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# [TNF superfamily control of tissue](https://www.frontiersin.org/articles/10.3389/fimmu.2023.1219907/full) [remodeling and](https://www.frontiersin.org/articles/10.3389/fimmu.2023.1219907/full) fibrosis

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Fibrosis is the result of extracellular matrix protein deposition and remains a leading cause of death in USA. Despite major advances in recent years, there remains an unmet need to develop therapeutic options that can effectively degrade or reverse fibrosis. The tumor necrosis super family (TNFSF) members, previously studied for their roles in inflammation and cell death, now represent attractive therapeutic targets for fibrotic diseases. In this review, we will summarize select TNFSF and their involvement in fibrosis of the lungs, the heart, the skin, the gastrointestinal tract, the kidney, and the liver. We will emphasize their direct activity on epithelial cells, fibroblasts, and smooth muscle cells. We will further report on major clinical trials targeting these ligands. Whether in isolation or in combination with other anti-TNFSF member or treatment, targeting this superfamily remains key to improve efficacy and selectivity of currently available therapies for fibrosis.

#### KEYWORDS

TNF superfamily, TNFSF, fibrosis, remodeling, mucosa

## 1 Introduction

Fibrosis is defined as the uncontrolled build-up of scar tissue. It is the end result of many inflammatory diseases and is responsible for 45% of death in USA [\(1\)](#page-20-0). Fibrosis can affect multiple organs and, irrelevant of the initiating disorder, it can ultimately lead to organ failure and death. Fibrosis originates after epithelial (or endothelial) injury, driving early alarmin expression, followed by inflammation that involves the production of the central fibrogenic cytokine TGF $\beta$  (transforming growth factor-beta). TGF $\beta$  allows for the differentiation of fibroblasts into pathogenic myofibroblasts. Myofibroblasts are responsible for collagen and extracellular matrix proteins deposition, in addition to smooth muscle hypertrophy. While TGF $\beta$  is central for fibrosis pathogenesis, its' targeting leads to severe side effects due to lymphoproliferative symptoms. Therefore, there is an urgent need to identify novel fibrotic mediators that could be therapeutic targets for the myriad of diseases

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presenting with fibrosis. Historically, tumor necrosis factor superfamily (TNFSF) ligands have been identified as proinflammatory mediators; however, our group has pioneered work implicating the TNF superfamily members in fibrosis [\(2](#page-20-0)–[5\)](#page-20-0). Currently, the TNF superfamily is known to consist of 19 ligands and 29 receptors. Current literature demonstrates growing evidence that the TNFSF members covered in this review (Table 1) play a role in fibrosis, including their upregulation in various fibrotic disorders; however, this does not rule out the potential contributions of other TNFSF members, which future research should address. In this review, we will summarize select TNFSF (Table 1) and their involvement in fibrosis of the lungs (interstitial lung disease, pulmonary fibrosis, idiopathic pulmonary fibrosis, acute respiratory distress syndrome, cystic fibrosis), the heart (atherosclerosis, myocarditis, ischemic myocardial infarction, non-ischemic hypertrophic cardiomyopathy), the skin (scleroderma, atopic dermatitis, atopic eczema, Dupuytren's disease), the gastrointestinal tract (eosinophilic esophagitis, ulcerative colitis, Crohn's disease), the kidney (acute kidney injury, chronic kidney disease), and the liver (non-alcoholic steatohepatitis, non-alcoholic fatty liver disease, primary biliary cholangitis) ([Figure 1](#page-2-0)). We will emphasize their direct activity on

TABLE 1 TNF superfamily members and receptors implicated in fibrosis.

stromal cells that perpetuate fibrosis, namely epithelial cells, fibroblasts, and smooth muscle cells [\(Figure 2\)](#page-2-0). We will further report on major active clinical trials targeting these ligands. Whether targeting each TNFSF ligand in isolation or in combination with another TNFSF member or treatment, targeting this superfamily remains key to improve efficacy and selectivity of currently available therapies for fibrosis.

# 2 TNF : TNFR1/TNFR2

Tumor necrosis factor (TNF), also referred to as TNF $\alpha$  or TNFSF2, is a pleiotropic cytokine known for its early and potent role in inflammation ([6](#page-20-0), [7\)](#page-20-0). TNF is first membrane bound (mTNF) on the cell surface and can then be cleaved by TNF-converting enzyme (TACE), a member of the disintegrin and metalloproteinase family, into its soluble form (sTNF) ([8](#page-20-0)). TNF is produced primarily by monocytes and macrophages; however, it can also be expressed by other cell types such as T cells, B cells, NK cells, mast cells, neutrophils, and fibroblasts [\(9\)](#page-20-0). TNF has two transmembrane receptors: TNF receptor I (TNFR1, also known as TNFRa, p55, or CD120a) and TNF receptor II (TNFR2, also known as TNFRb or



TNFSF members and their corresponding receptors discussed in this review article. Common ligand and corresponding receptor names are listed in bold. Alternative ligand and receptor names are listed in parenthesis.

<span id="page-2-0"></span>

p75) [\(10\)](#page-20-0). TNFR1 is ubiquitously expressed across human tissues, while TNFR2 is limited to mainly hematopoietic and endothelial cells ([11\)](#page-20-0). TNFR1 can be stimulated by either mTNF or sTNF, while TNFR2 is preferentially activated by mTNF [\(12](#page-20-0)–[14\)](#page-20-0). TNFR1 and TNFR2 share similar extracellular structures but, their intracellular structures differ. The cytoplasmic tail of TNFR1 contains a death domain (DD), which can recruit TNFR1-associated DD (TRADD), while TNFR2 instead recruits TNFR-associated factor (TRAF) 1 and 2 proteins [\(15,](#page-20-0) [16](#page-20-0)). Due to their intracellular domains, both TNFR1 and TNFR2 may signal to induce NF-kB activation and cell survival responses, whereas TNFR1 also has potential to induce cell death response.

Food and Drug Administration (FDA)-approved TNF antagonists (infliximab, etanercept, adalimumab, certolizumab and golimumab) have shown to be extremely efficacious in the treatment of inflammatory diseases presenting with end-stage fibrosis, such as rheumatoid arthritis, spondylarthropathies, Crohn's disease, and ulcerative colitis. Historically, the role of TNF in fibrosis was considered controversial, with many perceiving TNF as antifibrotic; however, current research suggests





that targeting TNF, either directly or by its receptors, could present a promising approach for treating fibrotic diseases (Figure 3).

Systemic sclerosis (SSc) is an idiopathic autoimmune disease that presents with fibrosis mainly in the skin but also in visceral organs including the lungs and heart. Elevated serum concentration of soluble TNFR1 correlates with SSc disease severity [\(17,](#page-20-0) [18](#page-20-0)) and soluble TNFR1 levels are increased in the bleomycin-induced murine model of SSc ([19](#page-20-0)). TACE processes pro-TNF and its receptors including soluble TNFR1. Blocking TACE, using tumor necrosis factor-alpha processing inhibitor-1 (TAPI-1), reduced skin thickness, the number of myofibroblasts, and mRNA expression of Col1a1, TGF $\beta$ , and  $\alpha$ SMA (alpha smooth muscle actin). TACE remains a potential therapeutic target in SSc patients, though further studies are needed to understand the potential impact of TAPI-1 treatment in humans. Additional work by Hügle et al. showed that TNFR1 and TNFR2 were up regulated on dermal T cells from patients with diffuse cutaneous SSc and that TNFR2 expression correlated with skin thickening [\(20](#page-20-0)). Further, TNF-costimulation after CD3/CD28 stimulation of these SSc patient T cells resulted in elevated type 1 collagen expression by fibroblasts and an increased secretion of profibrotic cytokines by the T cells, albeit a decreased production of IL-10, indicating that SSc patient T cells may reinforce fibrosis while lacking the ability to resolve inflammation. Recent work has also shown that sTNFR1 is increased in the fibroblast supernatant from IPF patients, and this pathway can likely induce T cell death, further contributing to disease by permitting fibroblast/myofibroblast survival [\(21](#page-20-0)).

