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TRAF Molecules in Inflammation and Inflammatory Diseases

Almin I. Lalani^{1,2} · Sining Zhu^{1,2} · Samantha Gokhale^{1,2} · Juan Jin^{1,3} · Ping Xie^{1,4}

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Abstract

Purpose of Review This review presents an overview of the current knowledge of tumor necrosis factor receptor (TNF-R) associated factor (TRAF) molecules in inflammation with an emphasis on available human evidence and direct in vivo evidence of mouse models that demonstrate the contribution of TRAF molecules in the pathogenesis of inflammatory diseases.

Recent Findings The TRAF family of cytoplasmic proteins was initially identified as signaling adaptors that bind directly to the intracellular domains of receptors of the TNF-R superfamily. It is now appreciated that TRAF molecules are widely employed in signaling by a variety of adaptive and innate immune receptors as well as cytokine receptors. TRAF-dependent signaling pathways typically lead to the activation of nuclear factor-κBs (NF-κBs), mitogen-activated protein kinases (MAPKs), or interferon-regulatory factors (IRFs). Most of these signaling pathways have been linked to inflammation, and therefore, TRAF molecules were expected to regulate inflammation and inflammatory responses since their discovery in the 1990s. However, direct in vivo evidence of TRAFs in inflammation and especially in inflammatory diseases had been lacking for many years, partly due to the difficulty imposed by early lethality of TRAF2^{-/-}, TRAF3^{-/-}, and TRAF6^{-/-} mice. With the creation of conditional knockout and lineage-specific transgenic mice of different TRAF molecules, our understanding about TRAFs in inflammation and inflammatory responses has rapidly advanced during the past decade.

Summary Increasing evidence indicates that TRAF molecules are versatile and indispensable regulators of inflammation and inflammatory responses and that aberrant expression or function of TRAFs contributes to the pathogenesis of inflammatory diseases.

Keywords TRAFs . Inflammation . Inflammatory diseases . TLRs . NLRs . Cytokines . NF-κB . IRFs

Introduction

The tumor necrosis factor receptor (TNF-R)-associated factor (TRAF) family of cytoplasmic proteins was initially identified

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 \boxtimes Ping Xie xie@dls.rutgers.edu

- ¹ Department of Cell Biology and Neuroscience, Rutgers University, 604 Allison Road, Nelson Labs Room B336, Piscataway, NJ 08854, USA
- ² Graduate Program in Cellular and Molecular Pharmacology, Rutgers University, Piscataway, NJ 08854, USA
- ³ Department of Pharmacology, Anhui Medical University, Meishan Road 81st, Shushan District, Hefei, Anhui Province, China
- ⁴ Rutgers Cancer Institute of New Jersey, New Brunswick, NJ 08901, **USA**

as signaling adaptors that bind directly to the intracellular domains of receptors of the TNF-R superfamily [[1](#page-18-0), [2](#page-18-0), [3](#page-18-0)••]. It is now recognized that TRAF molecules are widely employed in signaling by a variety of adaptive and innate immune receptors as well as cytokine receptors [[3](#page-18-0)••, [4](#page-18-0)•, [5](#page-18-0)]. Adaptive immune receptors that can directly recruit TRAF proteins include T cell receptor, CD28, and co-stimulatory receptors of the TNF-R superfamily (such as CD40, BAFF-R, TACI, BCMA, 4-1BB, OX-40, GITR, CD27, CD30, DR3, HVEM, and TNF-R2) [\[3](#page-18-0)••, [4](#page-18-0)•, [5\]](#page-18-0). Innate immune receptors that can indirectly employ TRAF proteins in signaling include Tolllike receptors (TLRs), NOD-like receptors (NLRs), RIG-Ilike receptors, and C-type lectin receptors [[3](#page-18-0)••, [5\]](#page-18-0). Cytokine receptors that can directly or indirectly recruit TRAF proteins include receptors for IL-1 β , IL-2, IL-6, IL-17, IL-18, IL-33, type I IFNs, type III IFNs, GM-CSF, M-CSF, and TGF-β [\[3](#page-18-0)••, [4](#page-18-0)•, [5](#page-18-0)].

Upon ligand engagement, one major role of TRAF molecules is to serve as adaptor proteins in the assembly of receptor-associated signaling complexes, linking upstream receptors to downstream adaptor proteins and effector enzymes [\[3](#page-18-0)••, [4](#page-18-0)•, [5\]](#page-18-0). This is mediated by the C-terminal TRAF domain, a distinct feature of all TRAF proteins except TRAF7 (a figure of TRAF1-7 structures is provided in a previous review [[3](#page-18-0)••]). The TRAF domain is further divided into N-terminal coiledcoil region (TRAF-N) and a C-terminal β-sandwich domain (TRAF-C or MATH domain) [\[2,](#page-18-0) [3](#page-18-0)••, [6\]](#page-18-0). The uniqueness and specificity of the binding of each TRAF molecule to various receptors is mainly mediated by minor structural differences in the TRAF-C domain that recognizes major and minor consensus sequences of the cytoplasmic tails of receptors or their associated adaptor proteins [[7,](#page-18-0) [8\]](#page-18-0). However, a recent study points out that the binding preferences of TRAF proteins may be more complicated than previously appreciated as TRAF molecules also exhibit binding preferences beyond the established core motifs [\[9](#page-18-0)], thus warranting further investigation on this aspect. In addition to their role as adaptor proteins, TRAFs (including TRAF2, 3, 5, and 6) also act as E3 ubiquitin ligases [[3](#page-18-0)••, [4](#page-18-0)•, [5](#page-18-0)]. TRAF-dependent signaling pathways typically lead to the activation of nuclear factor-κBs (NF-κB1 and NF-κB2), mitogen-activated protein kinases (MAPKs: ERK1/2, JNK1/2, and p38), or interferonregulatory factors (IRFs: IRF3, IRF5, and IRF7). Therefore, TRAFs function as both adaptor proteins and E3 ubiquitin ligases to regulate receptor signaling in adaptive and innate immune responses as well as other biological processes [\[3](#page-18-0)••, [4](#page-18-0)•, [5](#page-18-0)].

Because of the prominent importance of the TNF superfamily in inflammation, TRAF molecules were expected to regulate inflammation and inflammatory responses since their discovery as TNF-R-interacting proteins in the 1990s [\[1,](#page-18-0) [2\]](#page-18-0). However, the in vivo functions of TRAFs in inflammation and especially in inflammatory diseases had remained elusive for many years, partly due to the difficulty imposed by early lethality and multiple organ abnormalities of TRAF2^{-/-}, TRAF[3](#page-18-0)^{-/-}, and TRAF6^{-*i*-} mice [3••]. With the creation of conditional knockout and lineage-specific transgenic mice of different TRAF molecules, our understanding about TRAFs in inflammation and inflammatory responses has rapidly advanced during the past decade. Here, we provide an overview of current knowledge of TRAF molecules in inflammation with an emphasis on available human evidence and direct in vivo evidence of mouse models that demonstrate or implicate the contribution of TRAF molecules in the pathogenesis of inflammatory diseases.

TRAF1

Increasing evidence indicates that as a signaling adaptor, TRAF1 regulates inflammatory responses to the proinflammatory cytokine $TNF\alpha$ and microbial ligands of

TLRs [[3](#page-18-0)••, [10](#page-18-0)–[13,](#page-18-0) [14](#page-18-0)••]. Expression of TRAF1 is restricted to the spleen, lung and testis under normal conditions [\[10](#page-18-0), [15,](#page-18-0) [16](#page-18-0)]. As a direct NF-κB target gene, TRAF1 expression is often upregulated by $TNF\alpha$ and other inflammatory stimuli [\[17](#page-18-0)–[20\]](#page-18-0). When expressed in cells, TRAF1 protein regulates inflammation by directly interacting with TNF-R2, TRAF2, TRIF, IKK2, NIK, and ASK1 [[3](#page-18-0)••, [10](#page-18-0), [13](#page-18-0), [15,](#page-18-0) [20](#page-18-0)–[25](#page-18-0)]. Therefore, TRAF1 is able to regulate both canonical and non-canonical NF-κB pathways as well as activation of the MAP kinases (JNK, p38, and ERK) to influence proinflammatory cytokine production and inflammatory responses [[3](#page-18-0)••, [10,](#page-18-0) [13,](#page-18-0) [20](#page-18-0), [22](#page-18-0)–[26](#page-18-0)]. Recent human and animal studies provide evidence implicating TRAF1 in rheumatoid arthritis, lung inflammation, liver inflammation, and atherosclerosis.

Sepsis and Rheumatoid Arthritis Genome-wide association studies first identified single-nucleotide polymorphisms (SNPs) at the TRAF1-C5 locus (encoding TRAF1 and complement component 5) on chromosome 9 as risk factors for rheumatoid arthritis (RA) in human patients [[27](#page-18-0)–[32](#page-19-0)]. It was subsequently found that SNPs of the TRAF1-C5 locus predict the clinical response to anti-TNF therapy in RA patients [[33,](#page-19-0) [34\]](#page-19-0) and that increased serum levels of TRAF1 correlate with disease activity and autoantibodies in RA patients [[35\]](#page-19-0). In particular, the TRAF1/C5 SNP rs3761847 GG homozygote status is associated with an increased risk of death from sepsis and malignancies in RA patients [[36\]](#page-19-0). Interestingly, it was recently revealed that this SNP (rs3761847 GG) leads to reduced levels of TRAF1 protein in monocytes and T cells [\[14](#page-18-0)••]. Monocytes from healthy human subjects with SNP rs3761847 GG of the TRAF1 gene produce increased amounts of pro-inflammatory cytokines in response to lipopolysaccharide (LPS) due to enhanced NF-κB activation [[14](#page-18-0)••]. Mechanistically, TRAF1 inhibits TLR4-induced NF-κB activation by interfering with the linear ubiquitination of NEMO through direct interaction of TRAF1 with three components of the linear ubiquitination (LUBAC) complex, SHARPIN, HOIP, and HOIL-1 [\[14](#page-18-0)••]. Consistent with the negative role of TRAF1 in LPS-induced inflammation observed in human monocytes, $TRAF1^{-/-}$ mice are more susceptible to LPSinduced septic shock [\[14](#page-18-0)••]. Furthermore, in a genetic mouse model of inflammatory arthritis, KRN/I-A(g7) (KxB/N) mice, the production of anti-GPI autoantibody is markedly impaired by TRAF1 deficiency [\[37](#page-19-0)]. These new findings elucidate how this RA-associated TRAF1 SNP could contribute to the increased incidence and severity of sepsis, arthritis, and other inflammatory diseases.

