs) and macrophages, and play essential roles in antigen uptake and presentation. In this regard, they are divided mainly into two subgroups: type I and type II CLRs. Two subsets of transmembrane CLRs can be classified based on their CRDs; type I and II. Type I CLRs are mannose receptor family (MR) and DEC-205, whereas type II CLRs are sialoglycoprotein receptor family, DC-associated C-type lectin 1 (dectin-1) and macrophage galactose C type lectin (MGL) [24]. MGLs are able to recognize particularly terminal α and β N-acetylgalactosamine (GalNAc or Tn) residues from filovirus, helminths, bacteria, and tumor-associated antigens in humans [25]. Human counterparts of MGL in mice are MGL1 and MGL2, which are expressed on DCs [26] and activated macrophages [27]. The potency of human MGL was shown by Napoletano *et al.* as an adjuvant for designing novel anticancer vaccines because MGL engagement led to the increased antigen presenting potential in DCs and enhancement in antigen-specific CD8⁺ cell activation [28]. Dectin-1 is another type II C-type lectin receptor, which is involved in the antifungal immunity by recognizing β -1,3-glucans in the cell wall of several pathogenic fungi. Dectin-1 is able to induce several responses including phagocytosis, through spleen tyrosine kinase (Syk)/CARD9 pathway, which results in the cytokine production [29, 30]. Besides innate immunity, dectin-1 is also capable of triggering adaptive immune responses. For instance, curdlan activated dectin-1 in DCs, skewed the T cell polarization into Th17 and Th1

CD4⁺ T cell subsets in mice *in vitro* [31]. Finally, C-type lectin receptor CD69 have been shown to control T cell development and homeostasis in mice along with miR155 as both CD69 and miRNA155 were simultaneously regulated to ensure a balanced immunity [32].

Due to lack of studies focusing on CLRs in Treg populations, we used the DICE database to evaluate the expression profiles of CLRs in naive and memory Tregs collected from PBMC fractions of healthy donors. As described in **Figure 2A** and **B**, among all CLRs with low expressions, CLEC4A (DCCR) is the one with higher representation in both cell types. Even though CLEC7A (Dectin 1) had low expression in both cell types, it was the only differentially expressed gene (**Figure 2C** and **Table 2**). Taken together, CLRs did not have a notable expression profile in Tregs, thus our analysis is in agreement with previously reported data [16–18].

2.3 Cytosolic NOD-like receptors (NLRs) in regulatory T cells

Nucleotide binding oligomerization domain (NOD)-like receptors (NLRs) are a family of cytoplasmic PRRs that are known to drive the initial innate immune responses. There are 22 NLR members in human and 34 in mice [33], and they are characterized by a C-terminal domain of leucine rich repeats (LRRs) which senses PAMPs and danger molecules (DAMPs); a central NACHT domain that facilitates NLR oligomerization; and an N-terminal signaling domain [34]. The NLR members have been classified in 5 subfamilies based on their N-terminal domain: i) NLRA (CIITA), which contains acidic transactivation domain; ii) NLRB (NAIP) subfamily having an N-terminal baculovirus inhibition of apoptosis repeat (BIR) domain; iii) NLRC subfamily that contains caspase activation and recruitment domain (CARD) and allows direct interaction of NLR family members; iv) NLRP subfamily that bears a pyrin domain (PYD); and v) NLRX subfamily that has a mitochondria-targeting sequence required for its trafficking [34]. Some of the NLR members including NLRP1, NLRP3, NLRP6, NLRP7, NLRP12, and NLRC4 are reported to assemble large multimeric protein complexes called “Inflammasomes” which regulate the activation of caspases-1 [35, 36]. The signaling pathway where the assembled inflammasome activates pro-caspase-1 into its catalytically active form is generally