In a bleomycin-induced mouse model of pulmonary fibrosis, early work showed elevated TNF upon bleomycin instillation and blocking TNF prevented fibrotic disease progression, including collagen deposition [\(22\)](#page-20-0). In later work also using the bleomycin model of pulmonary fibrosis, TNF<sup>-/-</sup> and TNF<sup>tm/tm</sup> (mice only expressing mTNF) mice were protected from pulmonary fibrosis as compared to WT controls [\(23](#page-20-0)). When recombinant TNF was added to the TNF<sup>tm/tm</sup>, however, collagen overexpression and fibrotic lesions were observed. This evidence, along with observations that sTNF appeared to be necessary for appropriate lymphocyte recruitment and TGF-b1 expression, led Oikonomou et al. to conclude that sTNF, as opposed to mTNF, mediates the transition from pulmonary inflammation to fibrosis. While this work focused on deletion of TNF, contrasting work by Redente et al. administered TNF as a therapeutic into the lungs of WT mice with pre-established pulmonary fibrosis driven by bleomycin [\(24\)](#page-20-0). After pulmonary delivery of TNF, there was a decrease in fibrotic burden and number of profibrotic alternatively programmed macrophages.

Furthermore, conditional macrophage depletion phenocopied the resolution seen in the mice receiving the therapeutic TNF delivery. TNF may resolve established pulmonary fibrosis by reducing numbers and/or programming status of profibrotic macrophages, however, the exact mechanism remains unclear and further work must be done to explain the apparent discrepancy that TNF is driving pulmonary fibrosis on one hand, while helping to resolve fibrosis on the other.

More recent work by Li et al. showed that impaired TNF/ TNFR2 signaling enhances Th2 and Th17 polarization and aggravates allergic airway inflammation ([25\)](#page-20-0). Inhibiting TNFR2 via antibody treatment led to the increased expression of Th2 and Th17 inflammatory cytokines both in serum and in bronchoalveolar lavage fluid (BALF). Flow cytometry data further showed an inhibition of Th1 and CD4+CD25+ T-cell differentiation with a promotion of Th2 and Th17 polarization in vivo, which was subsequently replicated in vitro. It may be that impaired TNFR2 signaling can help facilitate traditionally fibrotic Th2/Th17 polarization, however, further studies are needed. In BALF from fibrotic and non-fibrotic hypersensitivity pneumonitis (HP) patients, transmembrane TNFR2 was elevated in fibrotic compared to non-fibrotic samples ([26\)](#page-20-0). In contrast, soluble TNFR2 and sTNF were both upregulated in non-fibrotic HP patients. Thus, TNFR2 signaling appears to be key for mediating fibrotic development; however, additional work needs to be done to understand whether this is a global or rather a diseasespecific trend.

In human dermal fibroblasts, Goldberg et al. found that the addition of TNF in vitro suppresses  $\alpha$ SMA expression ([27\)](#page-20-0). Similarly, while the addition of TGF $\beta$ 1 increased  $\alpha$ SMA, adding both TGF $\beta$ 1 and TNF suppressed  $\alpha$ SMA to below the baseline. Furthermore, TNF was found to suppress TGF $\beta$ 1- induced myofibroblast genes at the mRNA level including Col1a1, fibronectin and  $\alpha$ SMA. TNF-mediated inflammation may prevent TGFβ1- driven normal wound healing and fibrosis development. In contrast, in normal fibroblasts from the palm of patients with Dupuytren's disease (DD), a localized fibrotic condition of the hand, TNF treatment drove their conversion to myofibroblasts via activation of Wnt signaling ([28\)](#page-20-0). Similarly, TNF inhibition by neutralizing antibodies resulted in reversal of myofibroblast phenotype, suggesting that TNF could be a promising therapeutic target for DD. In continuation of this work, Izadi et al. demonstrate that TNF signals through TNFR2 on stromal cells to initiate lowlevel IL-33 production ([29](#page-20-0)). In turn, they argue that IL-33 can then signal via ST2 (suppression of tumorigenicity 2 aka IL1RL1) on local immune cells to further drive TNF expression. Future studies may explore inhibition of TNFR2 in combination with IL-33 inhibition, which may represent a more efficacious approach than TNFR2 inhibition alone to prevent further disease development in DD.

Stimulation of intestinal myofibroblasts with TNF increased proliferation and collagen accumulation by acting primarily via TNFR2 [\(30\)](#page-20-0). Theiss et al. found that TNF also induced expression of tissue inhibitor of metalloproteinase-1 (TIMP-1) and activation of ERK1/2. Thus, limiting TNFR2 action may have potential for the treatment of intestinal inflammation or Crohn's disease. In a model of liver fibrosis induced by carbon tetrachloride (CCl4) injections, deletion of TNFR1, but not TNFR2, inhibits liver fibrosis ([31\)](#page-20-0). TNFR1<sup>-/-</sup> mice exhibited reduced procollagen and TGF $\beta$  synthesis as well as reduced levels of IL-6 mRNA as compared to WT and  $TNFR2^{-/-}$  mice, indicating that TNFR1 may play a key role in liver fibrosis formation. In a study of liver cirrhosis induced by thioacetamide in rats, Abdul-Hamid et al. tested the antifibrogenic effect of etanercept, one of the five FDA-approved TNF antagonists ([32\)](#page-20-0). They observed that etanercept decreased TNFR1 expression and accumulation of both collagen and hemosiderin, concluding that etanercept may attenuate fibrosis progression but also may be a therapeutic approach for hepatic iron overload-associated disorders. Finally, in a high-fat diet (HFD) mouse model of NAFLD, Wandrer et al. tested a novel antibody that selectively inhibits TNFR1, but not TNFR2 [\(33\)](#page-20-0). Inhibition of TNFR1 markedly reduced liver steatosis, apoptotic liver injury, NAFLD activity and liver fibrosis as compared to control mice. Taken together, these studies emphasize the profibrotic role of TNFR1 in the liver, regardless of the model, and indicate that selective TNFR1 inhibition could be a promising therapeutic approach for treatment of liver fibrosis.

Cardiac inflammation, together with edema and fibrosis, are common features of many cardiovascular diseases (CVD), including ischemic myocardial infarction (MI), non-ischemic hypertrophic cardiomyopathy (HCM) and myocarditis. However, the type of fibrosis leading to heart failure (HF) will differ depending on the biological origin of HF. Upon mTNF cleavage by the TNFalpha-converting enzyme (TACE) ([34](#page-20-0)) or ADAM17 (a disintegrin and metalloproteinase 17) ([35](#page-20-0)), the soluble (sTNF) form of mTNF can be released with higher affinity for TNFR1 and indirectly balance TNFR2 signaling, as shown in the control of atherosclerosis. Conversely, ADAM17 deficiency favors overactivation of TNFR2 and atherosclerosis progression in lowdensity lipoprotein receptor (Ldlr)-deficient mice [\(35](#page-20-0)), suggesting that each receptor has distinct modes of signaling and cellular functions. Moreover, it has also been reported that the lymphotoxin-  $\alpha$  homotrimer (LT $\alpha$ 3) signals through TNFR1 ([36\)](#page-20-0), and has unique roles in initiation and exacerbation of some inflammatory diseases. In a mouse model of HCM induced by infusion of angiotensin II (Ang II), Ang II induced the synthesis of monocyte chemoattractant protein-1 (MCP-1), which mediates the cardiac infiltration of CD34<sup>+</sup>CD45<sup>+</sup> monocytic cells that can differentiate into collagen-producing fibroblasts that are responsible for the Ang-II-induced development of non-adaptive cardiac fibrosis. In response to continuous Ang-II, TNFR1-KO

mice, but not TNFR2-KO, have shown reduced cardiac collagen deposition and CD34<sup>+</sup>CD45<sup>+</sup> monocytic infiltration, while double receptor knockout mice were protected from cardiac fibrosis after 1 week of Ang-II infusion [\(37](#page-20-0)). In the same model, authors show that absence of TNFR1 signaling is essential for decreasing the amount of cardiac pro-fibrotic M2-like cells (day7 post-Ang-II), however, this loss of signal does not affect early pro-inflammatory M1-like infiltration (day 1 post-AngII). Reconstitution with WT-bone marrow into TNFR1-KO mice abrogated the protective loss of TNFR1 signaling effect by restoring cardiac M2 infiltration, upregulation of proinflammatory/profibrotic genes and development of fibrosis. Indeed, an in vitro mouse monocyte-tofibroblast differentiation assay demonstrated an essential role of TNFR1 signaling in the sequential progression of monocyte activation and fibroblast formation ([38\)](#page-20-0). Moreover, in a model of cardiac pressure-overload induced by transaortic constriction (TAC model), TNFR2 activates the AKT pathway and inhibits the NF-k<sup>B</sup> pathway via mTNF-induced signaling, which alleviates mechanical stress and mediates cardiac hypertrophy rather than directly inducing cardiac fibrosis [\(39](#page-20-0), [40](#page-20-0)).

