Involvement of tumor necrosis factor receptor superfamily (TNFRSF) members in the pathogenesis of inflammatory diseases

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Abbreviations: DC, dendritic cell; GITR, glucocorticoid-induced TNF receptor family-related gene; SLE, systemic lupus erythematosus

Overview

Current therapies for autoimmune diseases are not cures but merely palliatives, aimed at reducing symptoms. For the most part, these treatments provide nonspecific suppression of the immune system and thus do not distinguish between a pathogenic autoimmune response and a protective immune response. Recently emerging evidence not only has indicated the involvement of members of the TNF receptor/ligand superfamilies but also has revealed exciting innovative strategies for the treatment of autoimmune diseases and other chronic inflammatory diseases without depressing the immune response in general. In this review, we will discuss the regulatory mechanisms of TNF receptor/ligand family members, such as HVEM/ LIGHT, 4-1BB/4-1BBL, and GITR/GITRL that regulate T and B cell functions and participate in the process of inflammatory diseases. We will also discuss how intervening in the costimulatory pathways mediated by these molecules might have some potential as a therapeutic approach to immune disorders.

Keywords: autoimmune diseases; inflammation; receptors, tumor necrosis factor; tumor necrosis factor

Introduction

TNF receptor superfamily members have common motifs containing cysteine-rich pseudorepeats in the extracellular domain (Locksley et al., 2001). In contrast to the extracellular domain, the cytoplasmic domain does not share any distinctive motifs or even any significant sequence homology, except that of the death domain-containing members such as Fas, TNFR1, DR3, DR4, DR5, and DR6. At present, more than 20 TNF receptor members have been identified. Members of the TNF receptor superfamily and their ligands are expressed mainly on immune cells. Their immunomodulatory functions have been well established in T-cell-mediated immune responses. These include enhancement of dendritic cell (DC) survival and priming capacity for T cells, optimal generation of effector T cells, optimal antibody responses, and amplification of inflammatory reactions.

The immune response is initiated by presentation of antigen-derived peptides in the complex of MHC by APCs to the T-cell receptor (TCR) of T cells. In this process, the axis of TNF receptor members and their ligands stimulate DCs and T cells in a mutual or unidirectional manner. Current evidence suggests that each member plays a distinct role in the generation of CTL, CD4⁺ type 1 helper T (Th1), or Th2 subsets, even though in some cases, there is redundancy and synergy among members. TNF receptor family members and their ligands are also involved in the effector phase of immune responses to effectively exert their effector mechanism.

4-1BB/4-1BBL in autoimmune diseases

4-1BB is expressed on activated CD4⁺ T cells and CD8⁺ T cells. Recent studies have shown 4-1BB expression and its functions in a variety of cells (Kwon *et al.*, 2000; Kwon *et al.*, 2002). For example, 4-1BB is expressed on natural killer (NK) cells, NKT cells and CD4⁺CD25⁺ regulatory T cells within the lymphoid cell lineage. Myeloid cells, including monocytes, neutrophils, DCs, and eosinophils, can also express 4-1BB. On the other hand, 4-1BB ligand (4-1BBL) expression is restricted on activated APCs, such as DCs, B cells, and macrophages. Importantly, the roles of 4-1BB have been revealed in these cells as well as in T cells that have been the major target for 4-1BB studies (Heinisch *et al.*, 2000; Heinisch *et al.*, 2001; Futagawa *et al.*, 2002; Gavin *et al.*, 2002;

MacHugh et al., 2002; Wilcox et al., 2002a, 2002b)

Two important observations by Shuford et al. (1997) and Takahashi et al. (1999) greatly contributed to understanding of 4-1BB's role in immune responses. The former group demonstrated that 4-1BB signals preferentially induce proliferation of CD8⁺ T cells, and the latter group demonstrated that 4-1BB stimulation markedly increases superantigen-stimulated CD8⁺ T cells in vivo. Two recent reports provided strong evidence that 4-1BB indeed regulates both clonal expansion and survival of CD8⁺ T cells, using elaborate experimental systems (Cooper et al., 2002; Maus et al., 2002). The molecular mechanism for promotion and prolongation of CD8⁺ T cell proliferation and survival by 4-1BB stimulation remains to be clarified but current evidence indicates that it is mediated, at least in part, through increased production of IL-2 and expression of Bcl-x_L, an antiapoptotic BCL-2 family member (Lee et al., 2002; Maus et al., 2002). Studies using 4-1BBL-deficient or 4-1BB-deficient mice also clearly suggest a critical role for the 4-1BB costimulatory pathway in the expansion and differentiation of CTLs against viruses (DeBenedette et al., 1999; Tan et al., 1999; Kwon et al., 2002).