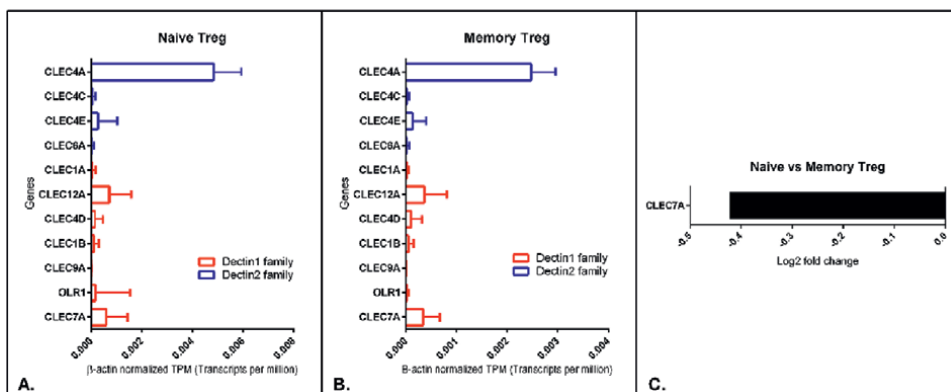


Figure 2. C type lectin expression in naive Tregs and memory Tregs; Expression of CLRs in A: naive (CD3⁺, CD4⁺, CD25^{high}, CD45RA⁺, CD127^{low}); B: memory (CD3⁺, CD4⁺, CD25^{high}, CD45RA⁻, CD127^{low}) regulatory T cells. C: Expression of genes reported as TPM was normalized to β -actin (TPM_{gene}/TPM β -actin) for individual representation of naive and memory Tregs. Results are depicted as bar plots in GraphPad Prism.

	Biotype	Naive treg mean expression (TPM)	Memory treg mean expression (TPM)	Log 2 fold change	Adjusted p-value
CLEC7A	Protein coding	2.05	2.44	-0.42	0.031

Table 2.

Differentially expressed C type lectin receptor family members in naive and memory tregs, p-values. (<https://dice-database.org/>).

referred to as the canonical inflammasome whose activation requires two steps: transcription and oligomerization. The first step is regulated by innate immune signaling, primarily by TLR signaling, and/or cytokine receptors such as TNF which leads to the production of biologically inactive pro interleukin-1 β (IL1 β), IL18, and NLR transcription via nuclear factor- κ B (NF- κ B) activation. The second step leads to inflammasome oligomerization and eventually caspase-1 activation which, in turn, results in IL1 β and IL18 processing and secretion [37]. Biologically active IL1 β and IL18 promote inflammatory and antimicrobial responses and activate different helper T cell subsets such as Th1 and Th17 cells [38]. Although NLRs activation leads to numerous signaling cascades which subsequently initiate the appropriate immune responses including the regulation of B and T cell functions [39], studies focusing on NLRs especially in Tregs are limited. Hence, utilizing open-source datasets, we evaluated the expression patterns of NLRs in Treg populations. Firstly, to address whether there is a Treg specific NLR expression, we compared 28 and 29 cell types studied by Ota *et al.*, and Monaco *et al.*, respectively and showed that there is no NLR specifically expressed in Tregs [17, 18]. Based on the current database, NLRC5 and NLRP1 appear to have higher expression levels in memory Tregs among 13 immune cells included by the DICE database. Next, we examined the data obtained from this database for NLR expression by focusing on Tregs separately (**Figure 3**). As detailed in **Figure 3A** and **B**, most NLR family members have low expressions in both I and memory Treg populations. NLRC3, NLRC5, and NLRP1 have higher expression levels than the rest of the NLRs in both cells. Interestingly, Schmiedel *et al.* listed NLRP2 transcripts as sex-biased (toward females) in both Treg populations [16]. Several NLRs are detected to be differentially expressed naive and memory Tregs are compared with one another (**Figure 3C** and **Table 3**). CIITA, NOD2, NLRC5 expressions were significantly higher in naive Tregs, while NLRP6 has a relatively higher differential expression profile than the remaining NLRs in memory Tregs. Critical roles, if any, of NLRs' expressional diversity within and in between Treg populations might need further investigation.

Apart from these, studies concentrating on NLRP3 and NOD2 roles in directing (Treg) differentiation and function demonstrated that NLRP3 negatively regulates Treg differentiation in an inflammasome-independent manner via translocation to the nucleus and subsequently interacting with Kpna2 [40]. Of note, immunoprotective roles were reported for NLRP3 inflammasome in controlling the Th1/Th17 immunity against fungal infection of pulmonary paracoccidioidomycosis by suppressing the expansion and migration of Tregs in mice [41]. In addition to NLRP3, NOD2 has been shown to get activated by muramyl dipeptide (MDP), resulting in NF- κ B translocation to nucleus in primary human FOXP3+ T cells thereby protecting from death receptor Fas-mediated apoptosis [42]. Finally, MDP-stimulated migration of Tregs has been shown to suppress the Th17 cells in the lungs of influenza A virus-infected