Although ischemic, and non-ischemic cardiomyopathies can both lead to HF, the mechanisms responsible for the development and progression of adverse ventricular remodeling are different. Whereas MI is characterized by ischemia-induced cardiomyocyte necrosis, leading to acute inflammation and replacement fibrosis ([41\)](#page-20-0), non-ischemic HCM, induced by chronic pressure overload due to hypertension or aortic valve stenosis in patients, does not result in significant cardiomyocyte death. Rather, non-ischemic HCM is characterized by pronounced cardiac hypertrophy, accompanied by blood vascular rarefaction and interstitial/ perivascular fibrosis, also called 'reactive fibrosis' ([41](#page-20-0)) related to chronic low-grade inflammation. Indeed, following a myocardial infarction, a so-called "replacement fibrosis" is occurring where extracellular matrix (ECM) replaces dying cardiomyocytes and muscle loss to maintain heart wall integrity, reinforcing the weakened myocardium. The resulting fibrotic scar is noncontractile, and its size, composition, and physical properties have major implications in the development of post-MI HF [\(42\)](#page-20-0).

In an MI model induced by ligating the left coronary artery, post-MI survival was significantly improved in TNFR1KO but not TNFR2KO mice, while infarct size showed no change in either knockout strain. A loss of TNFR1 signal significantly ameliorated contractile dysfunction after MI, whereas a loss of TNFR2 signal significantly exaggerated ventricular dilatation and dysfunction ([43\)](#page-20-0). In WT mice, MI significantly increased both TNF and  $LT\alpha$ levels in plasma, but in distinct temporal manners. While plasma TNF peaked 1 day after MI, and decreased toward baseline 3 days after MI, plasma  $LT\alpha$  is significantly upregulated 3 days post-MI, and stayed elevated thereafter ([44](#page-20-0)). Thus, TNF and  $LT\alpha$  mediate post-MI cardiac dysfunction via TNFR1 stimulation, whereas TNFR2 activation is cardioprotective against ischemic injury. Thus, simultaneous inhibition of TNF and  $LT\alpha$  or specific TNFR1 function blockade may represent superior cardioprotective approaches over general TNF activity suppression.

While TNF inhibitors have already proven successful in treatment of multiple inflammatory diseases presenting with endstage fibrosis, there is evidence of potential additional uses of these inhibitors for treatment of tissue remodeling and fibrosis. Followup studies should focus on distinct pathogenic roles of TNFR1 versus TNFR2 and their selective inhibition as promising therapeutics for tissue-specific fibrosis.

# 3 LIGHT: HVEM/LT $\beta$ R/DcR3

First described in 1998 by Mauri et al., LIGHT (homologous to Lymphotoxins, shows Inducible expression, competes with HSV Glycoprotein D for HVEM, a receptor expressed on T cells), also known as TNFSF14, HVEM-L (Herpesvirus Entry Mediator Ligand), or CD258, is a pleiotropic cytokine expressed primarily by activated T cells and dendritic cells with critical function in tissue fibrosis [\(2](#page-20-0)–[4](#page-20-0)). Additionally, it is expressed in both soluble and membrane bound form  $(45)$ . The receptors for LIGHT are LT $\beta$ R (lymphotoxin-beta receptor), HVEM, and the Fas-ligand soluble receptor DcR3 (Decoy receptor 3), or TNFRSF3, TNFRSF14, and TNFRSF6B, respectively [\(45](#page-20-0), [46\)](#page-21-0). HVEM is a coreceptor for herpesvirus expressed broadly on structural and hematopoietic cells, including endothelial cells, adipocytes, macrophages, eosinophils, and T cells. HVEM-LIGHT interaction triggers intracellular signaling through NF-kB, stimulating cytokine production ([47,](#page-21-0) [48\)](#page-21-0). LT $\beta$ R is necessary for lymphoid organ development and organization, cell proliferation, and apoptosis ([49](#page-21-0), [50](#page-21-0)). LT $\beta$ R is similarly expressed on all the cell types mentioned except T lymphocytes. Most importantly, one or both receptors are expressed on the main cell types contributing to tissue remodeling and fibrosis: fibroblasts, smooth muscle cells, and epithelial cells. LIGHT is induced in several inflammatory diseases and autoimmune connective tissue disorders with fibroproliferative features, including asthma, idiopathic pulmonary fibrosis (IPF), atopic dermatitis (AD), SSc, eosinophilic esophagitis (EoE), and non-alcoholic fatty liver disease (NAFLD), and many others ([51\)](#page-21-0). Given its receptor expression and induction in diseased states, LIGHT is a key regulator of fibrosis in many organs.

In the lung, LIGHT has been shown to control fibrosis in models of severe asthma and models of IPF. In a house dust mite (HDM)-induced model of chronic asthma, Doherty et al. showed that pharmacological inhibition of LIGHT using an LT $\beta$ R-Fc fusion protein significantly reduced smooth muscle hyperplasia, airway hyperresponsiveness, and lung fibrosis, which identified LIGHT as a target for asthmatic airway remodeling ([52](#page-21-0)). A key finding from these studies in chronic asthma is that LIGHT acts on lung macrophages via LT $\beta$ R, resulting in their accumulation and inducing their expression and subsequent release of TGFB, the primary fibrotic cytokine. Furthermore, this work demonstrated that LIGHT can act on eosinophils via HVEM, significantly increasing their production of IL-13, another potent regulator of tissue remodeling that can synergize with TGF $\beta$  ([52\)](#page-21-0).

In an intratracheal bleomycin-induced model of PF, using both genetic deficiency of LIGHT and antagonistic blockade of LIGHT binding to HVEM and LT $\beta$ R, Herro et al. demonstrated that LIGHT controls thymic stromal lymphopoietin (TSLP) expression

([2\)](#page-20-0). Recombinant LIGHT induces PF similarly to bleomycin induction, indicated by significant elevation in collagen deposition, aSMA accumulation around the bronchioles, and upregulation of mRNA transcripts for TGF $\beta$  and IL-13 ([2\)](#page-20-0). Additionally, abrogating LIGHT signaling significantly reduces TSLP and subsequent lung remodeling and fibrosis. Most notably, LIGHT not only synergizes with IL-13 and TGF $\beta$ , but it also acts directly on bronchial epithelial cells, inducing their expression of TSLP [\(2\)](#page-20-0). This work suggests that LIGHT is playing a critical role in the fibrotic response in many pulmonary diseases.

A recent study by Qu et al. suggests that LIGHT plays a role in viral and bacterial sepsis induced acute respiratory distress syndrome (ARDS) [\(53\)](#page-21-0). From a cohort of 280 patients, in the bacterial sepsis cases (n=189), significantly elevated LIGHT was associated with ARDS, higher Apache III scores, acute kidney injury (AKI), and acute hypoxic respiratory failure (AHRF). Given its profibrotic activity, LIGHT is likely a driver of worsened outcomes in bacterial sepsis.

LIGHT has been shown to be critical for fibrosis in SSc and AD. In a 2015 study, Herro et al. demonstrated that, similarly to its action in IPF, recombinant LIGHT given either subcutaneously or intratracheally induced features of SSc [\(3\)](#page-20-0). LIGHT-deficient mice had significantly reduced skin fibrotic activity following bleomycin induction ([3\)](#page-20-0). Importantly, this work demonstrates that LIGHT acts through HVEM and LTβR expressed on epidermal keratinocytes to promote skin fibrosis. Similar to its activity in bronchial epithelial cells in IPF, LIGHT directly and indirectly (through synergy with TGFβ) controls TSLP expression in keratinocytes promoting skin fibrosis ([3\)](#page-20-0).

In another study by Herro et al., LIGHT signaling in keratinocytes was further investigated ([4\)](#page-20-0). Most notably, LIGHT-HVEM signaling in keratinocytes is required for HDM-induced AD, as it induced strong keratinocyte hyperplasia and periostin production [\(4\)](#page-20-0). In LIGHT-deficient mice, clinical symptoms of AD were abrogated (i.e., skin eruption, bleeding, redness, and scaling). In addition, all type II cytokines were lower and  $TGF\beta$  was nearly absent ([4](#page-20-0)). Periostin, a characteristic feature of type II skin inflammatory disease, was also absent [\(4,](#page-20-0) [54](#page-21-0)). During HDMinduction, mice with a keratinocyte specific HVEM deletion phenocopied LIGHT-deficient mice. It was previously thought that periostin expression by keratinocytes was controlled by IL-13 and TGFB, however, this work shows that it is directly controlled by LIGHT.