Considering the importance of 4-1BB in the requiation of CD8⁺ T cell response, the manipulation of the 4-1BB costimulatory pathway would be a conceivable immuntherapeutic approach. Indeed, it was shown that the systemic administration of agonistic anti-4-1BB monoclonal antibody was highly effective in eradicating large established tumors (Melero et al., 1997). In influenza virus lung infection, 4-1BB stimulation enhanced the primary CD8⁺ T cell responses by preferentially expanding CD8⁺ T cells that re-cognized nondominant epitopes, accompanied by great increase of cytotoxicity (Halstead et al., 2002). Interestingly, anti-4-1BB-mediated tumor elimination is a complex process that requires CD4⁺ T cells and NK cells as well as CD8⁺ T cells. In this case, it seems that augmentation of the tumor-specific cytotoxicity of CD8⁺ T cells is regulated by anti-4-1BB-stimulated NK cells via their proliferation and IFN-y secretion in response to anti-4-1BB monoclonal antibody (Wilcox et al., 2002b). An observation by Ye et al. (2002) has indicated the existence of another mechanism for tumor eradication by 4-1BB stimulation. They introduced a gene into mouse melanoma tumors that encodes a single-chain Fv (scFv) of anti-4-1BB monoclonal antibody. Using these transfected tumors that enhanced the strength of 4-1BB signaling better than anti-4-1BB monoclonal antibody itself, they demonstrated that both NK cells and CD4⁺ T cells but not CD8⁺ T cells were required for the anti-tumor effect for the scFv specific for 4-1BB. One suggested explanation for this observation is that NK cells are key

effector cells to lyse tumors whose function can be enforced by IFN-y secreted by activated CD4⁺ T cells (Chen, 2002). In sum, two methods to improve costimulation via 4-1BB signals provide a promising strategy to cure poorly immunogenic tumors. One is to use tumor cells expressing cell-bound scFv fragments of anti-4-1BB monoclonal antibody as a therapeutic vaccine or to combine vaccination with tumor antigens with infusion of agonistic 4-1BB monoclonal antibody, which was shown to be effective in breaking immunological ignorance of poorly immunogenic tumors by Wilcox et al. (2002c). Another is to use 4-1BB stimulation to ex vivo expand tumor-specific CTLs for adoptive therapy. A promising system to achieve this goal has been developed by Carl June's group. They showed that artificial APCs, which were transfected by the 4-1BBL gene and were also engineered to be able to coat anti-CD3/CD28 monoclonal antibodies on their cell surface, enabled longterm expansion of bulk CD8⁺ cultures (Maus et al., 2002). Since recent clinical trials have validated the adoptive therapeutic capacity to treat melanoma patients (Dudley et al., 2002, Yee et al., 2002), the approach developed by Maus et al. might provide an invaluable tool to grow tumor-reactive T cells ex vivo.

Less has been known about 4-1BB regulation of CD4⁺ T cells. However, there is accumulating evidence that 4-1BB is implicated in immune responses mediated by CD4⁺ T cells, including alloimmune responses (Blazar et al., 2001, Nozawa et al., 2001) and inflammation (Seko et al., 2001, Sun et al., 2002a). Although there is a controversy regarding the mechanism by which 4-1BB regulates CD4⁺ T cellmediated responses, as with CD8⁺ T cells, signaling through 4-1BB appears to promote cell proliferation and survival of CD4⁺ T cells in vitro (Gramaglia et al., 2000, Cannons et al., 2001, Wen, et al., 2002). Using 4-1BB transgenic mice that constitutively expressed 4-1BB on mature T cells, we have recently demonstrated the involvement of 4-1BB in CD4⁺ T cell responses by regulating the clonal expansion and survival of CD4⁺ T cells in vivo (manuscript in submission).