Lung Inflammation TRAF1 has been shown to be involved in lung inflammation with several different mouse models, including intratracheal TNFα-induced inflammation, LPS inhalation-induced inflammation, and allergic lung

inflammation. Intratracheal TNF α -treated TRAF1^{-/−} mice exhibit more severe TNFRI-dependent liver injury due to increased production of TNFα by bronchoalveolar cells, suggesting a negative role of TRAF1 in TNFα-induced lung inflammation [[38\]](#page-19-0). Inhaled LPS induces an inflammatory response that may contribute to the pathogenesis of asthma and other airway diseases. Interestingly, $TRAF1^{-/-}$ mice are deficient in recruiting lymphocytes to the lower respiratory tract after inhalation of LPS, due to decreased expression of ICAM1, VCAM1, CCL17, and CCL20 in the lungs [\[39](#page-19-0)]. Experiments of bone marrow chimeras demonstrate that TRAF1 in resident lung cells, but not hematopoietic cells, is responsible for this phenotype [\[39](#page-19-0)]. Mice lacking TNFR1 but not TNFR2 show a phenotype similar to the TRAF1^{$-/-$} mice, suggesting a positive role of the TNFR1-TRAF1 pathway in the induction of chemokines and adhesion molecules in resident lung cells after LPS inhalation [\[39](#page-19-0)]. Similarly, TRAF1 expressed in resident lung cells is also required for the development of allergic lung inflammation as revealed by adoptive transfer experiments of ovalbumin (OVA)-immune wild type (WT) CD4+ T cells. In response to OVA exposure, $TRAF1^{-/-}$ recipient mice fail to display eosinophilic inflammation and airway hyperresponsiveness in this model of asthma [[40](#page-19-0)]. In sharp contrast, transfer of OVA-immune TRAF1^{$-/-$} T cells into naive WT recipients confers significantly more intense pulmonary inflammation and higher airway hyperresponsiveness following inhaled OVA challenge [[41\]](#page-19-0). This is caused by the T cell-intrinsic bias of $TRAF1^{-/-}$ T cells to produce increased amount of the Th2 cytokines (IL-4, IL-5, and IL-13) in response to antigen stimulation [[41\]](#page-19-0). Biochemical analyses revealed that TRAF1 inhibits the induction of Th2 responses by associating with NIP45 in the cytoplasm and thereby preventing the nuclear translocation of NIP45, a Th2 cell-associated transcription factor [\[41](#page-19-0)]. Therefore, TRAF1 proteins expressed in resident lung cells and T cells play differential roles in lung inflammation.

Atherosclerosis A recent study by Hessler et al. identified a SNP rs2416804 (GC alleles) of the TRAF1 gene as being associated with carotid intima-media thickness, a marker for subclinical atherosclerosis that predicts subsequent clinical cardiovascular events [\[42](#page-19-0)]. TRAF1 expression is significantly upregulated in atherosclerotic plaques of patients with atherosclerosis and also in the blood of patients with acute coronary syndrome [[43](#page-19-0), [44\]](#page-19-0). Consistent with the human evidence, TRAF1 deficiency in mice attenuates atherogenesis and impairs monocyte recruitment to the vessel wall as demonstrated by studies with TRAF1^{-/-}LDLR^{-/-} mice on a high-cholesterol diet [\[44\]](#page-19-0). Bone marrow transplantations revealed that TRAF1 deficiency in both hematopoietic and vascular resident cells contributes to the observed reduction in atherogenesis in mice [\[44](#page-19-0)]. Impaired monocyte recruitment is associated with decreased expression of the adhesion molecules ICAM1 and

VCAM1 on endothelial cells [\[44\]](#page-19-0). Together, the above evidence warrants further investigation of TRAF1 in the pathogenesis of atherosclerosis.

Liver Inflammation and Hepatic Steatosis Xiang et al. recently reported that TRAF1 expression is elevated in the livers of human patients with non-alcoholic fatty liver disease (NAFLD) [\[45](#page-19-0)]. Interestingly, both high-fat diet (HFD)-treated mice and genetic obese mice (ob/ob) exhibit an increase in TRAF1 expression in the liver compared with lean controls [\[45](#page-19-0)]. Palmitate, an inducer of lipid accumulation and insulin resistance in hepatocytes, also increases TRAF1 expression in hepatocytes [[45\]](#page-19-0). Xiang et al. further investigated the role of TRAF1 in insulin resistance, inflammation, and hepatic steatosis using mice with global TRAF1 deficiency or liverspecific TRAF1 overexpression. In response to HFD treatment or in ob/ob mice, TRAF1 deficiency is hepatoprotective, whereas TRAF1 overexpression in hepatocytes exacerbates the pathological development of insulin resistance, inflammatory response and hepatic steatosis. A similar liver protective role of TRAF1 deficiency was also demonstrated in a mouse hepatic ischemia/reperfusion (I/R) injury model by Zhang et al. [[25](#page-18-0)]. Mechanistically, hepatocyte TRAF1 directly interacts with ASK1 to promote hepatic steatosis through enhancing the activation of ASK1-mediated P38 and JNK cascades in response to HFD or palmitate stimulation [\[45](#page-19-0)]. Indeed, overexpression of a constitutively active form of ASK1 in the liver reverses TRAF1 deficiency-mediated amelioration of obesity and insulin resistance, while overexpression of a dominant negative form of ASK1 in the liver reverses TRAF1 overexpression-induced exacerbation of inflammation and hepatic steatosis [[45\]](#page-19-0). Thus, the TRAF1-ASK1 axis acts to induce insulin resistance, inflammation, and hepatic steatosis in response to HFD or palmitate stimulation [\[45](#page-19-0)].

Brain Inflammation and Ischemic Stroke In an experimental I/ R stroke model, TRAF1 expression is markedly induced in the cortex and stratum of WT mice at 6 h after middle cerebral artery occlusion (MCAO)-induced stroke onset [\[24\]](#page-18-0). In cultured primary cortical neurons, oxygen and glucose deprivation also rapidly increases TRAF1 protein levels [[24](#page-18-0)]. Neuron-specific TRAF1 transgenic mice exhibit enlarged inflammatory stroke lesions and detrimental behavioral and neurological dysfunction following MCAO, which is attributable to the enhancement of neuronal apoptosis [[24](#page-18-0)]. Conversely, $TRAF1^{-/-}$ mice have reduced inflammatory stroke lesions and ameliorated behavioral and neurological dysfunction associated with reduced neuronal apoptosis [[24\]](#page-18-0). Mechanistically, TRAF1 directly interacts with ASK1 to induce the MKK4/7-JNK1 pro-apoptotic pathway while inhibiting the Akt-mTOR-CREB pro-survival pathway in neurons [[24\]](#page-18-0). Together, these in vivo studies demonstrate the pathogenic roles of TRAF1 in neurons during ischemic stroke.

TRAF2

TRAF2 is ubiquitously expressed in various cell types and is especially important for inflammation in keratinocytes, macrophages, dendritic cells (DCs), T cells, hepatocytes, epithelial cells, and fibroblasts [[3](#page-18-0)••, [4](#page-18-0)•, [5](#page-18-0), [46,](#page-19-0) [47](#page-19-0)••, [48](#page-19-0)–[50](#page-19-0)]. As a signaling adaptor protein and an E3 ubiquitin ligase, TRAF2 regulates inflammatory responses mediated by receptors of the TNF-R superfamily, TLRs, NLRs, RIG-I, cytokine receptors, S100A8 receptors, and S100A9 receptors [\[3](#page-18-0)••, [4](#page-18-0)•, [5](#page-18-0), [46](#page-19-0), [49,](#page-19-0) [51,](#page-19-0) [52\]](#page-19-0). TRAF2 transduces receptor signals to induce the activation of both canonical and non-canonical NF-κB pathways as well as the activation of the MAPKs (JNK, ERK1/2 and p38) and IRFs (IRF3, IRF5 and IRF7) [\[3](#page-18-0)••, [4](#page-18-0)•, [5,](#page-18-0)[46,49](#page-19-0)]. Intracellular TRAF2 is also required for ER stress-induced inflammatory responses via the IRE1 α -TRAF2-Nur77 signaling axis [[53](#page-19-0)–[55\]](#page-19-0). TRAF2 directly interacts with a variety of receptors, adaptor proteins, and enzymes that regulate inflammation. These include receptors of the TNF-R superfamily, IL-17Rs, IL-15Rα, IFNAR1, EMMPRIN, TRAF3, TRAF5, cIAP1/2, Ubc13, TRADD, TRIF, RIP, Act1, MAVS, SOCS3, TAK1, IKKε, A20, CYLD, MCPIP1, HGK, MLKL, IRE1α, and Nur77, among others [[3](#page-18-0)••, [4](#page-18-0)•, [5](#page-18-0), [46,](#page-19-0) [49](#page-19-0)–[52,](#page-19-0) [54](#page-19-0)–[74](#page-20-0)]. Current human and mouse evidence indicates that TRAF2 plays complex roles in skin inflammation, cardiovascular inflammation, inflammatory bowel diseases, liver inflammation, and autoimmune inflammatory diseases (such as lupus, arthritis, and multiple sclerosis).

Skin Inflammation In primary human keratinocytes, exposure to ultraviolet (UV) light triggers association of TRAF2 with TNF-R1 to induce NF-κB activation and inflammation [[75\]](#page-20-0). In mice, keratinocyte-specific deletion of TRAF2 (K-TRAF2−/[−]) causes epidermal hyperplasia and psoriatic skin inflammation with excessive leukocyte infiltration and apoptotic death in the inflamed area by 15 weeks of age [[76](#page-20-0)]. This phenotype partially depends on TNF-induced apoptosis in keratinocytes, as compound deletion of TNF in K-TRAF2^{$-$ /} mice reduces apoptotic death and delays the development of skin inflammation [\[76](#page-20-0)]. Another essential pathway underlying this phenotype is the constitutive NF-κB2 activation and increased expression of inflammatory molecules observed in TRAF2−/[−] keratinocytes, including M-CSF, IL-23, 4-1BBL, CR1L, and CXCL-16 [[76\]](#page-20-0). Indeed, compound deletion of TNF and NF- κ B2 in K-TRAF2^{-/-} mice prevents the skin inflammation caused by TRAF2 deficiency in keratinocytes [\[76\]](#page-20-0). Interestingly, S100A8 and S100A9, two inflammatory proteins highly upregulated in skin lesions of human patients with atopic dermatitis, are found to bind to receptors named Neuroplastin-β and EMMPRIN, which recruit GRB2 and TRAF2 to induce NF-κB1 activation, keratinocyte proliferation, and skin inflammation [[51](#page-19-0), [52](#page-19-0)]. Consistent with the critical roles of TRAF2 in skin inflammation, mutations of the

TRAF2-deubiquitinating enzyme CYLD are identified in patients with familial cylindromatosis (with benign tumors of skin appendages), and $CYLD^{-/-}$ mice are highly susceptible to chemically induced skin tumors [\[72](#page-20-0)]. Therefore, TRAF2 expressed in keratinocytes plays protective roles in skin inflammation through multiple pathways.