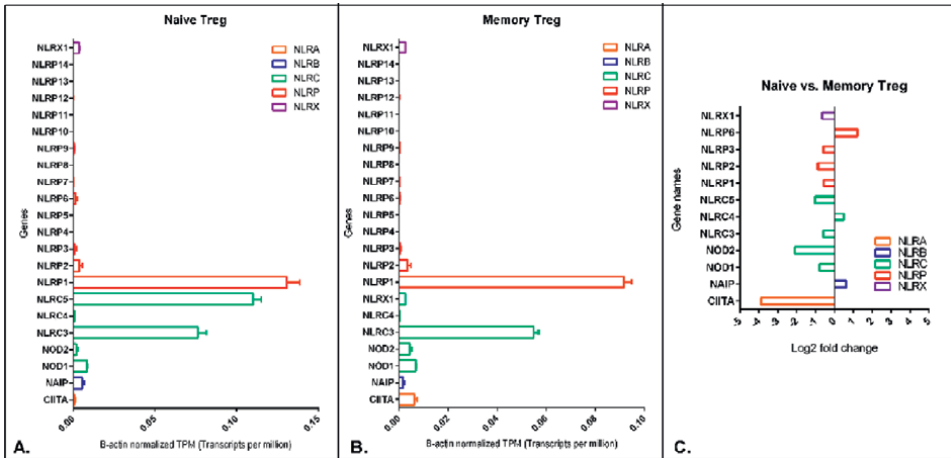


Figure 3. NLR expression profile in naive Tregs and memory Tregs: Expression of NLRs in A: naive (CD3+, CD4+, CD25 high, CD45RA+, CD127low); B: memory (CD3+, CD4+, CD25 high, CD45RA-, CD127low) regulatory T cells. C: Expression of genes reported as TPM was normalized to β -actin (TPM_{gene}/TPM β -actin) for individual representation of naive and memory Tregs. Results are depicted as bar plots in GraphPad Prism.

mice [43]. Together, these results suggest that the control of inflammation during fungal and viral infections is mediated by Tregs, with the contribution of NLRs.

2.4 Cytosolic retinoic acid-inducible Gene (RIG-i) like receptor

Type I interferons are proven to be indispensable during viral infections for their ability to generate an antiviral state. Although they are expressed at low levels, they are induced during the course of an infection which is detected by the presence of the foreign nucleic acids [44]. One example for such sensors is retinoic acid-inducible gene (RIG) I like receptors (RLR) whose activation results in type I interferons [45, 46]. RLRs sense viral RNA in the cytosol. The RLR family comprises three proteins: i) RIG-I; ii) melanoma differentiation-associated antigen 5 (MDA-5); and iii) laboratory of genetics and physiology 2 (LGP2) [47]. All these RLRs share a common structure including a central helicase domain responsible for ATP hydrolysis to unwind RNA and a C-terminal regulatory (CTR) domain adjacent to the helicase core. The CTR domain aids to distinguish the self RNAs from the foreign RNA fragments within the cellular environment. Added to these domains, RIG-I and MDA-5 have N-terminal caspase activation and recruitment domains (CARDs) that are required for downstream signaling through the interaction with CARDs of CARD containing adaptor proteins. Dissimilar to RIG-I and MDA5, LGP2 lacks the CARD domain. Instead, LGP2 is of importance to regulate the RIG-I and MDA5 directed antiviral responses [48–50].

To investigate the RLR expressions in Treg cells, we used the expression data from the DICE database (Figure 4). Similar to other PRRs, we did not observe a Treg specific expression of RLRs. As depicted in Figure 4A and B, RLRs have similar expression patterns among their members, DDX58 (RIG1) having a relatively higher expression trend as compared to IFIH1 (MDA5) and I8 in both naive and memory Tregs. Next, we listed the differentially expressed genes (Figure 4C and Table 4). Interestingly, Schmiedel *et al.* identified IFIH1 (MDA5) transcripts to have

	Biotype	Naive TREG mean expression (TPM)	Memory treg mean expression (TPM)	Log 2 fold change	Adjusted p-value
CIITA	Protein coding	1.6	16.65	-3.89	8.50E-262
NAIP	Protein coding	20.72	13.32	0.62	1.10E-09
NOD1	Protein coding	16.61	26.42	-0.79	2.90E-116
NOD2	Protein coding	3.1	11.2	-2.1	5.90E-169
NLRC3	Protein coding	168	237.03	-0.61	7.40E-50
NLRC4	Protein coding	1.39	0.96	0.5	4.40E-09
NLRC5	Protein coding	222.01	418.41	-1.03	1.50E-81
NLRP1	Protein coding	272.66	376.61	-0.57	6.90E-54
NLRP2	Protein coding	8.35	14.42	-0.88	7.40E-08
NLRP3	Protein coding	1.33	1.81	-0.59	7.00E-08
NLRP6	Protein coding	3.59	1.33	1.21	5.90E-17
NLRX1	Protein coding	6.78	9.8	-0.65	2.20E-19

Table 3.