A critical role of 4-1BB in the CD4⁺ T cell response suggests that intervening in the 4-1BB costimulatory pathway could provide an immunotherapeutic approach to the treatment of inflammatory diseases (Kwon *et al.*, 2002). The first *in vivo* evidence that 4-1BB plays an important role in the inflammatory process has been provided by Seko *et al.* (2001). They have shown that *in vivo* administration of anti-4-1BBL monoclonal antibody (thus blocking the 4-1BB/4-1BBL interactions) significantly decreased the myocardial inflammation induced by coxackievirus B3. Similarly, our recent results have demonstrated that herpetic stromal keratitis (HSK) induced by herpes

simplex virus type 1 (HSV-1) was completely prevented either by deleting 4-1BB (in 4-1BB-deficient mice) or by introducing anti-4-1BB monoclonal antibody (Seo et al., 2003). Puzzlingly, administration of agonistic anti-4-1BB monoclonal antibody resulted in the amelioration of experimental autoimmune encephalomyelitis (EAE), a mouse disease model corresponding to human multiple sclerosis (MS) (Sun et al., 2002a). The mechanism underlying the preventive effect of anti-4-1BB monoclonal antibody for EAE described in this study seems to be that anti-4-1BB monoclonal antibody induces activation-induced cell death of antigen-specific CD4 * T cells, thereby inhibiting effector T cell responses. Importantly, treatment with anti-4-1BB monoclonal antibody was effective in inhibiting the relapse of EAE. The same group of researchers has further proved the therapeutic effect of anti-4-1BB monoclonal antibody for inflammatory diseases by showing that anti-4-1BB monoclonal antibody blocks the disease progression of spontaneous systemic lupus erythematosus (SLE) (Sun et al., 2002b). This had been predictable, since anti-4-1BB monoclonal antibodies abrogate T-cell-dependent humoral immune responses (Mittler et al., 1999), and since SLE is a Th2-mediated autoimmune disease (i.e., autoantibodies are pathogenic).

It has been shown that anti-4-1BB monoclonal antibody can induce the suppression of antigen-specific humoral immune responses in primates (Hong et al., 2000). Thus, the possibility is high that humanized anti-4-1BB monoclonal antibody can be used to cure inflammatory diseases, especially Th2-mediated autoimmune diseases. Before a human clinical trial, it would be needed to understand the mechanisms how strong stimulation of the 4-1BB costimulatory pathway can make an abrogation of the production of antibodies that leads to curing autoimmune diseases. Emerging evidence suggests that the abrogation of antigen-specific humoral immune responses by agonistic anti-4-1BB monoclonal antibody may be due to depletion of antigen-specific B cells (autoreactive B cells in the case of SLE) in an IFN-y-dependent manner (Sun et al., 2002b). According to the studies by Sun et al., treatment of Fas-deficient MRL/lpr mice (naturally prone to SLE) with anti-4-1BB monoclonal antibody induced drastic increase in apoptosis of double-negative T cells and B cells, accompanied by remarkable increase in granulocyte population in their spleens. Neutralization of these mice with anti- IFN-y monoclonal antibody reversed the effect of anti-4-1BB monoclonal antibody. In addition, IFN-y-activated macrophages induced apoptosis of B cells. The proposed mechanisms for anti-4-1BB immunotherapy are diagrammed in Figure 1. In sum, even though it appears that 4-1BB may have several functions that depend on the activation status of the cell and subset

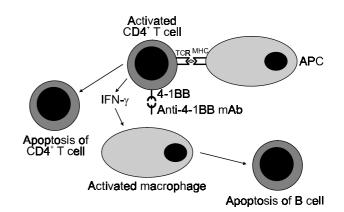


Figure 1. Anti-4-1BB immunotherapy in Th2-mediated inflammatory diseases. If 4-1BB on CD4⁺ T cells are stimulated by anti-4-1BB monoclonal antibody (mAb) during antigen presentation process, CD4⁺ T cells are activated and they secrete a large amount of IFN- γ . IFN- γ strongly activates macrophages, which in turn can produce a death signal for B cells. On the other hand, anti-4-1BB monoclonal antibody induces activation-induced cell death (AICD) of activated CD4⁺ T cells. As a result, the pathogenic antigen-specific CD4⁺ T cells and B cells might be depleted from the body, resulting in curing of Th2-mediated inflammatory diseases.