Cardiovascular Inflammation Increasing evidence indicates an important role for inflammation in cardiac hypertrophy and failure [\[77](#page-20-0), [78](#page-20-0)]. TRAF2 expression is upregulated in human atherosclerotic plaques and failing mouse hearts [\[43,](#page-19-0) [79](#page-20-0)]. Two groups independently demonstrated that cardiac-specific TRAF2 overexpression in mice leads to remarkably enhanced cardiac hypertrophy, left ventricular dysfunction, and adverse cardiac remodeling, which are associated with increased activation of NF-κB, JNK and Akt-GSK3 β [\[79,](#page-20-0) [80](#page-20-0)]. It would be interesting to further verify these findings using cardiacspecific TRAF2^{$-/-$} mice and to investigate the roles of TRAF2 in mouse models of atherosclerosis.

Inflammatory Bowel Diseases In humans, the expression of TRAF2 is significantly higher in inflamed and non-inflamed tissues of IBD patients than those in healthy control [\[81,](#page-20-0) [82\]](#page-20-0). TRAF2 expression is also higher in inflamed colonic mucosa tissues than in non-inflamed tissues in patients with Crohn's disease (CD), ulcerative colitis (UC), and nonspecific colitis [\[81](#page-20-0), [82](#page-20-0)]. Moreover, higher expression of TRAF2 has been identified as a prognosis factor of UC relapse [[82](#page-20-0)]. Liu et al. recently reported that TRAF2 overexpression may result from EZH2 downregulation-mediated epigenetic mechanism in IBD patients [[83](#page-20-0)]. In mice, the roles of TRAF2 in colitis have been demonstrated in both germline $TRAF2^{-/-}$ and myeloid cell-specific TRAF2−/[−] (M-TRAF2−/[−]) mice. Germline $TRAF2^{-/-}$ mice spontaneously develop severe colitis and succumb within 3 weeks after birth, which result from TNF α -TNFR1-mediated apoptosis of TRAF2−/[−] colonic epithelial cells and altered colonic microbiota (Fig. [1](#page-4-0)) [[48\]](#page-19-0). In the absence of TRAF2, compromised epithelial barrier allows commensal bacteria to induce the accumulation of IL-10-secreting neutrophils in the bone marrow, peripheral blood, and lamina propria (Fig. [1\)](#page-4-0) [\[84](#page-20-0)]. Combined treatment with neutralizing antibodies against $TNF\alpha$ and IL-10 substantially ameliorates colitis and prolongs survival in TRAF2^{$-/-$} mice [[84](#page-20-0)]. Myeloid cell-specific TRAF2 ablation promotes DSS-induced colitis in mice, which is associated with increased production of proinflammatory cytokines (TNFα, IL-1 β, IL-6, and IL-12) and decreased levels of IL-10 [\[47](#page-19-0)••]. The anti-inflammatory function of TRAF2 is independent of NIK-NK-κB2 and is mediated by elevated protein levels of c-Rel and IRF5 in macrophages [\[47](#page-19-0)••]. Mechanistically, c-Rel and IRF5 are constitutively targeted for K48-linked ubiquitination and proteasomemediated degradation by the TRAF3-TRAF2-cIAP1/2 complex similar to that previously described for NIK [\[47](#page-19-0)••]. Thus,

Fig. 1 Cell- and receptor-specific roles of TRAF molecules in inflammatory bowel diseases. The cell types with direct in vivo evidence of TRAFs in IBDs include macrophages (MØ), DCs, neutrophils, T_H2 cells, T_H17 cells, and epithelial cells (EPC). TRAF molecules (TRAF2, 3, 5, and 6) with anti-inflammatory roles in IBDs are depicted in blue in each specific cell type, and TRAF6 with proinflammatory roles in IBDs is depicted in pink in T_H 17 cells. The dominant TRAF-dependent receptors, TRAF-interacting transcription factors, and TRAF-dependent downstream cytokines and chemokines

TRAF2 plays protective roles against colitis by acting in both epithelial cells and myeloid cells (Fig. 1).

Liver Inflammation Expression of TRAF2 is downregulated during hepatic differentiation of human pluripotent stem cells, and infection with hepatitis B virus (HBV) induces the expression of TRAF2 in normal primary human hepatocytes [[85,](#page-20-0) [86\]](#page-20-0). Studies of mouse models revealed that TRAF2 regulates liver inflammation by inhibiting apoptosis and necroptosis in hepatocytes. Tamoxifen-induced TRAF2 deletion in adult mice leads to increased hepatic necroptosis and rapid lethality, which is delayed by co-deletion of RIPK3 or treatment with blocking reagents for TNF-R1 and IFNAR1 [[50\]](#page-19-0). Hepatic

are shown for each specific cell type as revealed by in vivo evidence obtained from mouse models of IBDs. In addition, TRAF6-mediated regulation of DCs indirectly controls the differentiation of T_H1 and Treg cells, which also contribute to the protective effects of DC TRAF6 against enteritis. The known roles of TRAFs in TCR signaling, the development and homeostasis of iNKT cells and T cell subsets, and the activation of CD4 and CD8 T cells are not included in the figure, as their contribution in IBDs has not been directly tested in vivo in whole animal models.

TRAF2 depletion by siRNA injection in mice exacerbates Fas-induced hepatic apoptosis and accelerates lethality, as TRAF2 mediates K48-linked ubiquitination and degradation of caspase 8 [\[87](#page-20-0)]. Interestingly, hepatocyte-specific deletion of TRAF2 in mice does not alter insulin signaling under normal or HFD conditions, but does attenuate HFD-induced hyperglycemia and obesity due to decreased hepatic gluconeogenesis, resulting in glucagon resistance [[88](#page-20-0)]. In mouse primary hepatocytes, TRAF2 directly promotes glucose production by enhancing glucagon-induced CREB phosphorylation and the expression of PEPCK and G6Pase [[88\]](#page-20-0). Furthermore, specific deletion of TRAF2 from liver parenchymal cells in mice leads to mild and focal spontaneous ductular reaction,

while co-deletion of TRAF2 and RIP in these cells results in spontaneous hepatocyte apoptosis, hepatitis, and hepatocellular carcinoma [\[57](#page-19-0)]. Taken together, TRAF2 plays complex and indispensable roles in regulating hepatocyte survival and function as well as liver inflammation.

Brain Inflammatory Diseases Upregulated expression of TRAF2 is detected in the brains of patients with Alzheimer's disease (AD) and Parkinson's disease (PD) as well as in the hippocampi of patients with mesial temporal lobe epilepsy [\[89](#page-20-0)–[91](#page-20-0)]. Interestingly, the 3′ UTR SNP rs7852970 GG of the Traf2 gene is significantly protective against AD as revealed by SNP association studies [\[89\]](#page-20-0). TRAF2 proteins are present within plaque-associated neurites and some neurofibrillary tangles in human AD brains [[89\]](#page-20-0). However, the causal role of TRAF2 in brain inflammatory diseases has not been demonstrated with in vivo models and needs further investigation.

Autoimmune Inflammatory Diseases In human, both downand upregulated expression of TRAF2 has been detected in peripheral blood mononuclear cells (PBMCs) of patients with systemic lupus erythematosus (SLE) [[92,](#page-20-0) [93\]](#page-20-0). TRAF2 expression is elevated in PBMCs of patients with RA and relapsingremitting multiple sclerosis (MS) [\[94](#page-20-0), [95](#page-20-0)]. Studies of mouse models revealed the critical role of TRAF2 in regulating T cell homeostasis and T cell tolerance, which are essential for controlling autoimmune inflammatory diseases. T cell-specific $TRAF2^{-/-}$ (T-TRAF2^{-/-}) mice display decreased naïve and memory CD8 T cell subsets and NKT cells in the spleen and liver due to reduced sensitivity to IL-15 [[49](#page-19-0)]. TRAF2^{$-/-$} $TNF\alpha^{-/-}$ mice develop an inflammatory disorder characterized by lymphocyte infiltration in multi-organs and accumulation of anti-dsDNA and anti-histone autoantibodies [\[96](#page-20-0)]. The pathogenic TRAF2^{-/-}TNF α ^{-/-}T cells show constitutive NF- κ B2 activation and produce elevated levels of T_H1 and T_H17 cytokines, including IFN γ , IL-17, IL-21, and IP-10 [\[96\]](#page-20-0). Interestingly however, T cell-specific deficiency of HGK, a MAP4K that directly phosphorylates TRAF2 and targets TRAF2 for lysosomal degradation, also leads to systemic inflammation involving multi-organs and insulin resistance in mice, which are associated with increased levels of IL-6, IL-17, and T_H 17 cells [\[74](#page-20-0)]. Therefore, a delicately balanced level of TRAF2 proteins in T cells is required to sustain T cell tolerance, and both increased or decreased TRAF2 protein levels can lead to autoimmune inflammatory diseases [[74,](#page-20-0) [96\]](#page-20-0).