In a recent study, Ikawa et al. investigated the role of LIGHT, in vitro, on dermal fibroblasts from SSc patients [\(55](#page-21-0)). LIGHT was significantly elevated in bulk RNA-seq of diffuse cutaneous SSc skin biopsies ([55](#page-21-0)). Conversely, HVEM was significantly decreased in mRNA from dermal fibroblasts. Given that HVEM deletion reduced dermal fibrosis to a greater extent than deletion of  $LT\beta R$ ([3](#page-20-0)), this may suggest that HVEM profibrotic signaling in dermal fibroblasts is more potent that LT $\beta$ R signaling. Further, in vitro recombinant LIGHT increases IL-6 expression and suppressed Th1 chemokine expression in diffuse cutaneous SSc dermal fibroblasts stimulated with IFN $\gamma$  ([55](#page-21-0)). This finding further asserts the role of LIGHT as a key regulator of fibrosis as the stimulation of IL-6 production by dermal fibroblasts would result in increased cellular activation, promoting both inflammation and fibrosis, and LIGHT suppression of Th1 chemokines is consistent with the fact that SSc is characterized by Th2/Th17 polarization.

In the liver, serum LIGHT was significantly increased in NAFLD patients, however, there were no differences found between NASH and simple steatosis  $(56)$  $(56)$ . HVEM and LT $\beta$ R mRNA expression was significantly increased in biopsied NAFLD tissue. LIGHT stimulated release of IL-8, a neutrophil chemokine, from human hepatoma cells (Huh7) was amplified by  $H_2O_2$ , which gives evidence to the role of oxidative stress in the pathogenesis of NAFLD. Genetic deletion of LIGHT resulted in reduced insulin resistance, hepatic steatosis, and expression of genes associated with NALFD to NASH transition in mice given a high-fat highcholesterol diet for 16 weeks compared to controls ([57](#page-21-0)). Furthermore, Liang et al. demonstrated that splenectomy improved liver fibrosis by decreasing the levels of serum LIGHT ([58\)](#page-21-0). Silencing of LT $\beta$ R in macrophages in vitro resulted in decreased levels of fibrosis and  $\alpha$ SMA in murine hepatic fibroblasts (JS1 cells) following treatment with recombinant murine LIGHT; and blocking TGFß abrogated the effects of LIGHT in vitro. These findings suggest that LIGHT may induce  $TGF\beta$  in hepatic macrophages, potentially driving liver fibrosis.

In the GI tract, LIGHT has been shown to play a role in esophageal fibroblast activation and differentiation into myofibroblasts, promoting inflammation and remodeling in EoE. In a study using cells from biopsied EoE tissue, LIGHT induced inflammatory gene transcription in fibroblasts and controlled tethering of eosinophils to fibroblasts via ICAM-1 ([59](#page-21-0)). Additionally, subsequent treatment of  $TGF\beta$  stimulated fibroblasts treated with LIGHT resulted in an inflammatory myofibroblast phenotype.

In the kidney, LIGHT has been implicated in controlling the development of renal fibrosis ([60](#page-21-0)). LIGHT, HVEM, and LTBR were significantly elevated in sera and renal tissue from patients with chronic kidney disease (CKD). This was also reflected in unilateral ureteral obstruction (UUO)-induced mice. Notably, genetic deletion of LIGHT significantly reduced renal fibrosis in UUO mice, indicated by reduction in collagen deposition, aSMA and fibronectin expression, and reduced mRNA expression of TGFb.

LIGHT has also been shown to play a significant role in connective tissue remodeling in primary acquired lacrimal duct obstruction (LDO), an idiopathic disease most common in the elderly. Bielecki et al. found that LIGHT and its receptors, HVEM and LT $\beta$ R, are expressed on mononuclear cell infiltrates, endothelial cells, fibroblasts, and columnar epithelial cells of the lacrimal sacs [\(61\)](#page-21-0). Notably, expression of LIGHT, HVEM, and  $LT\beta R$  were significantly correlated with fibrosis severity in the lacrimal sac walls.

Given the findings from the studies described, LIGHT is a key regulator of fibrosis through both direct and indirect mechanisms (Figure 4). Additionally, signaling through either HVEM, LT $\beta$ R, or both is necessary for LIGHT driven fibrosis. Thus, LIGHT is critical in the control of tissue remodeling and represents a promising therapeutic target for many fibrotic disorders.

# 4 TL1A : DR3/DcR3

The TNF-Like Ligand TL1A (TNFSF15) is a membrane-bound protein identified as a death receptor 3 (DR3) ligand in 2002 ([62](#page-21-0)). It was found to be largely expressed on endothelial cells ([62](#page-21-0)), though it has since been shown to be expressed cells of the immune system, including macrophages, plasma cells, and T lymphocytes [\(63\)](#page-21-0). TL1A signals through DR3 (TNFRSF25) to induce the NF-kB pathway and acts as a costimulatory molecule for both activated T cells and ILC2s, leading to T cell expansion and the secretion of proinflammatory cytokines [\(62,](#page-21-0) [64\)](#page-21-0). Additionally, TL1A signal can be neutralized by its soluble decoy receptor, DcR3 (TNFRSF6B) ([65\)](#page-21-0). The function of TL1A as a regulator of immunity and inflammation has led to numerous investigations of the role of TL1A expression in inflammatory disorders. Indeed, though its expression is usually systemically low, TL1A overexpression has been implicated in conditions such as inflammatory bowel disease and allergic inflammation of the lung and airways [\(63,](#page-21-0) [64](#page-21-0), [66\)](#page-21-0).



Blocking the TL1A signaling pathway using an anti-TL1A antibody in colitis or asthma animal models has been shown to attenuate pathology and inflammation in these disease models ([67](#page-21-0)), further highlighting TL1A as a promising marker for therapeutic strategies against inflammatory disease.

Additional studies indicate a potential for tissue-specific targeting of inflammation through the TL1A pathway. While it is initially expressed as a transmembrane protein, TL1A can be cleaved and expressed in a soluble form [\(62](#page-21-0), [68\)](#page-21-0). Transgenic mice expressing membrane-restricted TL1A were found to have elevated expression of several proinflammatory cytokines in the lung–indicating activation of both innate and adaptive immunity–whereas membrane-restricted TL1A in the small intestine primarily activated T cells, with a combination of soluble and membranebound TL1A required for severe bowel pathology ([68](#page-21-0)). Of note, a consistently upregulated cytokine included IL-13, a major indicator of TL1A-driven inflammation through ILC2 activation [\(64,](#page-21-0) [66](#page-21-0), [68,](#page-21-0) [69](#page-21-0)). In contrast, mice receiving soluble TL1A were found to have elevated expression of IL-13 and associated pathology of the bowel, but not in the lung [\(68\)](#page-21-0). While potential therapies have been proposed that equally target both transmembrane and soluble forms [\(67\)](#page-21-0), tissue-specific functional differences of TL1A indicate a potential for tissue-targeted therapies and may elucidate physiological implications of complete TL1A blockade.

Attenuating TL1A-mediated inflammation will have major implications for the prevention or treatment of chronic inflammatory complications leading to fibrosis. Disease models involving the gastrointestinal tract have frequently been used to study the role of TL1A in the development of fibrosis. While earlier studies indicated a role for TL1A in inducing intestinal inflammation ([64,](#page-21-0) [66](#page-21-0)–[69\)](#page-21-0), recent studies have correlated elevated TL1A with intestinal fibrosis in mice, with affirming a direct role for TL1A-DR3 signaling on colonic fibroblasts and promoting intestinal fibrosis [\(70,](#page-21-0) [71](#page-21-0)). Treatment of Ulcerative colitis (UC) patients with anti-TL1A antibody has been shown to reduce expression of fibrotic pathway markers, including matrix metalloproteinases (MMP7 and MMP10) [\(72](#page-21-0)), and treatment of the induced colitis mouse model with anti-TL1A antibody led not only to the reduction but also to the reversal of collagen deposition in mice with established fibrosis ([73](#page-21-0)). Such results raise the potential for TL1A-DR3 signaling pathways to serve not only as a preventative therapeutic target, but also as a target for treatment of early fibrosis of the gastrointestinal tract.