of cell involved, it is believed that the type of immune response initiated is the most important factor to determine the outcome of 4-1BB stimulation by aqonistic anti-4-1BB monoclonal antibody. In general, agonistic anti-4-1BB monoclonal antibody may turn out to be a valid therapeutic approach to treat Th2mediated autoimmune diseases such as SLE, rheumatoid arthritis, ulcerative colitis, whereas tools to block the 4-1BB costimulatory pathway such as anti-4-1BBL monoclonal antibody may provide immunotherapy to treat Th1-mediated inflammatory diseases such as multiple sclerosis and Crohn's disease, and to prevent rejection of organ transplant (manuscript in submission). Agonistic anti-4-1BB monoclonal antibody may also be used as an immunotherapeutic agent to eradicate tumor or viral infection.

HVEM/LIGHT in atherosclerosis and other inflammatory diseases

Even though its etiology is complex, atherosclersosis is believed to be a chronic inflammatory disease (Ross, 1999). To date, many theories to account for the initiation of atherosclersosis have been proposed: namely, responses to injury, altered cholesterol metabolism, clonal proliferation of smooth muscle cells, autoimmunity against autoantigens which may or may not have a cross-reactivity with pathogen-derived antigens, or inflammation induced by infectious pathogens (Wick *et al.*, 2001, Ludewig *et al.*, 2002). Currently, there is a controversy regarding specific immune responses to antigens present in the vascular wall could initiate atherosclerotic processes. However, there is no doubt that the disease processes are manifested as inflammation involving interactions of a variety of molecules on immune cells. Thus, during the progression of atherosclerosis, immune cells such as T cells and macrophages play a key role in maintaining/perpetuating immune-mediated vascular inflammation, on which process atherogenic risk factors such as altered cholesterol could exert an immunmodulatory effect locally.

Atherosclerosis is initiated by the accumulation of LDL in the subendothelial matrix (Luis, 2000). After modification, the LDL is able to stimulate the overlaying endothelial cells to produce proinflammatory molecules, including adhesion molecules, cytokines, and chemokines, which in turn mediate the entry of monocytes into the artery wall. During the initial inflammation, the recruited monocytes can be differentiated into macrophages and rapidly take up extensively modified LDL to form form cells, a major player of atherosclerosis. Puzzlingly, immunohistochemical studies demonstrate that from the beginning of atherosclersosis, fatty streak lesions contain a significant amount of activated T cells (especially CD4⁺ T cells) as well as macrophages (Waltner-Romen et al., 1998). T cells from atherosclerostic plaques are of polyclonal origin (Stemme et al., 1991) and can respond specifically to oxidized LDL (Stemme et al., 1995). These observations indicate that antigen-specific immune responses are involved in the initiation of atherosclerosis, and also suggest that T cells may contribute to the initiation of atherosclerosis. However, it is possible that bystander T cells could be antigen-independently activated to secrete cytokines (Houtkamp et al., 2001). In general, inflammatory responses are orchestrated by Th1 cells. Activated Th1 cells secrete proinflammatory cytokines, which play a key role in recruiting and activating macrophages and neutrophils. In this regard, even though Th1 cells may not be sufficient to induce atherosclerosis, Th1 cells may be important component of the atherosclerotic process, together with other proatherogenic cells such as macrophages.

CD40, a member of the TNF receptor superfamily, plays a critical role in the process of atherosclerosis (Lutgens and Daemen, 2002). CD40 is expressed on B cells and APCs such as DCs and macrophages and its ligand, CD40L (CD154), is expressed on activated CD4⁺ T cells (Noelle, 1996). Stimulation of DC CD40 by CD40L on activated T cells results in DC activation in such a way that DCs secrete cytokines for T-cell differentiation and also induce upregulation of costimulatory molecules such as B7-1 and B7-2, ligands for CD28, an important costimulatory molecule for T cells. On the other hand, engagement of CD40 on B cells by CD40L on activated CD4⁺ T cells induces enhanced B-cell survival and plasma