TRAF3

TRAF3 is closely related to TRAF2 in terms of both structure and function [\[5,](#page-18-0) [9\]](#page-18-0). TRAF3 is ubiquitously expressed in various cell types and is pivotal in regulating inflammation in macrophages, dendritic cells (DCs), neutrophils, B cells, T cells, hepatocytes, cardiocytes, osteoclasts, microglia, and neurons (Fig. [2\)](#page-6-0) [\[3](#page-18-0)••, [4](#page-18-0)•, [5](#page-18-0), [47](#page-19-0)••, [97,](#page-21-0) [98](#page-21-0)•, [99](#page-21-0)–[110](#page-21-0)]. Similar to TRAF2, TRAF3 acts as both a signaling adaptor protein and an E3 ubiquitin ligase in inflammatory responses mediated by receptors of the TNF-R superfamily, TLRs, NLRs, RIG-I, and cytokine receptors [[3](#page-18-0)••, [4](#page-18-0)•, [5](#page-18-0), [100,](#page-21-0) [111](#page-21-0)]. TRAF3 has overlapping functions with TRAF2 in inducing the activation of both canonical and non-canonical NF-κB pathways as well as the activation of the MAPKs (JNK1/2, ERK1/2 and p38) and IRFs (IRF3, IRF5 and IRF7) [[3](#page-18-0)••, [5,](#page-18-0) [100](#page-21-0), [111](#page-21-0)]. However, TRAF3 also has distinct roles and unique binding proteins, and therefore cannot be substituted by TRAF2 in inflammation and inflammatory responses. Direct TRAF3-interacting proteins that are important for inflammation include: (1) receptors: members of the TNF-R superfamily that do not contain death domains, NLRP12, and IL-17R [\[3](#page-18-0)••, [5,](#page-18-0) [97,](#page-21-0) [112](#page-21-0)]; (2) adaptor proteins: TRAF2, TRAF5, MyD88, TRIF, RIP, RIP2, MAVS, Act1, STING, and ASC [\[3](#page-18-0)••, [5,](#page-18-0) [113](#page-21-0)–[115](#page-21-0)]; (3) enzymes: NIK, IKKε, TAK1, TBK1, Peli1, A20, DUBA, OTUB1, OTUD7B, USP25, CHIP, MYSM1, PTPN22, Syk, CK1ε, DNA-PKc, and NDR1, among others [\[3](#page-18-0)••, [5,](#page-18-0) [116](#page-21-0)–[131](#page-21-0)]; (4) transcription factors: c-Rel and IRF5 (Fig. [2](#page-6-0)) [\[47](#page-19-0)••]. Increasing human and mouse evidence indicates that alterations in TRAF3 expression or function contribute to the pathogenesis of systemic inflammation, cardiac hypertrophy, inflammatory bowel diseases, liver inflammation, diabetes, bone inflammatory diseases, brain inflammation, and autoimmune inflammatory diseases (such as lupus, arthritis, and multiple sclerosis) (Fig. [2\)](#page-6-0).

Systemic Multi-organ Inflammation We recently investigated the roles of TRAF3 in myeloid cells during inflammatory responses using myeloid cell-specific TRAF3^{$-/-$} (M-TRAF3−/[−]) mice [[98](#page-21-0)•]. We found that myeloid cell-specific deletion of TRAF3 leads to increased serum levels of the pro-inflammatory cytokines IL-6 and IL-12 but decreased serum levels of the anti-inflammatory cytokine IL-10 in response to LPS (TLR4 ligand) or polyI:C (TLR3 ligand) challenge [\[98](#page-21-0)•]. Interestingly, aging M-TRAF3−/[−] mice (15-22 months old) spontaneously develop chronic inflammation often affecting multiple organs, including the liver, spleen, intestines, lung, pancreas, and heart [[98](#page-21-0)•]. These findings point to an indispensable anti-inflammatory role for TRAF3 in myeloid cells.

Cardiovascular Inflammation TRAF3 expression is upregulated in human atherosclerotic plaques and failing human hearts [\[43](#page-19-0),[107\]](#page-21-0). Epigenetic modifications of the *Traf3* gene have been observed in cardiovascular inflammation, including DNA methylation that has been associated with vascular recurrence after ischemic stroke in patients treated with clopidogrel and histone acetylation that has been associated

with cardiac hypertrophy in mice [[132,](#page-21-0) [133](#page-22-0)]. Consistent with human evidence, cardiac-specific TRAF3−/[−] mice exhibit reduced cardiac hypertrophy, fibrosis, and dysfunction [[107](#page-21-0)]. Conversely, transgenic mice overexpressing TRAF3 in the heart develop exaggerated cardiac hypertrophy in response to pressure overload [[107\]](#page-21-0). TRAF3 also promotes an

angiotensin II- or phenylephrine-induced hypertrophic re-sponse in isolated cardiomyocytes [[107](#page-21-0)]. Mechanistically, TRAF3 directly binds to TBK1, causing increased TBK1 phosphorylation and Akt activation in response to hypertrophic stimuli [\[107\]](#page-21-0). The above evidence identified TRAF3 as a key regulator of cardiac hypertrophy.

Fig. 2 Cell-specific roles and signaling networks of TRAF3 in inflammatory diseases. Direct in vivo evidence not only demonstrated the major anti-inflammatory roles of TRAF3 in macrophages (MØ), DCs, neutrophils (NTP), microglia (MG), osteoclast precursors (OP), B cells, and Treg cells but also revealed the pro-inflammatory roles of TRAF3 in hepatocytes, cardiomyocytes, and neurons. The proximal TRAF3-interacting complexes that are critical to inflammatory responses are depicted for each specific cell lineage, with the symbol "-" depicting direct interactions and the symbol "-" depicting indirect connections. The inflammatory disease phenotype of each cell lineagespecific TRAF3 knockout (KO) and transgenic (Tg) mice are also shown, respectively. Spontaneous inflammation or exacerbated inflammatory diseases are depicted in red, and delayed or reduced inflammatory diseases are depicted in green. Evidence shows that the function of TRAF3 in myeloid cells is dynamically modulated according to the metabolic states. In lean mice, TRAF3 plays anti-inflammatory roles in myeloid cells. However, under genetic (ob/ob) or HFD-induced obese state, TRAF3 plays pro-inflammatory roles and promotes metabolic inflammation in myeloid cells. It is also noticed that a delicate balance level of TRAF3 proteins is required to maintain B cell homeostasis and B cell tolerance, as either TRAF3 deficiency or overexpression in B cells leads to systemic autoimmune inflammation in mice. The known roles of TRAF3 in TCR and CD28 signaling, the development and homeostasis of iNKT cells and CD8 memory T cells, and the activation of CD4 and CD8 T cells are not shown in the figure, as their contribution in inflammatory diseases has not been directly demonstrated in vivo in whole animal models.

Inflammatory Bowel Diseases TRAF3 expression is significantly higher in the inflamed colonic mucosa, PBMCs, and plasma in human patients with CD and UC than in healthy controls [\[82,](#page-20-0) [134](#page-22-0)]. In the DSS-induced colitis model, M-TRAF3−/[−] mice exhibit exacerbated colon inflammation with increased levels of IL-1 β, IL-6, TNF, and IL-12, which is mediated by elevated protein levels of c-Rel and IRF5 in TRAF3−/[−] macrophages [\[47](#page-19-0)••]. Mice genetically deficient in NLRP12, a cytosolic NLR protein that directly interacts with TRAF3 and NIK, are also highly susceptible to DSS-induced colitis and exhibit reduced TRAF3 level and increased activation of NF-κB2, ERK, and Akt [\[112\]](#page-21-0). Similarly, mice deficient in PTPN22, a protein tyrosine phosphatase that directly binds to TRAF3 and promotes K63-linked polyubiquitination of TRAF3, show increased severity of DSS-induced colitis due to decreased TRAF3-type I IFN-mediated protection of colonic mucosa [\[126](#page-21-0)]. Furthermore, mice deficient in NDR1, a TRAF3-interacting protein that prevents the recruitment of TRAF3 to the IL-17R-Act1-TRAF6 complex, are resistant to TNBS-induced colitis with decreased IL-17 signaling and IL-17-mediated inflammation in epithelial cells [[130\]](#page-21-0). Thus, TRAF3 plays protective roles in colon inflammation by acting on multiple signaling pathways in myeloid cells and colonic epithelial cells (Fig. [1](#page-4-0)).

Liver Inflammation, Hepatic Steatosis, and Diabetes In humans, TRAF3 expression is decreased in PBMCs of patients with chronic HBV infection and is upregulated in livers of patients with hepatic steatosis or subjected to liver transplantation [[106](#page-21-0), [135](#page-22-0), [136](#page-22-0)]. The in vivo roles of TRAF3 in liver inflammation have been elucidated in several different mouse models. Myeloid cell-specific deletion of TRAF3 markedly attenuates metabolic inflammation, insulin resistance, glucose intolerance, and hepatic steatosis in mice with either genetic (*ob/ob*) or HFD-induced obesity [[103](#page-21-0)]. Hepatocyte-specific TRAF3^{-/−} mice also show ameliorated HFD-induced inflammatory responses, hepatic steatosis, insulin resistance, and type 2 diabetes, while transgenic mice overexpressing TRAF3 in hepatocytes exhibit the opposite phenotype [\[104,](#page-21-0) [136](#page-22-0)]. In response to hepatic I/R injury, hepatocytespecific, but not myeloid cell-specific, TRAF3 deficiency reduces cell death, inflammatory cell infiltration, and cytokine production, whereas hepatic TRAF3 overexpression results in the opposite effects in mice [[106](#page-21-0)]. Mechanistically, glucose directly increases TRAF3 levels in primary hepatocytes, and TRAF3 binds to TAK1 to modulate the NF-κB, JNK, and insulin-AKT signaling cascades in hepatocytes [\[104](#page-21-0), [106,](#page-21-0) [136\]](#page-22-0). Therefore, TRAF3 proteins expressed in both myeloid cells and hepatocytes promote liver inflammatory responses in obesity and I/R settings (Fig. [2\)](#page-6-0).

Bone Inflammatory Diseases TNF and RANKL mediate bone destruction in common bone diseases, such as osteoarthritis and RA, via TRAF3-dependent mechanisms [[108](#page-21-0), [109,](#page-21-0) [137\]](#page-22-0). TNF increases TRAF3 expression in osteoclast precursors (OPs), and RANKL decreases TRAF3 protein levels by inducing lysosome/autophagy-dependent degradation of TRAF3 [\[108](#page-21-0), [109](#page-21-0), [137\]](#page-22-0). Both TNF and RANKL induce more osteoclasts from TRAF3−/[−] OPs, whereas overexpression of TRAF3 reduces osteoclast formation from WT OPs induced by TNF, RANKL, and TNF + RANKL [[109](#page-21-0), [137](#page-22-0)]. OPspecific TRAF3^{-/−} mice have increased osteoclastogenesis and osteoporosis mediated by increased NF-κB1 and NF-κB2 signaling [\[109](#page-21-0)]. In particular, the importance of the noncanonical NF-κB2 signaling is highlighted by the evidence that TNF transgenic (TNF-Tg) mice lacking NF-κB2 p100 exhibit more severe joint erosion and inflammation as well as systemic bone loss than TNF-Tg WT mice [\[108\]](#page-21-0). Furthermore, osteoclast-lineage expression of a mutant form of NIK that lacks its TRAF3 binding domain results in constitutive NF-κB2 activation, osteoporosis, and enhanced inflammatory osteolysis in mice following injection of serum from arthritic K/BxN mice (a model of serum transfer arthritis) [\[138\]](#page-22-0). Thus, TRAF3 expressed in the osteoclast-lineage plays protective roles against bone inflammatory diseases.