As elevated TL1A expression has also been implicated in inflammation of the airway, recent studies have examined and affirmed the role of TL1A in promoting fibrosis of the lung. Treatment of mice with recombinant TL1A (rTL1A) has been shown to increase collagen deposition in the lung ([5](#page-20-0), [74](#page-21-0)), and treatment of human lung fibroblasts with rTL1A led to cell-specific proliferation and differentiation to myofibroblasts, as well as production of collagen ([5](#page-20-0)). Blockade of TL1A-DR3 signaling in mice intranasally challenged with the HDM airway irritant resulted in decreased levels of collagen deposition compared to mice administered IgG control, which was accompanied also by a reduction in mucus production–an immediate threat to airway integrity driven by TL1A-driven IL-13 signaling ([5](#page-20-0), [74,](#page-21-0) [75\)](#page-21-0). Interestingly, while a previous study suggested activation of both innate and adaptive immunity in the lung in the presence of overexpression of membrane-bound transgenic TL1A [\(68](#page-21-0)), rTL1A appears to promote mucus production in the absence of lymphocytes and independently of adaptive immunity [\(5\)](#page-20-0). TL1A may therefore have temporal functions in the lung, signaling through innate and adaptive immune systems to differentially elicit an acute muco-secretory or chronic inflammatory response. Additional studies may enable targeted therapeutic strategies upon elucidating the different pathways leading to each pathology.

As TL1A continues to be investigated as a potential therapeutic target for intestinal and lung inflammation, it is becoming increasingly clear that TL1A may be a systemically relevant target for fibrotic conditions in multiple body systems (Figure 5). TL1A was found to be upregulated in liver tissue in a recent study on mice with liver fibrosis, and TL1A transgenic mice exhibited higher levels of MMPs, collagen, and macrophage recruitment in the liver [\(76\)](#page-21-0); however, studies linking TL1A with fibrotic disorders of the liver or other organ tissues are limited. TL1A has been established as a promising therapeutic target for inflammatory, fibrotic, and asthmatic disorders, pending further investigation of tissuespecific signaling pathways and mechanisms of action.



(macrophages, T cells, ILC2s) to drive pro-fibrotic and anti-fibrotic effects. Figure was created with [BioRender.com](https://www.biorender.com/).

## 5 APRIL/BAFF : TACI/BCMA/BAFFR

APRIL (TNFSF13), a proliferation-inducing ligand, and BAFF (also known as BLyS; TNFSF13B), a B lymphocyte stimulator, are two members of the TNF Superfamily [\(77](#page-21-0)–[80](#page-21-0)). While BAFF can exist in membrane bound or soluble forms, APRIL exists only in soluble form ([80](#page-21-0)–[82\)](#page-21-0). The ligands share two receptors of the TNFRSF family, TACI (TNFRSF13B) and BCMA (TNFRSF17), in addition to BAFF's unique receptor, BAFF-R (TNFRSF13C) [\(83](#page-21-0)– [88](#page-21-0)). Though APRIL and BAFF share receptors, their reported affinities differ significantly. On one hand, BAFF has high affinity for both BAFF-R and TACI, with a lesser affinity for BCMA; however, APRIL binds both TACI and BCMA with high affinity, but not at all to BAFF-R [\(89\)](#page-21-0). All three receptors are expressed in circulating B lymphocytes, T lymphocytes, and monocytes [\(90](#page-21-0)). It also has been shown that TACI is expressed in macrophages, playing a role in M1 polarization and inflammation [\(91,](#page-21-0) [92](#page-21-0)). The roles of APRIL and BAFF in B cell maturation and differentiation have been thoroughly described ([93](#page-22-0)–[95](#page-22-0)); however, more recently, it has been shown that these TNFSF members contribute to pathogenic tissue remodeling and fibrosis (Figure 6).

Recent work has implicated elevated serum BAFF levels with elevated non-alcoholic steatohepatitis (NASH) severity. Miyake et al. showed that higher serum BAFF levels were associated with hepatocyte ballooning and advanced fibrosis in these patients, concluding that serum BAFF levels may be a useful tool for distinguishing NASH from simple steatosis [\(96\)](#page-22-0). Similarly, in patients presenting with autoimmune hepatitis, BAFF levels were significantly higher in those with advanced fibrosis (a fibrosis score of F3 or higher) as opposed to those with less severe fibrosis ([97\)](#page-22-0). Concordantly, in an in-vivo study of nonalcoholic fatty liver disease (NAFLD), high fat diet-fed BAFF-/- mice displayed reduced adipose tissue fibrosis and hepatic steatosis despite a lack of body weight reduction ([98\)](#page-22-0).

In patients with mixed connective tissue disease complicated by interstitial lung disease (ILD), serum levels of BAFF and APRIL were elevated compared to those presenting without ILD ([99\)](#page-22-0). However, only BAFF was elevated in the BALF, with no detected increase in APRIL, in a mouse model of bleomycin-driven PF. Additionally, BAFF inhibition in this PF mouse model by genetic ablation or neutralization by a soluble receptor, significantly reduced PF and IL-1 $\beta$  levels [\(100](#page-22-0)). Since BAFF is differentially upregulated in pulmonary fibrosis and correlative with disease severity, BAFF may represent an attractive therapeutic target,

though further work examining the efficacy of pulmonary BAFF inhibition is needed.

Though BAFF is predominantly implicated in liver and lung fibrosis, research indicates that APRIL may play a role in atopic skin diseases. In studies of AD patients, elevated serum levels of APRIL, but not BAFF, are associated with disease severity [\(101,](#page-22-0) [102](#page-22-0)). High serum APRIL levels also strongly correlate with severity in pediatric atopic eczema (AE), both during flare and quiescence, implicating APRIL as a reliable marker of AE severity in children and highlighting APRIL as a promising target for treatment of AE ([103](#page-22-0)). Further mechanistic and in-vivo studies are needed, however, to validate these correlations and understand the relationship between APRIL and fibrotic skin diseases.

Early work showed elevated serum BAFF levels in patients with SSc, with BAFF mRNA expression up regulated in affected skin of patients with early diffuse cutaneous SSc and B cell BAFFR expression increased in SSc patients as compared to healthy controls [\(104](#page-22-0)). Tight skin (TSK/+) mice are used to model development of skin fibrosis in SSc. In these TSK/+ mice, serum BAFF levels are significantly elevated and BAFF antagonist inhibits the development of skin fibrosis and suppresses fibrogenic cytokine production, such as IL-6 and IL-10 ([105](#page-22-0)). Work by Matsushita et al. showed that increased levels of APRIL and BAFF are mutually exclusive in SSc patients, with high APRIL levels indicating pulmonary involvement and high BAFF levels serving as a marker for severe skin fibrosis ([106](#page-22-0)). Opposing these findings, Bielecki et al. found significant association between increased production of APRIL by PBMC and greater skin fibrosis, in addition to pulmonary involvement and increased anti-topo I antibodies ([107\)](#page-22-0). Further work must be done to elucidate the distinct and overlapping roles of BAFF and APRIL in SSc pathogenesis.

Recent studies also explore the pathogenic role of B cells and BAFF in fibrosis and systemic sclerosis. B cells stimulated with BAFF can upregulate profibrotic markers such as collagen,  $\alpha SMA$ , and TIMP1 in SSc human dermal fibroblasts ([108\)](#page-22-0). BAFF inhibition can attenuate fibrosis in a bleomycin-induced mouse model SSc with reduction of fibrotic IL-6 producing Beffs, but not regulatory IL-10 producing Bregs ([109\)](#page-22-0). The exact contribution of B cells to fibrotic processes, however, remains unclear and needs further investigation.

BAFF and APRIL, along with their shared and distinct receptors, remain promising therapeutic targets for inflammatory and fibrotic disorders; however, further studies must be done to understand disease and tissue-specific signaling of these molecules.



# 6 RANKL : RANK/OPG

The receptor activator of nuclear factor kappa-B ligand (RANKL) is a TNFSF member (TNFSF11) most well-known for its role in osteoclastogenesis, maintaining bone homeostasis, and degradation of ECM in bone tissue [\(110\)](#page-22-0). The effects of RANKL are mediated by its binding to its specific, high affinity receptor, the receptor activator of nuclear factor kappa-B (RANK; TNFRSF11A). RANK it is expressed on cells of macrophage/monocyte lineage, which includes bone osteoclasts ([111](#page-22-0)). When RANKL binds RANK, it activates and differentiates osteoclasts and degrades the extracellular bone matrix ([110\)](#page-22-0). RANKL also has a decoy receptor, osteoprotegrin (OPG; TNFRSF11B), which is soluble protein expressed mostly by osteoblasts and an inhibitor of osteoclast activation, counteracting bone resorption ([110](#page-22-0), [111\)](#page-22-0). OPG binds RANKL, limiting RANKL/RANK binding and thus preventing activation and differentiation of osteoclasts. Under normal physiological conditions, the RANKL/RANK/OPG axis is vital for regulating bone turnover and maintaining bone homeostasis. However, in a disease state, the axis can become unbalanced and drive fibrosis. Elevated levels of OPG can inhibit ECM degradation by blocking RANKL-RANK interactions, leading to the buildup of ECM characteristic of fibrotic diseases.