cell development with production of high affinity antibody. Further studies on the CD40-CD40L system revealed a broad spectrum of its roles beyond hematopoietic cells, as indicated by its expression on a variety of cells such as fibroblasts, endothelial cells, and smooth muscle cells (Mach *et al.*, 1997). Recent studies have provided evidence that the CD40-CD40L system is key elements for initiating the arterial plaque formation (Mach *et al.*, 1998) and for progressing established atherosclerotic lesions to more advanced unstable lesions (Lutgens *et al.*, 1999; Schonbeck *et al.*, 1999). Importantly, these studies have opened a promising possibility that disruption of the CD40 and CD40L system is a potential therapeutic tool for atherosclerosis.

Recently, our group has demonstrated that HVEM (TNFRSF14), another member of the TNF receptor superfamily, is implicated in atherosclerosis (Lee et al., 2001). HMEM was originally identified as one of many entry receptors for *a*-herpesviruses (Montgomery et al., 1996). HVEM expression is most prominent in lymphoid tissues and cells, including CD4⁺ and CD8⁺ T cells, CD19⁺ B cells, monocytes, DCs (Harrop et al., 1998, Morel et al., 2001), and neutrophils (our unpublished data), even though HVEM has a wide tissue distribution in the mRNA level (Kwon et al., 1997). The ligand for HVEM, LIGHT (TNFSF14), is expressed on activated CD4⁺ and CD8⁺ T cells, and immature DCs (Morel et al., 2000, Tamada et al., 2000a). HVEM stimulation by LIGHT leads to costimulation of T cells (Tamada et al., 2000a) and DC activation (Morel et al., 2000). HVEM plays a role in immune responses such as tumor rejection (Tamada et al., 2000b), graft-versus-host disease (Tamada et al., 2000b; Tamada et al., 2002, Wilcox et al., 2002c), and autoimmune diseases (Shaikh et al., 2002; Wang et al., 2002).

We investigated the potential involvement of HVEM in atherosclerosis (Lee et al., 2001). First, our immunohistochemical analysis showed that HVEM colocalized with HLA-DR and CD69 in regions rich in foam cells of atherosclerotic plaques, indicating that HVEM is specifically expressed on foam cells. Even though we did not identify LIGHT-expressing cells in atherosclerotic plaques, Western blot analysis showed higher levels of LIGHT expression in atheromatous regions, compared with fibrous regions of the plagues. Indeed, HVEM expression is quickly upregulated by monocyte-activating stimuli such as TNF- α or LPS. Further, in vitro-differentiated macrophages expressed HVEM constitutively. Second, we demonstrated that using a monocytic cell line, THP-1, ligation of HVEM with an immobilized anti-HVEM monoclonal antibody induced the secretion of proatherogenic (proinflammtory) cytokines, TNF- α and IL-8, in the presence of IFN-y. We further confirmed IL-8 secretion by stimulation with LIGHT in THP-1. Third, we demonstrated the production of metalloproteases, MMP-1, MMP-9, and MMP-13 and their inhibitors, TIMP-1 and TIMP-2, in THP-1 by HVEM stimulation. We further found colocalization of HVEM with the metalloproteases but not with the two metalloprotease inhibitors in foam cell-rich regions of the atherosclerotic plaques. In sum, our data indicated that HVEM play a role in the progression of atherosclersosis.

Currently, we don't know the mechanism how the HVEM-LIGHT system mediate the atherosclerotic processes. Based on our observations, we want to propose several explanations for the HVEM action mechanism in atherosclerosis. First, HVEM may be involved in the amplification/perpetuation of chronic inflammation by inducing monocytes to secrete proinflammatory cytokines (i.e., TNF- α) and chemokines. It is also possible that like CD40, HVEM expression is not restricted to foam cells in atherosclerotic lesions but could be found in smooth muscle cells and endothelial cells. Thus, signaling via HVEM may induce the production of proinflammatory cytokines and chemokines in a variety of cells during the processes of atherosclerosis. Second, metalloproteases produced by HVEM stimulation in macrophages may contribute to determining the stability of atherosclero-