Brain Inflammation and Ischemic Stroke An autosomal dominant mutation of TRAF3 has been identified as a causative mutation in a patient with a history of herpes simplex virus-1 (HSV-1) encephalitis in childhood, which resulted from impaired TLR3-type I IFN signaling [[139](#page-22-0)]. DNA methylation of

the Traf3 gene is downregulated in patients with ischemic stroke, and this *Traf3* epigenetic regulation is associated with vascular recurrence and also correlated with an increased platelet aggregation [\[140](#page-22-0)]. Consistent with human evidence, the in vivo roles of TRAF3 in brain inflammation and ischemic stroke have been demonstrated with several mouse models. Transgenic mice overexpressing TRAF3 show decreased levels of IL-17-induced inflammatory factors IL-6, KC, and MMP3 in the brain and also exhibit delayed onset and reduced incidence and severity of experimental autoimmune encephalomyelitis (EAE) after MOG immunization [\[141\]](#page-22-0). Conversely, M-TRAF3^{-/-} mice, which have TRAF3 deleted in microglia and other myeloid cells, display exacerbated EAE [[120](#page-21-0)]. TRAF3 ablation also restores TLR-induced inflammatory responses and EAE severity in mice deficient in Peli1, an E3 ubiquitin ligase that mediates K48-linked ubiquitination and degradation of TRAF3 in microglia [\[120](#page-21-0)]. Interestingly, in a mouse model of ischemic stroke, TRAF3 expression is induced in neurons in response to I/R [\[110](#page-21-0)]. Neuron-specific TRAF3−/[−] mice reduces neuronal death and inflammation following I/R, whereas transgenic mice overexpressing TRAF3 in neurons exhibit more severe ischemic stroke [[110](#page-21-0)]. Neuronal effects of TRAF3 are mediated by TAK1-NF-κB/JNK/Rac-1 signaling [[110\]](#page-21-0). Furthermore, mice deficient in $CK1\varepsilon$, a kinase that interacts with and phosphorylates TRAF3 at Ser349, show aggravated and sustained brain inflammation after infection with West Nile virus [[129](#page-21-0)]. Taken together, TRAF3 plays antiinflammatory roles in microglia/myeloid cells and proinflammatory roles in neurons via distinct signaling pathways during brain inflammation (Fig. [2](#page-6-0)).

Autoimmune Inflammatory Diseases TRAF3 expression is upregulated in synovial fluid mononuclear cells and PBMCs of patients with juvenile idiopathic arthritis, and genome-wide association studies (GWASs) identified TRAF3 as a susceptibility gene for human multiple sclerosis [[142](#page-22-0), [143\]](#page-22-0). A PTP22 variant (PTPN22_R620W) that is strongly associated with human SLE and RA fails to promote TRAF3 ubiquitination [\[126\]](#page-21-0). Mechanistically, TRAF3 is a critical regulator of B cell homeostasis and activation, Treg and iNKT development and function, CD4 and CD8 T cell activation, and medullary thymic epithelial cell (mTEC) development [[101,](#page-21-0) [102,](#page-21-0) [127,](#page-21-0) [144](#page-22-0)–[147](#page-22-0)], all of which could impact autoimmune responses. Indeed, B cell-specific TRAF3−/[−] (B-TRAF3−/[−]) mice exhibit an autoimmune inflammatory phenotype affecting multi-organs, including the liver and kidney [[101](#page-21-0)]. Paradoxically, B cell-specific TRAF3 transgenic mice also develop systemic autoimmune inflammation in multi-organs, including pancreas, kidney, and joints [\[105](#page-21-0)]. Treg-specific TRAF3 ablation leads to mild tissue inflammation mostly seen in the lung and liver in mice [\[144](#page-22-0)]. Furthermore, TRAF3 plays a central role in inhibiting the NF-κB2 pathway during mTEC development, and mice lacking NF-κB2 components fail to develop mTECs and exhibit systemic autoimmune inflammation [\[147\]](#page-22-0). Therefore, TRAF3 dysregulation plays causal roles in the pathogenesis of various autoimmune inflammatory diseases.

TRAF4

Unique among the TRAF family, TRAF4 is mainly involved in developmental, morphogenic, and oncogenic processes [\[148](#page-22-0)–[153](#page-22-0)]. However, TRAF4 also regulates inflammation and inflammatory responses mediated by GITR, TLRs, NOD2, IL-17R, and IL-25R [[3](#page-18-0)••, [153](#page-22-0)–[161\]](#page-22-0). TRAF4 modulates inflammatory responses by directly interacting with GITR, NOD2, IL-17R, IL-25R, TRIF, Act1, TRAF6, IKKα, MEKK3, MEKK4, SMURF2, and $p47^{pbox}$ (a component of cytosolic NADPH oxidase) to control NF-κB, JNK, and reactive oxygen species (ROS) pathways [[149,](#page-22-0) [153](#page-22-0)–[162](#page-22-0)]. Current human and mouse evidence implicates TRAF4 in airway inflammation, inflammatory bowel diseases (IBD), and autoimmune encephalomyelitis.

Airway and Pulmonary Inflammation Initial characterization of TRAF4−/[−] mice revealed that loss of TRAF4 expression results in developmental defects of the upper respiratory tract, respiratory air flow abnormalities, and increased rates of pulmonary inflammation [[150](#page-22-0), [151](#page-22-0)]. However, Zepp et al. recently found that $TRAF4^{-/-}$ mice exhibit blunted airway eosinophilia and Th2 cytokine production in response to IL-25 administration [[161](#page-22-0)]. Mechanistically, IL-25/IL-25R ligation induces the recruitment of TRAF4, which is required for the Act1/IL-25R interaction as well as the recruitment the E3-ligase SMURF2 to degrade the IL-25R inhibitory molecule DAZAP2 [\[161\]](#page-22-0). Thus, TRAF4 plays a negative role in pulmonary inflammation during development, but a positive role in IL-25-induced airway inflammation.

Inflammatory Bowel Diseases TRAF4 is overexpressed in patients with IBDs, and TRAF4 overexpression appears to be an indicator of endoscopic disease activity in UC patients [\[163\]](#page-22-0). Interestingly, TRAF4 is identified as a key negative regulator of signaling by the Crohn's disease susceptibility protein NOD2 [\[158,](#page-22-0) [159](#page-22-0)]. In response to stimulation with bacterial ligands of NOD2, TRAF4 directly binds to NOD2, MEKK4, and IKKα, which leads to phosphorylation of Ser426 on TRAF4 by $IKK\alpha$ and disruption of the NOD2-RIP2 complex [\[158,159](#page-22-0)]. Consequently, TRAF4 inhibits NOD2-induced NF-κB activation and bacterial killing in macrophages (Fig. [1\)](#page-4-0) [\[158](#page-22-0), [159](#page-22-0)]. However, direct in vivo evidence of pathological or protective roles of TRAF4 in IBDs is still lacking and awaits further investigation.

Brain Inflammation and Autoimmune Encephalomyelitis TRAF4 expression is downregulated in the brain of patients with schizophrenia [\[164\]](#page-22-0), which is associated with high levels of pro-inflammatory cytokines in the blood and cerebrospinal fluid [\[165\]](#page-22-0). Characterization of TRAF4^{$-/-$} mice revealed that TRAF4 is required for myelin homeostasis in the central nervous system (CNS) [[166\]](#page-22-0). TRAF4−/[−] mice exhibit myelin perturbation and degeneration of a high number of Purkinje cells, which is linked to the activation of the Nogo receptor-p75NTR-RhoA pathway in the CNS [\[166\]](#page-22-0). In a T_H 17-mediated EAE model, adoptive transfer of MOG35-55-specific WT T_H17 cells into irradiated TRAF4^{$-/-$} recipient mice induces an accelerated onset of disease with increased numbers of immune cell infiltration in the brain [[160](#page-22-0)]. Biochemical analyses revealed that IL-17/IL-17R engagement recruits Act1, TRAF6, and TRAF4 [\[153](#page-22-0)]. Interestingly, TRAF4 competes with TRAF6 for binding to Act1 on the same site, thereby inhibiting IL-17-induced production of pro-inflammatory cytokines (such as GM-CSF and IL-6) and chemokines (such as CXCL1 and CCL2) in brain resident cells (such as astrocytes). Taken together, TRAF4 is important in restricting the effects of IL-17 signaling and disease pathogenesis in T_H 17mediated autoimmune encephalomyelitis [\[160\]](#page-22-0).

TRAF5

As a close structural homolog of TRAF2 and TRAF3, TRAF5 regulates inflammatory responses mediated by receptors of the TNF-R superfamily, TLRs, RIG-I, IL-17R, and gp130 (a component of IL-6 receptor) [[3](#page-18-0)••, [116](#page-21-0), [167](#page-22-0)–[173\]](#page-23-0). TRAF5 is important in the inflammatory responses mounted by CD4+ T_H 2 and T_H 17 cells, neutrophils, macrophages, hepatocytes, B cells, endothelial cells, and fibroblasts [[67](#page-20-0), [168,](#page-22-0) [169,](#page-22-0) [171](#page-22-0)–[174](#page-23-0)]. Upon receptor engagement, TRAF5 has been shown to induce the activation of both NF-κB1 and NF-κB2 pathways as well as the activation of the MAPKs (JNK and ERK1/2) by directly interacting with the upstream receptors and downstream adaptor proteins or enzymes[[3](#page-18-0)••, [116,](#page-21-0) [167](#page-22-0)–[169](#page-22-0)]. TRAF5-interacting proteins that participates in inflammation include OX40, IL-17R, gp130, TRAF2, TRAF3, MyD88, MAVS, TAB2, Act1, USP25, and RORγt, among others [\[3](#page-18-0)••, [116,](#page-21-0) [167](#page-22-0)–[170,](#page-22-0) [172](#page-23-0)••, [173](#page-23-0)–[177](#page-23-0)]. Available human and mouse evidence implicates TRAF5 in lung inflammation, cardiovascular inflammation, inflammatory bowel diseases, liver inflammation, and autoimmune inflammatory diseases (such as encephalomyelitis, arthritis, lupus, and uveitis).