Differentially expressed NOD like receptor family members in naïve and memory tregs, p-values (<https://dice-database.org/>).

female-biased sex ratios. Data analysis indicates that all RLRs are expressed in Tregs from healthy donors [16].

RLRs, MDA-5, and RIG-I are ubiquitously expressed in the cytoplasm of immune cells including Tregs. Although exhaustion of Tregs following bacterial ligand treatments has been demonstrated [14, 51, 52], the impact of viral infection on Treg derived suppression remained elusive. A study by Anz *et al.* suggested a direct suppression mechanism through the activation of RLRs. In this particular study, regulatory and effector T cells from wild-type and MDA-5 deficient mice were cocultured and infected with encephalomyocarditis virus. Results suggested that MDA-5 deficient Tregs lost their ability to suppress the immune responses when compared with wild type counterparts during the viral infection [53].

Because IFN-beta promoter stimulator (IPS-1) is the main adaptor protein of RLR signaling [54], its influence on the RLR signaling during West Nile Virus (WNV) infection were studied with respect to Tregs using IPS-1 deficient mice. Conceivably, uncontrolled inflammatory responses including the more pronounced immune cell responses and failure in virus neutralization were identified with the lack of Tregs expansion which is a characteristic of WNV infection [55]. Moreover, Xu *et al.* showed the intrinsic suppression ability of RNA stimulated RIG-I in Treg

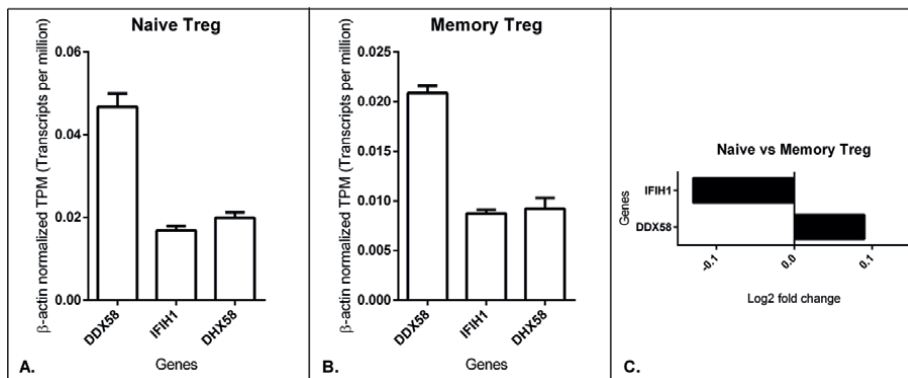


Figure 4. RIG-I expression profile in naive Tregs and memory Tregs: Expression of RLRs in A: naive ($CD3^+$, $CD4^+$, $CD25$ high, $CD45RA^+$, $CD127$ low); B: memory ($CD3^+$, $CD4^+$, $CD25$ high, $CD45RA^-$, $CD127$ low) regulatory T cells. C: Expression of genes reported as TPM was normalized to β -actin ($TPM_{gene}/TPM_{\beta-actin}$) for individual representation of naive and memory Tregs. Results are depicted as bar plots in GraphPad Prism.

	Biotype	Naive treg mean expression (TPM)	Memory treg mean expression (TPM)	Log 2 fold change	Adjusted p-value
DDX58	Protein coding	65.92	58.75	0.09	0.026
IFIH1	Protein coding	29.18	29.88	-0.13	0.0012

Table 4. Expression levels of mRNA for each RIG-I like Receptor family member naive and memory Tregs, p-values (<https://dice-database.org/>).

differentiation in a IFN regulatory transcription factor (IRF)-3 dependent manner [56]. Another study investigated the role of RNA-unprimed RIG-I (apo RIG-I) in Treg differentiation. In contrast to the suppression of Treg differentiation by RNA ligand primed RIG-I, this study showed that apo-RIG-I maintains the Treg/Th17 cell balance [57]. Taken together, ever expanding novel findings from large datasets and state-of-the-art approaches may change the way we evaluate PRRs of Tregs in most bewildering ways.

3. Functionality of regulatory T cells in disease in the context of PRRs

3.1 Regulatory T cells in infections

Immune system as a whole represents a quite complex and interacting vast network of cells and biochemical signals circulating in blood and tissues. Therefore, this complexity necessitates a tight regulation. Tregs maintain the homeostasis by suppressing the immune response after the infection is resolved. As discussed earlier, Tregs can be activated by a variety of pathogens and their suppressive functions may differ depending on the pathogen and the progression of the infection. Not only pathogens, but also non-pathogenic environments with endogenous proteins are essential in regulating Treg responses. Heat shock protein gp96 is a chaperone for

several TLRs including TLR4 and acts as a ligand as well [58, 59]. Tregs suppress the T cell proliferation and cytokine release to protect the host against excessive immune response. There are few aspects still being investigated, especially which receptors are expressed in Tregs and regulate Tregs during viral, bacterial, and fungal infections [60]. In this part of the chapter, we will continue to discuss the Tregs in terms of infectious and non-infectious disease conditions.