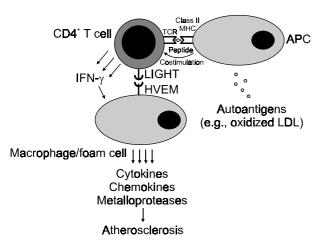


Figure 2. A schematic illustration for the potential contribution of the HVEM-LIGHT system to atherosclerosis. 1) Autoantigens (e.g., oxidized LDL) may be captured and processed by professional antigenpresenting cells (APCs) such as DCs. 2) Processed peptides then may be presented to the T-cell receptor (TCR) of CD4⁺ T cells in the context of MHC class II molecules by APCs. 3) Following TCR stimulation together with costimulation, CD4⁺ T cells will be activated, leading to expression of LIGHT and secretion of IFN- γ in atherosclerotic lesions. 4) LIGHT on activated CD4⁺ T cells then stimulates HVEM on macrophages in an IFN- γ -dependent manner, which will result in the induction of macrophages to produce proinflammatory cytokines, chemokines, and metalloproteases. 5) These inflammatory mediators and enzymes ultimately contribute to amplifying/perpetuating atherosclerotic processes.

tic plaques. Other cytokines such as IL-8 secreted by HVEM stimulation may also be an important factor regulating the stability of atherosclerotic plaques in such a way that IL-8 downregulate metalloprotease inhibitors.

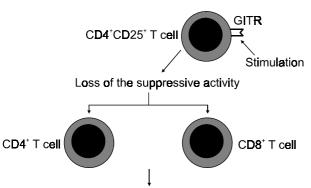
As with other members of the TNF and TNF receptor superfamilies, it is likely that the regulatory mechanism by which the HVEM-LIGHT system mediates the processes of atherosclerosis is complex. Biological activities mediated by HVEM are thought to be regulated by a complex network consisting of other TNF and TNF receptor family members: Natural ligands for HVEM are LIGHT and LTa. LIGHT can also serve as a ligand for LTB receptors (Mauri et al., 1998) and for a decoy receptor called DcR3 (TR6), which can also bind to FasL (Yu et al., 1999). Despite these known facts, a more feasible scenario as to the involvement of the HVEM-LIGHT system in atherosclerosis is that LIGHT on activated atherogenic CD4⁺ T cells may provide macrophages/foam cells with a strong inflammatory signal via HVEM during the development and progression of atherosclerotic lesions (Figure 2). This idea is supported by the studies by Wang et al. (2001). They have demonstrated that constitutive expression of LIGHT on T cells leads to severe inflammatory diseases in various peripheral tissues such as intestine, skin, and kidney. The autoimmune phenotypes in LIGHT transgenic mice is due to hyperactivation of T cells, since LIGHT transgenic mouse T cells exhibit upregulation of activation markers, increased cytokine production, and expanded macrophage and granulocyte population, thereby resulting in splenomegaly and lymphoadenopathy. Currently it is not known whether the tissue destruction observed in the LIGHT transgenic mice is due to nonspecific inflammation by activated T cells or true autoimmunity due to loss of central tolerance (Granger and Ware, 2001). Wang et al. have also provided evidence that the HVEM-LIGHT system is involved in the effector phase of immune responses. When HVEM-Fc fusion protein was treated into 5-to 6-week-old nondiabetic (NOD) mice, which spontaneously develop insulin-dependent diabetes mellitus (IDDM), the development of the disease was significantly prevented. Therefore, blockade of the HVEM costimulatory pathway may be of immunotherapeutic value in preventing acute GVHD or autoimmune diseases.

Since the involvement of the HVEM-LIGHT system in atherosclerosis has just begun to be revealed, further studies will be needed. In particular, meticulous expression analysis of HVEM/LIGHT and related molecules in atherosclerotic lesions, definition of HVEM/LIGHT in atherogenic T cells, and definition of the receptor/ligand pairs in appropriate animal model should provide novel insights into the significance of the HVEM-LIGHT system in atherosclersosis.