Airway and Pulmonary Inflammation So et al. reported that in the presence of OX40 stimulation by an agonistic anti-OX40 antibody, TRAF5^{$-/-$} mice display enhanced T_H2 response to immunization with the T-dependent antigen KLH in adjuvant CFA or alum [\[174\]](#page-23-0). Similarly, in a model of OVA-induced allergic airway inflammation, in which endogenous OX40/ OX40L interactions are essential for the priming of T_H2 cells in asthmatic-like responses, TRAF5−/[−] mice show exaggerated T_H 2-driven airway and lung inflammation [[174\]](#page-23-0). TRAF5 deficiency leads to increased numbers of inflammatory cells and elevated levels of T_H2 cytokines IL-5 and IL-13 in bronchoalveolar lavage (BAL) fluid as well as OVA-specific IgE in the plasma following OVA challenge [\[174](#page-23-0)]. Interestingly, Bulek et al. found that in a mouse model of IL-17-induced pulmonary inflammation, the IL-17-Act1-TRAF2- TRAF5-IKK ε signaling axis is required for neutrophilia and lung inflammation [\[67](#page-20-0)]. This is mediated by IL-17 induced expression of chemokines (CXCL1 and CXCL2) and cytokines (TNF, IL-6 and G-CSF) in the lung tissue and especially in airway epithelial cells [[67,](#page-20-0) [175](#page-23-0)]. Therefore, TRAF5 plays a negative role in T_H2 induced airway and lung inflammation but a positive role in IL-17-induced airway and lung inflammation via distinct cell types and signaling pathways.

Atherosclerosis and Cardiac Fibrosis TRAF5 is overexpressed in human atherosclerotic plaques and is downregulated in total blood RNA of patients with stable or acute coronary heart disease [[43,](#page-19-0)[178](#page-23-0)]. TRAF5^{-/-}LDLR^{-/-} mice on a highcholesterol diet exhibit accelerated atherosclerosis with increased rolling and adhesion of inflammatory leukocytes [\[178\]](#page-23-0). This is mediated by (1) increased uptake of LDL by TRAF5−/[−] macrophages likely via their elevated expression of CD36; (2) increased production of chemokines KC and MCP-1 by TRAF5−/[−] macrophages and endothelial cells; (3) enhanced JNK activation and expression of adhesion molecule ICAM-1 on TRAF5^{-/−} endothelial cells; (4) increased expression of VCAM-1 on TRAF5^{$-/-$} monocytes; and (5) reduced number of TRAF5^{$-/-$} Treg cells in the spleen [[178](#page-23-0)]. Interestingly, in a mouse model of cardiac hypertrophy, TRAF5 expression is robustly induced in the heart in response to transthoracic aorta constriction [\[179\]](#page-23-0). TRAF5 deficiency promotes cardiac hypertrophy and fibrosis, which is associated with elevated levels of pro-inflammatory cytokines IL-6, TNF α , and MCP-1 in heart tissues and cardiomyocytes [\[179\]](#page-23-0). Thus, TRAF5 has a protective role in cardiovascular inflammation by acting in cardiomyocytes, blood vessel endothelial cells, and leukocytes.

Inflammatory Bowel Diseases Like TRAF2 and TRAF3, TRAF5 expression is significantly upregulated in inflamed colonic mucosa, PBMCs, and plasma of patients with CD and UC [[134](#page-22-0)]. TRAF5−/[−] mice are more susceptible to DSSinduced colitis with increased frequencies of CD4+ T_H2 and T_H 17 cells as well as enhanced cytokine levels of IFN- γ , IL-4,

and IL-17A in the colons after DSS treatment [\[171\]](#page-22-0). Thus, TRAF5 deficiency aggravates DSS-induced colitis, most likely by regulating T_H2 and T_H17 -mediated inflammation in mice [\[171\]](#page-22-0). These findings are consistent with previous evidence that TRAF5 controls T_H2 and T_H17 development by regulating the OX40, gp130, and IL-17R signaling as well as RORγt stability [[67](#page-20-0),[172](#page-23-0)••, [173,](#page-23-0) [174](#page-23-0),[176](#page-23-0)]. Therefore, TRAF5 plays anti-inflammatory roles in colitis mainly by acting in CD4+ T_H2 and T_H17 T_H17 T_H17 cells (Fig. 1).

Liver Inflammation and Hepatic Steatosis It has recently been reported that TRAF5 expression is decreased in the fatty livers of both NAFLD patients and obese mice and also in palmitate-treated hepatocytes in vitro [\[180\]](#page-23-0). TRAF5^{$-/-$} mice exhibit deterioration of HFD-induced metabolic disorders and have increased levels of pro-inflammatory cytokines (IL-1 β, IL-6, TNF α , and MCP-1) in the liver and serum [[180](#page-23-0)]. Conversely, transgenic TRAF5 overexpression in the liver significantly suppresses nonalcoholic steatohepatitis (NASH)-like phenotypes in mice after HFD treatment and also inhibits the progression of NAFLD in ob/ob mice [\[180](#page-23-0)]. Mechanistically, TRAF5 regulates hepatic steatosis by targeting JNK1 signaling, as evidenced by the fact that JNK1 ablation markedly ameliorates the detrimental effects of TRAF5 deficiency on obesity, inflammation, insulin resistance, hepatic steatosis, and fibrosis [\[180](#page-23-0)]. These findings identify TRAF5 as a protective factor in liver inflammation and hepatic steatosis.

Brain Inflammation and Ischemic Stroke Wang et al. reported that TRAF5 protein levels are upregulated by cerebral I/R in the neurons of ischemic mouse brains [[181](#page-23-0)]. TRAF5^{$-/-$} mice exhibit reduced infarct size and improved neurological function following MCAO-induced ischemic stroke [\[181\]](#page-23-0). This is associated with decreased neuronal apoptosis and attenuated blood-brain barrier (BBB) disruption, which is mediated by decreased expression and activity of MMP2 and MMP9 as well as decreased expression of iNOS, COX-2, TNFα, IL-1 β, MCP-1, and ICAM-1 [[181](#page-23-0)]. In contrast, neuron-specific TRAF5 transgenic mice show exacerbated brain injury and edema following cerebral I/R [[181\]](#page-23-0). Mechanistically, TRAF5 induces NF-κB activation and inhibits the Akt/ FoxO1 pathway in neurons to promote inflammatory responses and brain injury following ischemic stroke [\[181](#page-23-0)].

Autoimmune Encephalomyelitis TRAF5 has recently been recognized as a critical regulator of T_H 17 development through multiple mechanisms. TRAF5 inhibits IL-6-induced early T_H 17 development by directly interacting with gp130 and antagonizing the recruitment of STAT3 to gp130 in CD4+ T cells [\[172](#page-23-0)••, [173](#page-23-0)]. Paradoxically, however, TRAF5 also directly interacts with and ubiquitinates the T_H17 lineagespecific transcription factor RORγt via K63-linked polyubiquitination, thereby stabilizing the RORγt protein to promote the expression of T_H 17-related genes such as IL-17A [\[176](#page-23-0)]. Despite the complex negative and positive roles of TRAF5 in T_H17 development and function, TRAF5^{$-/-$} mice exhibit greatly exaggerated T_H 17-mediated inflammation and autoimmune encephalomyelitis in the EAE model [\[172](#page-23-0)••]. On the other hand, in IL-17-responding cells such as epithelial cells and fibroblasts, IL-17R signaling induces Act1 mediated K63-linked ubiquitination of TRAF5 and the subsequent interaction of TRAF5 with the splicing factor SF2 (ASF) to stabilize the mRNA transcripts of chemokines and cytokines [\[67,](#page-20-0) [175](#page-23-0), [182](#page-23-0)]. Deficiency in USP25, an enzyme that removes K63-linked ubiquitination of TRAF5 and TRAF6, also leads to exacerbated EAE severity [\[177](#page-23-0)]. Together, the above evidence implicates TRAF5 dysregulation in autoimmune encephalomyelitis mediated by T_H 17 cells and IL-17-responding epithelial cells and fibroblasts.

Other Autoimmune Inflammatory Diseases As a key signal transducer of the IL-17R-Act1 axis, TRAF5 is also involved in other IL-17-associated autoimmune inflammatory diseases, including arthritis, lupus, and uveitis (eye inflammation) [\[168,](#page-22-0) [176,](#page-23-0) [183](#page-23-0), [184](#page-23-0)]. For example, an increase in the TRAF5 mRNA level is detected in CD4+ T cells of patients with SLE [[176\]](#page-23-0). Interestingly, three SNPs (rs6540679 AG, rs12569232 GG, and rs10863888 AG) of TRAF5 are associated with two autoimmune uveitis entities, Behçet's disease and Vogt-Koyanagi-Harada syndrome in humans [[183\]](#page-23-0). Two of these SNPs (rs6540679 AA and rs12569232 GG) are also associated with pediatric uveitis [[184](#page-23-0)]. However, the causal roles of TRAF5 dysregulation in these autoimmune inflammatory diseases remain to be determined with animal models.