RANKL is upregulated in multiple fibrotic liver diseases, indicating it may play a key role in pathogenesis. Primary biliary cholangitis (PBC) is a disease characterized by injury to the small intrahepatic bile ducts. PBC patient cholangiocytes express elevated levels and RANKL and RANK, which can be associated with disease severity [\(112\)](#page-22-0). Although the exact role of the RANKL/RANK axis in PBC is unclear, activating this signaling pathway inhibits the proliferation of cholangiocytes. The RANKL/RANK axis may have a protective role in PBC and represents a strong potential target for treating PBC [\(112](#page-22-0)). RANKL and OPG expression are both significantly elevated in serum of patients with liver cirrhosis, a disease in which low bone density and bone mass loss can be potential complications. Fabrega et al. suggest that RANKL is stimulated by disease-associated pro-inflammatory cytokines, causing enhanced osteoclast formation, and that the elevated OPG may be an attempt to counteract the bone loss caused by this osteoclast formation ([111\)](#page-22-0).

The RANKL-RANK-OPG axis has been implicated in fibrotic lung disease, though further work is needed to better understand its exact role. In silicosis, a type of pulmonary fibrosis caused by silica inhalation, silica activates lung macrophages and bone osteoclasts via RANKL and TLR4 signaling pathways. This process is thought to increase proteolytic activity of macrophages with a TRAP+ and high MMP-12 phenotype, which may lead to elastin degradation and promote lung fibrosis ([113\)](#page-22-0). In a mouse model of silicosis, work by Jin et al. showed that treatment with the naturally occurring tetrapeptide N-acetyl-seryl-aspartyl-lysyl-proline (Ac-SDKP) reduces RANKL signaling in macrophages and RANKL-induced osteoclast differentiation, highlighting a potential therapeutic role for blocking RANKL-signaling via Ac-SDKP [\(113](#page-22-0)). In cystic fibrosis (CF), CF-related bone disease, characterized by low bone mineral density and increased risk of fracture, is a rising cause of morbidity ([114\)](#page-22-0). Human osteoblasts with a CFTR mutation showed RANKL overexpression and decreased OPG production. This combination shows an increased RANKL-to-OPG ratio, which can drive decreased bone resorption that leads to CF-associated bone loss ([114\)](#page-22-0).

The involvement of OPG pathways in the pathology of cardiac fibrosis is evidenced by several studies. In addition to MI HF, two other forms of cardiac fibrosis may occur and often co-exist: interstitial and perivascular fibrosis. While not necessarily resulting of cardiomyocytes death, these may result in pressure overload or metabolic dysfunction, due to endothelial and immune change in response to hypoxia. Both reactive forms of fibrosis lead to accumulation of fibrous tissue in the perivascular space of coronary arteries and drive cardiac muscle bundle thickening.

Ageing OPG-KO mice developed less interstitial cardiac fibrosis and concomitant activation of MMP-2 ([115\)](#page-22-0), which is known to be associated with fibrosis resolution ([116\)](#page-22-0), tissue inhibitors of MMP-1, -2 and the inactivation of procollagen  $\alpha$ 1 synthesis, while developing cardiac left ventricle hypertrophy and significant loss of contractile function. Moreover, in OPG-KO mice, cardiac hypertrophy following Ang-II-induced hypertension is significantly increased, while less interstitial fibrosis and pro $collagen-\alpha1$  mRNA expression but increased numbers of apoptotic cells is observed ([117\)](#page-22-0). Moreover, blocking IgE-FcERI pathways in TAC- or Ang-II-induced-HCM alleviate pathological heart remodeling and dysfunction. Indeed, in vitro IgE treatment of neonatal cardiomyocytes or cardiac fibroblast induced hypertrophy and activation with matrix protein production and OPG gene expression, respectively [\(118\)](#page-22-0). In human, OPG levels are significantly higher in patients with chronic fibrosis after myocardial infarction than those with no fibrosis, associated with aortic stenosis severity and poorer prognosis [\(119\)](#page-22-0). In addition, higher OPG levels were associated with increased left ventricular mass index and myocardial stiffness in patients suffering of HF with preserved ejection fraction ([120\)](#page-22-0). Collectively, these data suggest a critical role for OPG/RANK/RANKL axis in pathological cardiac remodeling.

The RANKL-RANK-OPG axis represents a potential avenue to develop novel diagnostics and therapeutics for fibrotic disease. OPG expression is upregulated in multiple fibrotic tissues, highlighting the RANKL-OPG interaction as a promising candidate to include in a biomarker panel to diagnose fibrosis [\(110](#page-22-0), [121\)](#page-22-0). Wang et al. showed RANKL mutants that can bind RANK but not OPG, which could be a strong therapeutic tool that warrants further investigation. This therapeutic works by allowing the RANKL-RANK interaction to occur, while limiting obstruction from elevated OPG levels. Future studies should be performed to further explore the therapeutic potential of targeting the RANKL-RANK-OPG signaling axis to treat fibrotic diseases.

## 7 GITRL : GITR

Glucocorticoid-induced TNF receptor family related protein (GITR), also known as TNFRSF18, is a type I transmembrane protein which is constitutively expressed by Tregs at a high level and by resting CD25<sup>-</sup>CD4<sup>+</sup> T cells at a lower level, though expression is markedly increased following T cell activation [\(122](#page-22-0)). In addition to activated effector T lymphocytes, GITR may also be found on other activated immune cells such as NK cells and neutrophils [\(123](#page-22-0)–[125\)](#page-22-0). GITR is activated by its ligand GITRL (TNFSF18), which is mainly expressed on B cells, DCs, macrophages and endothelial cells ([126,](#page-22-0) [127\)](#page-22-0). GITR possesses an intracellular domain bearing significant homology to those of fellow TNFRSF members CD27, OX40, and 4- 1BB, all of which act as powerful costimulatory signals for T cells ([128](#page-22-0)–[130](#page-22-0)). GITR itself is no exception in this regard as it functions as a powerful costimulatory molecule for all T cell subpopulations ([124\)](#page-22-0). Stimulation of CD25 CD4<sup>+</sup> T cells with agonistic anti-GITR antibody (DTA-1) results in promotion of proliferative responses, cytokine production, and expression of activation antigens ([131\)](#page-22-0). Interestingly, while GITR stimulation of CD25<sup>+</sup>CD4<sup>+</sup> T cells (Tregs) results in increased proliferation, it also leads to abrogation of Treg mediated suppression ([122,](#page-22-0) [132](#page-22-0)).

This relationship between GITR and Tregs was further investigated by Kim and Youn through in-vitro cocultures of arthritic mouse derived fibroblast-like synoviocytes (FLS) and Tregs to simulate inflamed synovia. In Tregs, GITRL-expressing FLS caused a reduction in the expression of Foxp3, the master transcription factor which drives Treg development and functionalization ([133\)](#page-22-0). Constitutive expression of GITR on Tregs has been implicated in generating signals which dampen Foxp3 mediated suppressive action and decrease expression stability ([134\)](#page-22-0). Further, anti-GITR mAb (DTA-1) treated Tregs resisted FLSinduced Foxp3 downregulation, which supports the evidence that this Foxp3 downregulation occurs due to GITR signaling ([132,](#page-22-0) [133\)](#page-22-0). This functional downregulation of Tregs subsequently creates a pro-inflammatory environment which can develop into fibrosis if unresolved; however, further in vivo studies investigating this phenomenon in fibrotic models are needed to unravel the relationship among GITR, Tregs, and fibrosis.