GITR/GITRL in inflammation

GITR (glucocorticoid-induced TNF receptor family-related gene) was originally identified by comparing untreated and dexamethasone-treated murine T cell hybridoma cells (Nocentini et al., 1997). Later, human GITR and its ligand were identified by searching an EST (expressed sequence tag) database (Gurney et al., 1999; Kwon et al., 1999a, 1999b). The expression pattern of GITR is similar to that of 4-1BB in T cells. Like 4-1BB, GITR expression is upregulated on T cells, and a high level of GITR is constitutively expressed on CD4⁺CD25⁺ regulatory T cells (McHugh et al., 2002; Shimizu et al., 2002). Initial characterization of GITR functions revealed that the receptor could inhibit TCR-induced apoptosis in the T cell hybridoma cells that were used to clone the GITR gene (Nocentini et al., 1999). This was confirmed in a human T cell line (Gurney et al., 1999). In fact, T cells of GITR-deficient mice exhibited a higher capacity to proliferate in response to TCR stimulation but underwent higher levels of activation-induced cell death (Ronchetti et al., 2002). Therefore, GITR plays an important role in the regulation of T cell proliferation and TCR-mediated apoptosis. It remains to be clarified whether GITR delivers a negative signal for T-cell proliferation or not.

Over the past few years there has been an explosion in the number of publications focused on $CD4^{+}CD25^{+}$ regulatory T cells (Figure 3). One field of regulatory T cell studies is to find a marker for regulatory T cells. A series of gene array analysis have identified surface molecules highly expressed in $CD4^{+}CD25^{+}$ regulatory T cells in comparison with non-regulatory CD4⁺ T cells (McHugh *et al.*, 2002). These include TNF receptor family members such as 4-1BB,



Enhancement of CD4⁺and CD8⁺ T cell responses

Figure 3. A model for GITR action. GITR signals break the immunosuppressive activity of $CD4^{+}CD25^{+}$ regulatory T cells for conventional $CD4^{+}$ and $CD8^{+}$ T cells. As a consequence, $CD4^{+}$ and $CD8^{+}$ T cell response might be enhanced.

OX40, and GITR. By using a different approach, Shimizu et al. (2002) also found that GITR was predominantly expressed on CD4⁺CD25⁺ regulatory T cells. Despite its high levels of expression on CD4⁺CD25⁺ regulatory T cells, like CD25 and CTLA4, there is a limitation of the use of GITR as a satisfactory marker for CD4⁺CD25⁺ regulatory T cells, since GITR is upregulated in conventional T cells upon activation. However, CD4⁺GITR⁺ T cells are equivalent to CD4⁺CD25⁺ regulatory T cells (Shimizu et al., 2002). In vitro studies showed that GITR signals abrogated the suppressive function of CD4⁺CD25⁺ regulatory T cells (Shimizu et al., 2002, McHugh et al., 2002). Furthermore, in vivo administration of anti-GITR monoclonal antibody induced autoimmune gastritis (Shimizu et al., 2002). Therefore, it is clear that stimulation of GITR can break immunological self-tolerance. Since elucidation of the role of GITR in immune responses is in the nascent stage, there are many outstanding questions to be answered. First, it will be needed to be verified whether GITR stimulation can break the suppressive activity of regulatory T cells in vivo. If this proves to be so, blockade of the GITR signaling pathway might be applied for treatment of inflammatory diseases. On the other hand, stimulation of the GITR signaling pathway might be used as a tool to enhance the anti-tumor activity of CTLs. Second, GITR may play a role in conventional T cells in that GITR functions as a costimulatory molecule in those cells (McHugh et al., 2002; Shimizu et al., 2002). Our unpublished results indicate that GITR stimulation increases CD4⁺ T cell responses but not CD8⁺ T cell responses. Moreover, it appears that the receptor differentially regulates the activity of Th1 and Th2 subsets of CD4⁺ T cells. Therefore, it will be interesting to define which branch of immune responses will be regulated by GITR. Finally, GITR may contribute to the development of CD4⁺CD25⁺ regulatory T cells. Even though GITR-deficient mice have the normal development of lymphoid organs and their cell populations (Ronchetii et al., 2002), it will be necessary to examine the population of CD4⁺CD25⁺ regulatory T cells in more details.

Concluding remarks

The evidence is now overwhelming that TNF receptor members participate in the process of inflammatory diseases. This indicates intervening in TNF receptor signals as a therapy of choice for inflammatory diseases, including autoimmune diseases. However, to take full therapeutic advantage of manipulation of the costimulatory pathways mediated by TNF receptor family members, more has to be learned about action mechanisms of action of these molecules.

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