3.1.1 Regulatory T cells in bacterial infections

Helicobacter pylori is a Gram-negative bacterium that infects the stomach and is a highly contagious pathogen [61]. Currently, studies covering PRRs in the context of Tregs are rather sparse when it comes to bacterial infections. However, TLR4 inhibition following *H. pylori* has been shown to increase the Foxp3 expression and the CD4⁺CD25⁺Foxp3⁺ Treg cell numbers in the gastric mucosa and enhance the bacterial colonization. However, blocking Tregs led to the limited colonization of *H. pylori*, resulting in the reduced inflammatory responses. This study indicated that the crosstalk between TLR4 signaling pathway and Tregs is crucial for limiting *H. pylori* colonization and suppressing the inflammation of infected mice [62].

3.1.2 Regulatory T cells in fungus infections

Paracoccidioidomycosis (PCM) is an endemic disease caused by the fungus *Paracoccidioides brasiliensis* [63]. In PCM disease, regulation of Treg functions is mediated by PRRs such as TLRs, CLRs, and NLRs and downstream proteins like MyD88 [41, 64–67]. In one study, TLR2-deficient mice had a reduced number of Tregs along with an excessive immune response, suggesting that TLR2 is required for Treg expansion to control the inflammatory response [67]. The study utilized MyD88-deficient mice to further analyze the effect of the downstream effectors of TLR2 signaling pathway in Tregs. The absence of MyD88 resulted in the impaired T cell responses and uncontrolled spread of fungal infection in the murine model of PCM infection [65]. Another study showed that Treg proliferation is decreased in WT mice compared to TLR4 deficient mice, therefore, the level of infiltration of activated T cells and macrophages into the lung increased, resulting in severe infection [64]. Dectin-1 is a CTL receptor involved in the antifungal immune response [68]. In Dectin-1-deficient mice with *P. brasiliensis*, low levels of activated effector/memory CD4⁺ and CD8⁺ T cells along with increased CD4⁺ CD25⁺ Foxp3⁺ Treg levels let the infection spread to tissues, eventually controlling the severity of the disease and causing the increased mortality in mice [66]. Besides the membrane bound Dectin-1 receptor, NLRP3 inflammasome complex mediated the activation and secretion of IL1 β and IL18 have been reported in *P. brasiliensis* infected mice. NLRP3 deficient mice infected with *P. brasiliensis* had an increased Th1/Th17 immune response and reduced Treg response [41].

During candidiasis, a fungal infection mediated by *Candida albicans*, TLR2 is of great importance to control Treg survival. In this study, Netea *et al.* reported that TLR2-deficient mice, but not TLR4, had increased Th1 immune response and a reduced IL10 producing CD4⁺ CD25⁺ Treg population as compared to the WT mice infected with *C. albicans*. Tregs were further stimulated with a TLR2 ligand, peptidoglycan, to assess the significance of TLR2 signaling. Findings from this study highlights the importance of TLR2 signaling in the maintenance of survival, expansion and suppression capacity of Treg and IL10 production in candidiasis [69].

3.1.3 Regulatory T cells in viral infections

One of the immune system mechanisms that are used to protect the host from viral infections is the recognition of viral nucleic acids by PRRs such as TLRs and RLRs [70]. The human genome encodes 10 different TLRs, four of which are responsible for the recognition of viral genome, and these are TLR3, TLR7, TLR8, and TLR9. Interestingly, unlike other TLRs located on the outer cell membrane, they are located in the endosomal membranes and induce downstream molecules through adaptor proteins [4]. RLRs sense viral RNAs in the cytosol. Among RLRs, RIG-I, and MDA5 have RNA helicase activity which give them the ability to bind viral RNA and induce immune response [46]. It is well established in the literature that innate immune cells are activated through these PRRs as the first line of host defense against viral attacks. Activated innate immune cells then phagocytose and process the virus to present it to naive T cells in the draining lymph nodes. Primed T cells eventually differentiate into different types of helper T cells including Tregs [60].