TRAF6

Among all TRAF molecules, TRAF6 has been the most extensively investigated in inflammatory responses. Historically, TRAF6 was initially considered as the only TRAF molecule that can regulate signaling of both the TNF-R and the TLR/IL-1R superfamilies [[185](#page-23-0), [186\]](#page-23-0). TRAF6 is ubiquitously expressed and important for inflammation in various cell types, especially in T cells, macrophages, dendritic cells (DCs), osteoclasts, mast cells, epithelial cells, fibroblasts, microglia, astrocytes, and neurons [\[3](#page-18-0)••, [90,](#page-20-0) [185](#page-23-0)–[193](#page-23-0)]. Serving as both a signaling adaptor and an E3 ubiquitin ligase, TRAF6 transduces signals that emanate from receptors of the TNF-R superfamily, TLRs, NLRs, RIG-I, cytokine receptors, and Ctype lectin receptors in inflammatory responses [[3](#page-18-0)••, [186\]](#page-23-0). TRAF6 is required for receptor-induced activation of both canonical and non-canonical NF-κB pathways as well as activation of the MAPKs (JNK1/2, ERK1/2, and p38) and IRFs (IRF3, IRF4, IRF5, and IRF7) [\[3](#page-18-0)••, [186](#page-23-0), [194](#page-23-0)–[196](#page-23-0)]. TRAF6 directly interacts with a variety of critical regulators of

inflammation and inflammatory responses. These include (1) receptors: members of the TNF-R superfamily, NLRX1, NLRC3, IL-17Rs, and TGF β receptors [[3](#page-18-0)••, [186,](#page-23-0) [197](#page-23-0)–[201](#page-23-0)]; (2) adaptor proteins: MyD88, TRIF, MAVS, TAB2, NEMO, Ubc13, DAB2, LAT, TRIP6, ECSIT, SOCS1, SOCS2, SOCS3, TAX1BP1, GIT2, and Keratin 8 [[3](#page-18-0)••, [186,](#page-23-0) [202](#page-23-0)–[211\]](#page-24-0); (3) enzymes: TAK1, TBK1, IRAK1, ASK1, Act1, WWP1, IRE1α, A20, CYLD, USP20, USP25, Pellino3, Itch, SHP, MST4, IPMK, and PINK1 [\[3](#page-18-0)••, [177,](#page-23-0) [186,](#page-23-0) [188](#page-23-0), [212](#page-24-0)–[223](#page-24-0)]; (4) transcription factors: IRF4, IRF5, IRF7, STAT1, STAT3, Smad6, HIF1α, Nur77, and DCP1a, among others [[3](#page-18-0)••, [186,](#page-23-0) [196,](#page-23-0) [219](#page-24-0), [224](#page-24-0)–[231](#page-24-0)]. Both human and mouse evidence indicates the pivotal importance of TRAF6 in sepsis, lung inflammation, cardiovascular inflammation, inflammatory bowel diseases, liver inflammation, diabetes, pancreatitis, neurodegenerative diseases, and autoimmune inflammatory diseases (such as autoimmune hepatitis, lupus, arthritis, and multiple sclerosis).

Sepsis TRAF6 expression is downregulated in PBMCs in critically ill patients with sepsis, and an intronic SNP of TRAF6 (rs4755453) is associated with susceptibility to sepsis-induced acute lung injury (a protective role identified for the C allele of rs4755453) [\[232](#page-24-0), [233](#page-24-0)]. TRAF6 deficiency leads to defective LPS-, IL1 β - and CD40- signaling in mice [\[234](#page-24-0), [235](#page-24-0)]. Multiple TRAF6-interacting proteins, including IRF5, ASK1, Akt2, and CRTC2, are activated by TRAF6 and play important roles in LPS-induced septic shock responses as demonstrated by in vivo evidence in mouse models [\[236](#page-24-0)–[239](#page-24-0)]. Notably, a variety of TRAF6-interacting proteins regulate LPS-induced septic shock responses in mouse models by directly targeting TRAF6 ubiquitination, degradation or complex formation, including IRAK1, IRAK2, IRAK-M, A20, NLRX1, NLRC3, CD204, β-arrestin, GIT2, MST4, Nur77, IPMK, SHP, and Keratin 8, among others [[198,](#page-23-0) [199,](#page-23-0) [210,](#page-24-0) [211,](#page-24-0) [215,](#page-24-0) [220](#page-24-0)–[222,](#page-24-0) [230,](#page-24-0) [240](#page-24-0)–[245\]](#page-25-0). Therefore, TRAF6 is a central regulator of sepsis.

Airway Inflammation In cultured human macrophages, cigarette smoke induces TRAF6 degradation, NF-κB activation and IL-8 production via TLR4-IRAK-dependent signaling [\[246\]](#page-25-0). During lung I/R injury, DAMPs induce autophagy to amplify the inflammatory response by enhancing K63-linked ubiquitination of TRAF6 and activation of the downstream MAPK and NF-κB signaling in alveolar macrophages [[247\]](#page-25-0). In mice, high doses of CpG oligodeoxynucleotides protect against allergic airway inflammation by stimulating the TLR9-TRIF-TRAF6-NF-κB2 pathway [\[195\]](#page-23-0). In the presence of TGF β, ligation of OX40 induces conventional CD4+ T cell polarization to T_H 9 cells, and OX40L-transgenic mice develop an extensive autoimmune disease with severe T_H 9driven airway inflammation. However, OX40 fails to induce T_H 9 polarization in CD4 T cells of T cell-specific TRAF6^{$-/-$}

mice due to defective OX40-TRAF6-NIK-NF-κB2 signaling in TRAF6^{$-/-$} T cells [[194](#page-23-0)]. In contrast, TRAF6 in DCs is required for the maintenance of tolerance in the lung to prevent allergic asthma. Specific deletion of TRAF6 from DCs leads to spontaneous generation of T_H 2-associated immune responses in the lung and increased susceptibility to the model antigen OVA-induced asthmatic airway inflammation with exacerbated eosinophil infiltration [\[248](#page-25-0)]. As a component of the IL-17R-Act1-TRAF6 signaling axis in macrophages, fibroblasts, and epithelial cells, TRAF6 is also required for IL-17 and IL-25-induced airway and pulmonary inflammation [\[177,](#page-23-0) [200,](#page-23-0) [249](#page-25-0)]. Furthermore, TRAF6^{-/-} mast cells show impaired production of cytokine IL-6, IL-13, TNF, and CCL-9 following FcεRI aggregation, suggesting a positive role for mast cell TRAF6 in allergic inflammatory responses [[189\]](#page-23-0). Thus, TRAF6 is an indispensable regulator of airway inflammation by acting in both immune cells and lung resident cells.

Cardiovascular Inflammation TRAF6 expression is upregulated in human atherosclerotic plaques and human hearts with hypertrophic cardiomyopathy, dilated cardiomyopathy, and atrial fibrosis [[43,](#page-19-0) [250](#page-25-0)–[252](#page-25-0)]. Using LDLR^{$-/-$} mice reconstituted with TRAF6−/[−] fetal liver cells and on a high cholesterol diet, Stachon et al. reported that TRAF6 is not required for atherogenesis. Interestingly, however, Polykratis et al. revealed the opposite protective versus pathogenic roles of TRAF6 in atherosclerosis using two different conditional TRAF6 knockout mouse models [[253](#page-25-0)]. Endothelial TRAF6 deficiency reduces atherosclerosis in female ApoE−/[−] mice by inhibiting NF-κB-dependent proinflammatory gene expression and monocyte adhesion to endothelial cells [\[253](#page-25-0)]. In contrast, myeloid cell-specific TRAF6 deficiency causes exacerbated atherosclerosis in both male and female ApoE−/[−] mice by increasing ER stress and apoptosis and by reducing IL-10 production and the efferocytosis capacity of TRAF6−/[−] macrophages [[253](#page-25-0)]. In mouse hypertrophic hearts, elevation of TRAF6 protein levels is induced by ROS generated during hypertrophic progression [\[250\]](#page-25-0). Cardiac-specific TRAF6 transgenic mice show exacerbated cardiac hypertrophy in response to pressure overload or angiotensin II challenge, whereas cardiac-specific TRAF6−/[−] mice exhibit an alleviated cardiac hypertrophy phenotype [[250\]](#page-25-0). Mechanistically, ROS triggers TRAF6 auto-ubiquitination and subsequent TRAF6- TAB2-TAK1 signaling, which regulates cardiac remodeling via the p38 and JNK1/2 pathways [\[250\]](#page-25-0). Thus, TRAF6 plays complex roles in endothelial cells, macrophages, and cardiomyocytes via distinct signaling pathways during cardiovascular inflammation.

Inflammatory Bowel Diseases In humans, epigenetic silencing of TRAF6 by hypermethylation and reduced TRAF6 expression are detected in PBMCs of IBD patients [[254\]](#page-25-0). Paradoxically, Shen et al. reported that TRAF6 expression is elevated in PBMCs and intestinal mucosa of IBD patients and that soluble TRAF6 levels in plasma are also significantly higher in patients with CD and UC than in healthy controls [\[163\]](#page-22-0). In mice, dendritic cell-specific deletion of TRAF6 (DC-TRAF6−/[−]) results in spontaneous eosinophilic enteritis and fibrosis in the small intestine associated with a T_H2 inflamma-tory response in the lamina propria [\[255](#page-25-0)•]. The aberrant T_H 2 response is linked to decreased Treg cell numbers in the small intestine and diminished induction of iTreg cells due to defective expression of IL-2 in TRAF6^{$-/-$} DCs [\[255](#page-25-0)•]. The T_H2associated small intestine inflammation is exacerbated in germ-free $DC-TRAF6^{-/-}$ mice compared to specific pathogen-free DC-TRAF6^{$-/-$} mice, suggesting that the enteritis phenotype is independent of gut microbiota [[256\]](#page-25-0). In contrast, young mice with T cell-specific TRAF6 deletion show attenuated DSS-induced colitis, which is associated with increased TGF β-Smad2/3 signaling in TRAF6^{$-/-$} T cells and increased T_H 17 differentiation [[257](#page-25-0)]. Interestingly, intestinal epithelial cell (IEC)-specific deletion of TRAF6 leads to exacerbated DSS-induced colitis in mice, which is dependent on gut microbiota but independent of TLR-MyD88/TRIF signaling in IECs [\[258\]](#page-25-0). Furthermore, activation of NOD2, a major susceptibility gene of CD, protects mice from TNBS-induced colitis by increasing the expression of IRF4, which binds to TRAF6 and RICK to inhibit their K63-linked polyubiquitination [[196](#page-23-0)]. Together, the above evidence indicates that TRAF6 plays diverse and critical roles in IBDs by differentially acting in various cell types in the intestines (Fig. [1\)](#page-4-0).