In a study by Chen et al., they used a co-culture model of bleomycin treated MLE-12 cells (immortalized mouse lung type II epithelial cell line) and human menstrual blood-derived mesenchymal stem cells (MenSC). MenSC were able to significantly reduce bleomycin induced cell injury and inhibit bleomycin induced epithelial to mesenchymal transition (EMT) ([135\)](#page-22-0). Bleomycin treated MLE-12 cells cocultured with MenSC showed significant downregulation of GITR compared to bleomycin treated MLE-12 cells cultured alone ([135\)](#page-22-0). Immunophenotyping of 79 patients of varying degrees of liver cirrhosis found significant upregulation GITR, CD40L, and OX-40 in patients with cirrhosis as compared to healthy controls [\(136\)](#page-22-0). Combined, these findings strongly suggest that GITR signaling plays a role in promoting fibrosis, and thus could serve as a potential therapeutic target.

The direct role of GITR signaling in the context of fibrosis is perhaps best illustrated by the findings of Cuzzocrea et al., where bleomycin treated GITR<sup>-/-</sup> mice displayed significantly diminished histological signs of lung injury as compared to  $GITR^{+/+}$  mice in a bleomycin model of pulmonary fibrosis [\(137](#page-22-0)). Further, cotreatment of GITR+/+ mice with bleomycin and a GITRL binding Fc-GITR fusion protein resulted in a phenotype resembling that of GITR-/ mice, suggesting that these results are indeed due to disruption of GITRL/GITR signaling. Analysis of BALF also shows that GITR-/- BALF has a lower degree of cellularity compared to that of  $\mathrm{GITR}^{+/+}$ mice. Histological findings correlate areas of lung injury with granulocyte infiltration and show significant reduction of myeloperoxidase (MPO) activity in both GITR<sup>-/-</sup> and Fc-GITR treated GITR<sup>+/+</sup> mice as compared to GITR<sup>+/+</sup> mice ([137\)](#page-22-0). Another potential contributing factor for the  $GITR^{-/-}$  phenotype is the responsiveness of fully polarized Th2 cells and lack of responsiveness of fully polarized Th1 cells to GITR stimulation, as shown by in vitro studies conducted by Motta et al. [\(138](#page-23-0)). This distinction is especially relevant as Th2 cytokine signaling is known to play a central role in the perpetuation of fibrotic processes ([139\)](#page-23-0). The reduction in leukocyte recruitment coupled with an absence of the GITR stimulated pro-Th2 signaling may generate a relatively anti-inflammatory and anti-fibrotic environment, thus possibly explaining the above findings. Though recent studies strongly imply GITR's involvement in fibrosis, additional studies are needed to identify the exact mechanisms responsible.

## 8 OX40 : OX40L

OX40 (also known as TNFRSF4 or CD134) was originally found to be a marker of T-cell activation, as it is only expressed transiently by effector T-cells following antigen binding of the T-cell receptor ([140\)](#page-23-0). Expression of OX40 ligand (OX40L, also known as TNFSF4 or CD252), is largely limited to professional antigen presenting cells such as dendritic cells or activated B cells [\(141](#page-23-0), [142](#page-23-0)). OX40-OX40L signaling is known to modulate activated T-cell activity through costimulatory signaling ([143\)](#page-23-0). More specifically, OX40 signaling promotes activated T-cell survival, proliferation, and cytokine secretion ([144\)](#page-23-0). OX40-OX40L interactions are thus unsurprisingly implicated in various autoimmune diseases such as SSc or systemic lupus erythematosus (SLE) ([145,](#page-23-0) [146](#page-23-0)). However, recent studies suggest that OX40-OX40L may play direct role in causing or promoting fibrosis.

The impact of OX40L expression within the context of a potential new animal model of pulmonary arterial hypertension (PAH) was investigated in a study by Rabieyousefi et al. PAH refers to a category of disease which typically presents clinically with severe pulmonary hypertension and presents histopathologically with pulmonary arteriole occlusion, medial muscular hypertrophy, and intimal fibrosis [\(147](#page-23-0)). Spontaneous PAH onset was stably identified in transgenic C57BL/6 (B6) mice which overexpressed OX40L (B6.TgL). Curiously, this spontaneous onset of PAH was found to be dependent on the presence of OX40L specifically in the B6 genetic background. Pathological manifestations in the colon and lung were observed in transgenic mice with constitutive OX40- OX40L signaling with a B6 genetic background but not in mice with a BALB/c genetic background. These findings aptly point out that the importance of OX40 signaling in fibrosis may become even further enhanced when in the presence of certain predisposing genetic factors.

In a study by Elhai et al., in vivo blockade of OX40L in murine models of SSc prevented the inflammation-driven fibrosis, fibrosing alveolitis, and lung vessel remodeling normally associated with this model [\(148\)](#page-23-0). Additionally, soluble OX40L levels were significantly higher in SSc patient serum samples compared to healthy controls, especially in patients with diffuse cutaneous SSc, the most severe presentation of SSc. Elevated OX40L serum levels at baseline were highly predictive for worsening of dermal and lung fibrosis, indicating that OX40L may serve as a potential biomarker for fibrosis. Current work further suggests OX40L expression may impact development and progression of fibrosis in a variety of different tissues and disease states.

In the skin, the same study by Elhai et al. also found that OX40L lacking mice were protected against bleomycin induced dermal fibrosis, as evidenced by decreased dermal thickness, hydroxyproline content, and myofibroblast count compared to OX40L expressing mice ([148](#page-23-0)). Blockade of OX40L with anti-OX40L monoclonal antibodies even caused regression of established dermal fibrosis in the bleomycin mouse model. Histological examination of biopsied fibrotic skin from SSc patients showed the presence of OX40L staining in cells positive for both CD90 and aSMA, suggesting OX40L is also expressed by fibroblasts and myofibroblasts in fibrotic skin.

OX40 signaling may also play a central role in the process of atherosclerosis. Atherosclerosis-prone receptor deficient mice  $(LDLR^{-/-})$  were placed on a Western-type diet for 10 weeks to induce atherosclerotic lesions in the aorta and aortic arch before being placed on a chow diet and receiving concurrent treatment with anti-OX40L antibody or PBS ([149\)](#page-23-0). While the decrease in dietary lipids alone did improve lesion stability, lesion regression did not occur unless anti-OX40 antibody was also administered. Lesion regression is likely largely due to the loss of Th2 promotion normally caused by OX40-OX40L signaling. This reduction of Th2 polarization is supported by flow cytometry showing a significant reduction in GATA-3 positive cells within the CD4 positive T-cell population. OX40-OX40L signaling disruption represents a potential therapy for established atherosclerotic lesions.

Interference of OX40-OX40L signaling presents as an attractive avenue of potential prophylaxis and/or therapy for a variety of fibrotic diseases including systemic sclerosis, pulmonary arterial hypertension, dermal fibrosis, and atherosclerosis. Soluble OX40L levels also possesses potential as a biomarker for fibrosis and is predictive of worsening dermal and lung fibrosis in systemic sclerosis patients. Recent studies have also demonstrated that OX40L expression extends beyond just professional antigen presenting cells to also include structural cells such as fibroblasts and myofibroblasts. Future studies should seek to further examine the impact of OX40-OX40L signaling in fibrotic diseases beyond the canonical co-stimulation of T-cells through antigen presenting cells.

## 9 CD70 : CD27

CD70 (TNFSF7) is the single natural cognate ligand for the transmembrane glycoprotein CD27 (TNFRSF7). CD70 is expressed on antigen presenting cells and select other cell types like fibroblasts ([150\)](#page-23-0), while expression of CD27 is found on specific subsets of B and T lymphocytes, NK cells and hematopoietic stem cells ([151\)](#page-23-0). The CD27:CD70 costimulatory pathway has previously been well characterized as an important axis for signal transduction among T and B cells ([152,](#page-23-0) [153\)](#page-23-0). This pathway is important for priming naïve T cells and promoting their survival, which directly affects the formation of effector and memory T lymphocytes. The activation of T cells leads to MMP-mediated proteolytic cleavage of CD27 from the cell surface, resulting in secretion of functionally active soluble CD27 (sCD27) ([154](#page-23-0)–[156](#page-23-0)). Thus, CD27 is expressed on naïve T cells and memory CD4+ lymphocytes, but not on activated effector cells ([152,](#page-23-0) [157](#page-23-0)). Concordantly, expression of CD27 is absent from naïve B cells, but upregulation occurs in activated and memory B lymphocytes [\(158](#page-23-0)). The CD70:CD27 cognate interactions in the B cell compartment are necessary for promotion of T cell dependent activation of B cells, the formation of germinal centers, as well as subsequent expansion and differentiation of B cells into plasma cells ([158](#page-23-0)–[161](#page-23-0)). While CD70:CD27 interactions have been thoroughly recognized as providing stimulatory signals for T and B cell activation, the involvement of this axis in fibrosis remains unclear.