TLR2 and TLR4 have been the focus of numerous studies which emphasized the effects on regulatory T cells in the course of viral infections. During hepatitis C virus infection, Tregs were suggested to suppress the HCV-specific antiviral responses resulting in viral persistence [71, 72]. In a different study by Zhai *et al.*, the core protein of hepatitis C virus (HCVc) in the blood of HCV-infected patients has been shown to induce the proliferation of Tregs which subsequently hampered the CD4⁺ T cell proliferation and IFN- γ production. Since HCVc binds TLR2 on Kupffer cells and dendritic cells, just like the TLR2 agonist lipoteichoic acid, which leading to the similar processes, they proposed that HCVc mediated Treg expansion was TLR2 dependent [73]. In a separate study, the number of Tregs, TLR2 and TLR4 expression levels in the peripheral blood monocytes of chronic hepatitis C patients have been shown to elevate in parallel to viral load [74]. To this end, literature on TLRs seem to report consistent results with respect to Treg regulation.

Additionally, cytosolic RLRs have roles during viral infections. Amphiregulin, known as EGFR ligand, is produced mainly by Tregs in lungs during influenza A virus infection and it is important for tissue protection [75–77]. Interestingly, EGFR signaling has been suggested to suppress RIG-I signaling during viral infections [78, 79]. Thus, amphiregulin produced by regulatory T cells may reduce RIG-I signaling to increase survival during viral infections.

3.2 Regulatory T cells in autoimmune diseases

Autoimmunity can be defined as immunologic aberrations which exclusively exhibit abnormal self-antigen tolerance. PRRs can govern autoimmunity by playing pivotal roles in distinct immunological mechanisms [80, 81]. Autoimmune diseases have been associated with viral, bacterial and, more recently, fungal infections after detection by PRRs because of the reduced number of Treg cells and increased pro-inflammatory cytokines, such as IL17, IL22 and IL23, which drive the differentiation into CD4⁺ Th17 T cells [82].

As we discussed previously in this chapter (**Figure 1**), TLRs are expressed and have functions in adaptive immune cells such as TCR alpha beta cells, TCR gamma beta T cells and regulatory T cells [83]. LPS induced TLR4 in CD4⁺CD25⁺ T cells have been shown to lead to activation and proliferation of Treg cells [12]. Although controversial, other TLRs including TLR5, TLR7, and TLR8 have been shown to express in human and murine CD4⁺CD45⁺ Tregs [11]. With regards to autoimmunity,

using a cohort of MS patients who were helminth-infected or non-infected, Correale and Farez investigated the roles of retinoic acid (RA) and TLR2 in parasite mediated protection in MS patients. Helminth-activated DCs not only inhibited IL-17 and IFN- γ production via autoreactive T cells but also led to the immunoprotection which was attributed to the involvement of TLR2 and RA and the augmentation of CD4⁺CD25⁺FOXP3⁺ Treg cells [84].

Multiple sclerosis (MS) is a central nervous system autoimmune disease [85] which is characterized by demyelination [86]. When healthy individuals were compared to MS patients, it was found that Tregs of the healthy group displayed higher TLR2 expression. Furthermore, the PBMC samples from these two separate groups were stimulated with an agonist of TLR1/2, Pam3Cys, which lowered Treg functions and induced Th17 in MS groups samples [87]. Another example of autoimmune disease is type 1 diabetes mellitus (T1DM) that is associated with pancreatic β cell deficiency which results in abnormal sugar level [88]. High mobility-group box (HMGB) proteins have a role to induce the innate immunity by interacting with nucleic acids and recruiting them to PRRs and they engage receptors for advanced glycation end products (RAGE) [89]. Wild *et al.* showed that HMGB1 enhanced IL-10 levels and prolonged survival of Treg cells [90]. Furthermore, the inhibition of HMGB1 during beta cell mass turnover at an early stage in NOD mice is followed by reduced incidence of diabetes. Additionally, TLR4 and RAGE were shown to be predominant HMGB1 receptors in Treg cells and blockade of either one diminished Treg instability whilst stimulation with recombinant HMGB1 remarkably increased the amount of phosphorylated downstream targets including PI3K, Akt and mTOR in Tregs [91]. Overall, PRRs and Tregs axis in certain immune conditions has been pending to be investigated more elaborately.