Liver inflammation, Diabetes, and Hepatic Steatosis TRAF6 expression is decreased in PBMCs of chronic hepatitis B virus-infected patients [[259\]](#page-25-0), but is elevated in PBMCs of patients with type 2 diabetes [[260](#page-25-0), [261](#page-25-0)]. Significant association is detected between the TRAF6 SNP rs16928973 TT and diabetic nephropathy (DN) in patients with type 2 diabetes [\[262\]](#page-25-0). In mice, specific deletion of TRAF6 from medullary thymic epithelial (mTEC) cells leads to autoimmune hepatitis associated with autoantibodies and abnormal hepatic T cell populations and functions, caused by impaired mTEC development and T cell tolerance to liver autoantigens [\[190\]](#page-23-0). In a model of concanavalin A-induced murine hepatitis, the OX40-TRAF6-MALT1-caspase 1-gasdermin D signaling is required to induce pyroptosis in hepatic iNKT cells and the subsequent liver inflammation and injury [[263\]](#page-25-0). In mouse primary hepatocytes, insulin induces TRAF6-mediated K63 linked ubiquitination of APPL1 and Akt activation, and TRAF6 silencing leads to insulin resistance in hepatocytes [\[264\]](#page-25-0). Interestingly, mice deficient in Pellino3, a negative regulator of TRAF6 activity, show exacerbated HFD-induced inflammation, hepatic steatosis, and insulin resistance with increased expression of IL-1 β, TNF, IL-6, and CCL2 in the liver [\[219\]](#page-24-0). These effects of Pellino3 deficiency result from

augmented TRAF6-mediated K63-linked ubiquitination and stabilization of HIF1 α in the liver [[219\]](#page-24-0). However, direct in vivo evidence of TRAF6 in hepatocytes, insulin resistance, and hepatic steatosis is still lacking and awaits further investigation with hepatocyte-specific TRAF6^{$-/-$} mice.

Pancreatitis Nishida et al. found that IL-36 α , a cytokine detected in fibrotic tissue of chronic pancreatitis, induces inflammatory mediators from human pancreatic myofibroblasts via the IL-36R-MyD88-TRAF6-IRAK1-TAK1 signaling path-way [\[265](#page-25-0)]. In mice, TRAF6 expression is significantly increased in caerulein-induced acute pancreatitis, and TRAF6 plays a protective role in acinar cells against caerulein-induced apoptosis [\[207\]](#page-24-0). LPS-induced SOCS1 and SOCS3 exacerbate caerulein-induced pancreatitis by directly interacting with TRAF6 and degrading TRAF6 protein via ubiquitination [\[207](#page-24-0)]. As a convergence point of the TLR4-dependent and the TLR4-independent signaling pathways, TRAF6 may play an important role in pancreatitis [\[207,](#page-24-0) [266](#page-25-0)], which remains to be directly elucidated using conditional TRAF6 knockout mice in pancreatitis models.

Brain Inflammatory Diseases TRAF6 has been implicated in the pathogenesis of a variety of human brain inflammatory diseases, including ischemic stroke, Alzheimer's disease (AD), Parkinson's disease (PD), and Huntington disease (HD). TRAF6 SNP haplotype rs5030416 (allele C) rs5030411 (allele C) has been associated with susceptibility to ischemic stroke [[267](#page-25-0)], and TRAF6 expression is upregulated in peripheral blood of stroke patients [[268](#page-25-0)]. TRAF6 protein levels are elevated in the brains of PD and HD patients [[90](#page-20-0), [193\]](#page-23-0). Interestingly, abnormal protein aggregates of TRAF6 are detected in the brains of patients with AD, PD, and HD [[90,](#page-20-0) [191](#page-23-0)–[193](#page-23-0)]. In human AD brains, TRAF6 associates with the ubiquitin-associating protein sequestosome1/ p62 and tau in neurofibrillary tangles, and TRAF6 catalyzes K63-linked polyubiquitination of tau to promote tau aggregation into insoluble tangles [[191](#page-23-0)]. Indeed, tau was recovered as a polyubiquitinated protein in brain lysates from WT mice, but was not polyubiquitinated in brain lysates recovered from the TRAF6^{$-/-$} mice [[191](#page-23-0)]. In human PD brains, TRAF6 interacts with and ubiquitinates misfolded mutant PARK7/DJ-1 and PARK1/aSYN to promote the accumulation of insoluble aggregates and Lewy bodies [[192\]](#page-23-0). Similarly in human HD brains, TRAF6 binds to mutant N-HTT proteins and also ubiquitinates mutant N-HTT to increase the formation of insoluble aggregates [[193\]](#page-23-0). Interestingly, however, instead of the conventional K63 linked polyubiquitination, TRAF6 promotes atypical ubiquitination of mutant DJ-1, aSYN and N-HTT with K6, K27, and K29 linkage formation [[192,](#page-23-0) [193\]](#page-23-0). Therefore, TRAF6 appears to act as a key pathogenic E3 ligase in neurodegenerative diseases.

Table 1 Genetic variations and alterations in expression of TRAF molecules in human inflammatory diseases

Table 1 (continued)

Autoimmune Inflammatory Diseases TRAF6 expression is elevated in human patients with SLE and RA [\[4](#page-18-0)•, [186,](#page-23-0) [269](#page-25-0)–[271](#page-25-0)]. Downregulated expression of TRAF6 has also been detected in PBMCs of SLE patients [[93\]](#page-20-0). Three TRAF6 SNPs (rs5030437 A allele, rs4755453 C allele, and rs540386 A allele) are associated with lupus, and the SNP rs5030437 A allele is also associated with RA [[271](#page-25-0), [272](#page-25-0)]. The causal roles of TRAF6 dysregulation in autoimmune inflammatory diseases have been demonstrated by several mouse models with TRAF6 deficiency. In addition to its essential roles in tolerance induction in DCs and mTECs described above, TRAF6 is also required for normal function of CD4+ T cells and Treg cells. An early study by Chiffoleau et al. showed that chimeric mice reconstituted with $TRAFG^{-/-}$ fetal liver cells develop a progressive lethal inflammatory disease associated with massive organ infiltration and activation of CD4+ T cells in a T_H2 -polarized phenotype [\[273](#page-25-0)]. King et al. verified the findings with T cell-specific TRAF6−/[−] (T-TRAF6−/[−]) mice, which also exhibit a systemic autoimmune inflammatory disease affecting multiple organs [\[274\]](#page-25-0). This autoimmune inflammatory phenotype is mediated by increased TCR-PI3K-Akt activation and reduced expression of Cbl-b and consequently independence from CD28 costimulation and impaired anergy induction in TRAF6^{-/−} CD4+ T cells [\[274](#page-25-0), [275\]](#page-25-0). Consistent with the notion that TRAF6 is required for Treg development and maintenance [\[257,](#page-25-0) [276](#page-25-0), [277](#page-26-0)], Treg-specific TRAF6^{$-/-$} mice spontaneously develop allergic skin diseases, arthritis, lymphadenopathy, and hyper IgE phenotypes [[277\]](#page-26-0). Mechanistically, TRAF6 deficiency results in reduced stability and protein level of FoxP3 in Treg cells, leading to rapid conversion of FoxP3 expressing Treg cells into T_H 2-like inflammatory cells in mice [\[277\]](#page-26-0). In summary, TRAF6 protects hosts from various autoimmune inflammatory diseases by acting in CD4+ T_H cell subsets, Treg cells, DCs, and mTECs.

TRAF7

TRAF7 protein does not have the TRAF homology domain that defines the TRAF family [\[3](#page-18-0)••]. Currently, there is no human evidence or direct in vivo evidence about TRAF7 in inflammation and inflammatory diseases.

Here, we summarize genetic variations and alterations in expression of TRAF molecules in human inflammatory diseases in Table [1](#page-13-0) and also provide a list of direct in vivo evidence of TRAF molecules in inflammatory diseases in mouse models in Table [2.](#page-15-0)

Conclusions

During the past decade, our knowledge of TRAF molecules in inflammation and inflammatory diseases has rapidly grown. Compelling evidence has demonstrated the central importance of TRAFs in regulating and controlling inflammation and inflammatory responses in both humans and mice. This is highlighted by mounting evidence of TRAF dysregulation or dysfunction in human patients with various inflammatory diseases. The causal roles of TRAF dysregulation or dysfunction in inflammatory diseases have been verified in a variety of mouse models as reviewed here. It is recognized that although TRAFs have overlapping roles, each TRAF molecule (TRAF1 to 6) also plays distinct and indispensable roles in inflammation and inflammatory responses as demonstrated by studies of mouse models with genetic engineering of the corresponding Traf gene. It is also increasingly clear that for each specific TRAF molecule, its role in inflammation may vary substantially depending on the specific receptor pathways engaged, the cellular and organ context, the functional or metabolic state of the cell, and the stoichiometry of other TRAFs and TRAF-interacting proteins in the cell as revealed by

Table 2 Direct evidence of TRAF molecules in inflammatory diseases in mouse models

Table 2 (continued)

Table 2 (continued)

comprehensive analyses of different inflammatory responses and disease models. In conclusion, TRAF molecules are versatile and indispensable regulators of inflammation and inflammatory responses, and aberrant expression or function of TRAFs contributes to the pathogenesis of inflammatory diseases.

Perspective

Given the central importance of TRAFs in inflammation and inflammatory diseases, it would be envisioned that TRAFs and TRAF-dependent signaling pathways represent rational therapeutic targets for human inflammatory diseases. Development of therapeutic strategies and agents that specifically targets TRAFs and TRAF-dependent signaling pathways will thus be the next major challenge in the field. This could be particularly difficult considering the broad and highly diverse roles of TRAFs in inflammation and other immune responses depending on the stimuli, cell type, tissue environment, and functional state of the hosts. In this regard, insights gained into the proximal TRAF signaling complexes and detailed structures of the interactions between each TRAF and its specific signaling partners will guide the design of contextspecific therapeutics. In addition, local or cell-specific drug

delivery would be beneficial to improve the therapeutic efficacy and avoid systemic side effects of TRAF-targeting therapeutics. To date, only TRAF6-specific therapeutic agents have been tested in inflammatory disease settings. Inhibition of TRAF6 expression using specific small interfering RNA reduces the severity of arthritis and joint inflammation in a mouse RA model [\[282](#page-26-0)]. Notably, structure-based in silico approaches have been employed to screen and identify compounds that specifically block TRAF6-CD40 or TRAF6- RANK interactions, which serve as lead compounds for further drug development and optimization [[283,](#page-26-0) [284\]](#page-26-0). The small molecule inhibitor (SMI) of CD40-TRAF6 interaction, 6877002, effectively reduces in vivo inflammation in mouse models of peritonitis, polymicrobial sepsis, and EAE [\[283,](#page-26-0) [285](#page-26-0)]. Another SMI of CD40-TRAF6 interaction, 6860766, potently ameliorates in vivo inflammation in mouse models of polymicrobial sepsis and HFD-induced obesity [[283](#page-26-0), [286\]](#page-26-0). These findings provide proof-ofconcept evidence that manipulation of TRAF expression and function holds therapeutic potential for inflammatory diseases. Further development of therapeutic strategies and agents that specifically target other TRAF molecules or signaling complexes will add to our armament to improve the treatment of human inflammatory diseases.

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Compliance with Ethical Standards

Conflict of Interest The authors have no competing financial interests.

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