3.3 Regulatory T cells in asthma and allergy

Persistent inflammation with the excessive production of cytokines by the immune cells can be harmful which is associated with numerous diseases including asthma and allergy [92]. Asthma is an inflammatory disease of airways which is linked to excessive T helper cell type-2 (Th2) immunity. Both allergic and non-allergic stimuli including house dust mites (HDM), pollens, viral infections and tobacco smoke trigger a cascade of events resulting in chronic airway inflammation which then leads to the airway hyperresponsiveness (AHR) [93]. Th2 cells in the airway release specific cytokines including IL4, IL5, IL9, and IL13; thereby promoting eosinophilic inflammation and immunoglobulin E (IgE) production which in turn, triggers the release of other inflammatory mediators, such as leukotrienes and histamines [94]. One of the hallmarks of asthma pathogenesis is the enhanced Th2 response and the inadequate differentiation and functional defects of Tregs. Baatjes *et al.* has reported that CD4⁺CD25^{high}Foxp3⁺ Tregs were lower in the peripheral blood of the asthma patients than non-asthmatic individuals [95]. *In vivo* animal model studies have shown that IL10 and TGF β secreted by Treg remarkably suppressed the airway inflammation and AHR [96] while blocking IL10 and TGF β worsened the airway inflammation and AHR [97].

Several studies also revealed the involvement of PRRs, especially TLRs and NLRs in asthma susceptibility. Simpson *et al.* firstly discovered the upregulation of TLR2, TLR4, and pro-inflammatory cytokines, IL1 β and IL18, in neutrophilic asthma [98]. Another study reported that TLR2 activation induces Treg and long-term suppression of asthma symptoms in OVA-sensitized mice [99]. Moreover, the important roles of

TLR7 in alleviation of airway inflammation, promoting Th1 immune responses and reversing AHR have been shown [100]. Meng *et al.* reported that TLR7 stimulation suppressed eosinophilic inflammation by reducing Th2 cytokines IL4 and IL5, eotaxin and IgE in numerous animal models of asthma [101]. Yet another study added that treatment with TLR7 agonist R848 induced Treg cell-mediated suppression of asthma symptoms in OVA-sensitized and challenged mice [102].

Although limited, the involvement of inflammasome activation in asthmatic airway inflammations has been studied as well. The prolonged administration of IL1 β , an inflammasome dependent cytokine, has been shown to induce AHR [103]. Also, increased levels of IL1 β in the serum and BALF of asthmatic patients were decreased after glucocorticoids inhalation [104]. Significantly higher inflammasome dependent IL18 levels in the serum of asthma patients were detected [105]. Moreover, Simpson *et al.* reported the elevated expression of the NLRP3 inflammasome in patients with neutrophilic asthma [106]. Another recent study using HDM-induced mouse models of allergic airway inflammation reported elevated expression of NLRP3, NLRC4, NLRC5, and caspase-1 genes as well as pro-IL1 β levels in the lungs, while mature IL1 β was not observed which suggested that inflammasome components are upregulated even if they do not form functional inflammasome complexes [107]. Unfortunately, studies as to the effects of inflammasomes on Treg functions in allergy and asthma conditions are limited. One study demonstrated that intranasal stimulation with NOD2 ligand disrupted the generation of Tregs and subsequently induced the development of eosinophil-associated airway inflammation [108]. Altogether, targeting NLRs and inflammasome components can be another potential therapeutic approach for the control of airway inflammation.

3.4 Regulatory T cells in cancer

Countless pathological conditions involve infections and tissue damage leading to chronic inflammation after the activation of PRRs. Innate immunity and PRRs in cancer initiation and progression are extensively studied because PRRs are expressed in different tumor tissues, such as lung, breast, colon, gastric cancer, and melanoma [21, 109]. The PRR activation in cancer cells can stimulate the production of many cytokines, chemokines, hormones, and vascular-promoting factors to induce the formation of an inflammatory tumor microenvironment that promotes the tumor progression [110]. The activation of PRRs on antigen presenting immune cells can induce dendritic cells, tumor-associated macrophages, and B cells for the generation of tumor-specific T cell responses. Tregs are found in tumor microenvironment and are able to suppress anti-tumor immune responses which is required for escaping immune system thereby cancer progression.

Signaling through PRRs results in robust pro-inflammatory responses by promoting antigen presenting cells and orchestrating adaptive immunity against tumor associated antigens [110]. Indeed, PRR ligands can both stimulate tumors and tumor-infiltrating immune cells to secrete cytokines and chemokines which modulate immune cell polarization and reprogramming the tumor microenvironment to reinforce innate and adaptive anti-tumor immunity [111]. Even though the roles of NLRs and RLRs in tumor immunity still largely unknown, TLRs have significant roles in stimulating DC maturation, antigen uptake and presentation, and the differentiation of CD4⁺ T cells. Additionally, Nyirenda *et al.* have reported the reversion of immunosuppressive skills of Tregs upon TLR stimulation and this is especially interesting for cancer research due to their activity in tumor microenvironment [112]. Given what we

know about TLRs and their ligands currently, different TLR agonists have been used in anticancer therapies. Studies on TLR8 have demonstrated that adoptive transfer of TLR8 ligand-stimulated Treg cells reduced the tumor growth in mice [14] by reprogramming Treg glucose metabolism [113]. On the contrary, peritumoral administration of TLR5 ligand flagellin did not affect the growth of murine breast carcinoma D2F2 [114].

Several inflammasome forming NLRs including NLRP1, NLRP3, NLRP6, and NLRC4 may both have protective and detrimental roles in tumor development by their modulation of innate and adaptive immunity, apoptosis and differentiation [115]. On one hand, Janowski *et al.* has reported the protective role of NLRC4 in melanoma progression independent of the inflammasome components ASC and caspase-1 [116]. On the other hand, a recent study has shown that in metastatic melanoma and sarcoma models, NLRP3 inflammasome activation increased Treg population while inhibiting both NK and T-cell mediated anti-tumor immunity [117]. Additionally, recent studies demonstrated that NLRP3 inflammasome inhibitor (MCC950) reduced IL1 β production and Tregs in head and neck squamous cell carcinoma mouse model [118]; and NLRP3 inhibitor (OLT1177) reduced melanoma growth and Foxp3⁺ cells in tumor microenvironment, and when given in combination with anti-PD-1 therapy, its efficacy increased as compared to monotherapy [119].

Even though CLRs are expressed by dendritic cells, they trigger distinct signaling pathways which induce the expression of cytokines and ultimately determine the T cell differentiation. There are several CLR agonists or antagonists that can be used as anti-cancer drugs, such as β -glucan as dectin-1 agonists [120]. With this, Osorio *et al.* have shown that a bacterial β -glucan, curdlan, skewed Tregs toward Th17 cells both in *vitro* and *in vivo* using 4 T1 mouse mammary tumor models [121]. Also, another study has demonstrated that LSECtin, a type II transmembrane protein, which belongs to the C-type lectin receptor superfamily inhibited the proliferation of tumor-specific effector T cells and induce more IL10 production from Treg cells [122].

In addition to these, cancer cells may mimic viral infections to activate interferon response pathway, and activation of RLR signaling in cancer cells may trigger cell death, activation of innate immune cells in tumor microenvironment or increased recruitment of adaptive immune cells into poorly immunogenic tumors [123]. RLRs could inhibit growth or induce apoptosis of different types of cancer cells upon recognition of RNA ligands. Jiang *et al.* has noted that intratumoral delivery of SLR14, RIG-I agonist induced strong anti-tumor immune responses through the reduction of CD4⁺ FoxP3⁺ Treg cells and induction of CD8⁺ T lymphocytes and NK cells [124]. In another study, high RIG-I expression in ovarian cancer was associated with increased FoxP3 expression and enriched PD-L1 and PD-1 mRNA expression [125]. Taken together, it is noteworthy that even though cancer disease and tumor microenvironment are highly heterogeneous, findings from completed and ongoing research raise the possibility of new targets for the treatment of cancer.

4. Conclusions

To study infectious and immune system related diseases is specifically difficult due to the genetic diversity of hosts and pathogens, the ever-changing nature of infection as it progresses, and the secession of host responses during the course of infection and the disease progression. Despite these challenges, utilization of more sophisticated, contemporary immunogenetic methods and tools such as single cell sequencing, high

throughput screenings, computational modeling along with the availability of novel *in vivo* disease models, 3D organoid cultures perhaps lead to exciting outcomes for the long-term control of both infectious diseases and non-infectious immune system related diseases. These approaches will eventually lay the foundation of a framework to understand the interactive relationship between PRRs and regulatory T cells.

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Conflict of interest

The authors declare no conflict of interest.


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In healthy humans, effector immune cells are activated by the presence of pathogens. Various signaling pathways coordinate the growth and proliferation of the immune cells to fight the invading pathogen and keep the host healthy. A portion of white blood cells known as regulatory T cells (Treg) help to control the rapid proliferation of effector immune cells including effector T cells as well as antigen-presenting cells to make sure the inflammation is kept in check. When Treg cells are depleted or undergo loss of suppressive functionality, hyperinflammatory disease results. However, Treg depletion can also provoke and enhance tumor immunity. Therefore, targeting Treg cells is a promising approach for both autoimmune disease and cancer immunotherapy. To attenuate or enhance Treg-mediated immune suppression, it is necessary to find a specific molecular marker that can selectively and reliably differentiate between Treg and effector T cells. Further elucidation of the cellular and molecular processes underlying the development and function of regulatory immune cells will help to establish new strategies for the treatment and prevention of immune-mediated disease.

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