Recent research investigating the interaction of CD70 on fibroblasts proposes CD70 as a possible target in fibrotic diseases. Tran-Nguyen et al. demonstrated that CD70 agonists, including Tcell–derived sCD27, were potent inhibitors of fibroblast extracellular matrix protein production such as collagen and fibronectin ([162](#page-23-0)). This work highlights CD70:CD27 axis modulated T cell-fibroblast interactions, linking T cell response to fibrogenesis. In an acute inflammatory state, high CD27 expression and sCD27 secretion by activated CD4 T cells drive elevated fibroblast CD70 activation, consequently inhibiting fibroblast ECM production. Conversely, chronic inflammation is predominated by highly differentiated CD4 T-cell effectormemory (Tem) that do not express or secrete CD27, resulting in enhanced fibrosis. Though these studies used in-vitro and ex-vivo modeling to suggest that stimulation of fibroblast CD70 with an agonist could be a strategy to target fibrosis in chronic disease, further development of in-vivo modeling is needed to confirm the potential for targeting CD70 as an antifibrotic treatment.

Mature CD20+ CD27+ B cells were found to be increased in chronic renal nephritis biopsies in the form of intrarenal lymphoid follicle-like structures and their levels are correlative with disease severity ([163](#page-23-0)). Though double labeling for CD27 and CD20 demonstrated a significant mature memory B cell population, whether these CD20+ CD27+ B cell-dominated structures represent a harmful or potentially beneficial occurrence for progression of renal diseases remains unclear. Future loss of function studies must be done to understand the potential contribution of these mature B cells to fibrosis development.

Doi et al. observed a depletion of CD27+ B cells in cirrhotic patients compared to healthy controls [\(164](#page-23-0)). In addition, the loss of this population was accompanied by impairment of activation, Tcell allostimulation, TNF-beta secretion and IgG production. Supporting these findings, Chang et al. also showed a lack of CD27+ memory B cells in cirrhotic patients [\(165\)](#page-23-0). Further, in this limited pool of CD27+ B cells from cirrhotic patients, there was a statistically significant increase of the pro-apoptotic CD95 (Fas/ TNFRSF6). They concluded that elevated sensitivity to Fasmediated apoptosis, directed by increased exposure surface FasL and endotoxin, was likely driving the depletion of CD27+ memory B cells and contributing to systemic infection risk. To resolve the role of these B cells in cirrhosis, further mechanistic and in-vivo studies are needed to clearly define any causal relationships between these phenomena.

In an in-vivo experimental autoimmune myocarditis (EAM) model, activated cardiac NK cells expressed CD27 and depletion of CD27+ NK cells during EAM resulted in increased disease severity, including elevated fibrosis and an influx of cardiac infiltrating eosinophils [\(166](#page-23-0)). In vitro, CD27+ NK cells limited infiltration of eosinophils both directly, through induction of eosinophil apoptosis, and indirectly, via alteration of eosinophil-related chemokines by cardiac fibroblasts. Thus, while this work proposes a pathway of NK cell-driven eosinophilic regulation, further confirmation in human models is needed to determine therapeutic potential of targeting CD27+ NK cells.

Serum levels of soluble CD27 positively correlated with disease severity in SSc biopsies, highlighting the potential for targeting the CD27:CD70 axis ([161\)](#page-23-0). Thus, skin tissue expression of CD27 and serum levels of sCD27 may be useful diagnostic markers for SSc. Similarly, Luo et al. emphasized epigenetic involvement in disease pathogenesis and highlighted the differential expression of CD70 in SSc patients, which is associated with disease severity ([167\)](#page-23-0). These studies remain correlative, however, and require in-vivo validation to determine the contribution of the CD27:CD70 axis in SSc development.

## 10 TRAIL : DR4/DR5/DcR1/DcR2

Tumor necrosis factor-related apoptosis-inducing ligand (TRAIL), also known as TNFSF10, Apo-2 ligand, or CD253, is a Type II membrane protein bearing high levels of homology to Fas ligand ([168\)](#page-23-0). TRAIL is primarily expressed by lymphocytes, monocytes, and natural killer cells ([169](#page-23-0)–[171](#page-23-0)). Though membrane bound, TRAIL can also undergo proteolytic cleavage and be released in a soluble form which then goes on to bind one of five different receptors. The canonical TRAIL signaling pathway involves its binding to either of two death domain containing death receptors, death receptor 4 (DR4, also known as TRAIL-R1 or TNFRSF10A) ([172\)](#page-23-0) or death receptor 5 (DR5, also known as TRAIL-R2 or TNFRSF10B) ([173](#page-23-0)), thus prompting receptor homotrimerization along with the recruitment of the adaptor protein Fas-associated death domain (FADD), resulting in the formation of death-inducing signaling complex [\(174\)](#page-23-0). FADD then recruits and activates procaspase-8 and downstream signaling events ultimately lead to apoptosis [\(174](#page-23-0)). TRAIL may also bind to either of two membrane decoy receptors, decoy receptor 1 (DcR1, also known as TRAIL-R3 or TNFRSF10C) which completely lacks a death domain ([175\)](#page-23-0) or decoy receptor 2 (DcR2, also known as TRAIL-R4 or TNFRSF10D) which possesses a truncated nonfunctional death domain [\(176](#page-23-0)). Finally, the secreted glycoprotein and TNF superfamily member OPG serves as a soluble decoy receptor for TRAIL, albeit with slightly reduced affinity compared to DcR1 and DR5 ([177\)](#page-23-0). Mice possess two TRAIL decoy receptors and a single TRAIL death receptor (mDR5) which bears greater similarity to human DR5 than to human DR4 [\(178](#page-23-0)).

Though TRAIL is mainly known for its ability to selectively induce apoptosis in cancer and transformed cells while sparing normal cells [\(179](#page-23-0), [180](#page-23-0)), its potential beyond the treatment of cancer has gained growing attention in recent years. TRAIL has robust applications in the context of liver fibrosis. Activated hepatic stellate cells (aHSCs) are the cell type primarily responsible for liver fibrosis and were found to have increased expression of DR4 and DR5 ([181\)](#page-23-0). This upregulation of DR4 and DR5 suggests that TRAIL may be capable of selectively targeting aHSCs to effectively treat liver fibrosis. Indeed, systemic administration of PEGylated TRAIL was found to ameliorate carbon tetrachloride  $(CCl<sub>4</sub>)$  induced liver fibrosis and cirrhosis in rats, as measured by reductions in  $\alpha$ SMA and collagen deposition, via selective killing of aHSCs without any off-target apoptosis. The remarkable specificity of this preparation is noted by the authors to contrast with the recombinant TRAIL formulations and TRAIL agonists used in cancer research. This suggests that the design of anti-fibrotic TRAIL/TRAIL agonist formulations will require additional considerations to limit offtarget effects and perhaps include a mechanism to eventually suspend apoptosis to allow for tissue healing. This work also emphasizes the importance of screening potentially targetable cell types in a fibrotic disease for TRAIL sensitivity, as aHSCs are known to not undergo spontaneous apoptosis and resist a myriad of proapoptotic stimuli ([182\)](#page-23-0).

The efficacious results of this approach are also demonstrated by Park et al. in the investigation of engineered TRAIL treatment in SSc. Dermal myofibroblasts are the principal cell type responsible for fibrosis in scleroderma and thus present as an obvious potential therapeutic target. RNA-seq data from skin biopsies of SSc patients revealed greatly upregulated DR4 and DR5 mRNA expression in addition to other typical fibrogenic components ([183\)](#page-23-0). In vitro studies of primary human dermal fibroblasts show that  $TGF- $\beta$ 1, the$ cytokine which induces dermal myofibroblasts transdifferentiation, also significantly induces both mRNA and protein expression of DR4 and DR5. Treatment with engineered TRAIL not only selectively killed dermal myofibroblasts but was even able to reverse established skin fibrosis to near-normal architecture in both an inducible (bleomycin) and genetic (Tsk-1) mouse model of SSc.

It is also becoming increasingly evident that TRAIL can play a major role in fibrotic diseases by affecting inflammatory processes. In investigating the role of TRAIL in the A fumigatus mouse model of EoE, TRAIL was significantly upregulated in EoE patients as compared to their healthy counterparts [\(184](#page-23-0)). TRAIL is also known to upregulate expression of the E3 ubiquitin-ligase midline-1 (MID-

#### TABLE 2 Clinical trials targeting TNF superfamily members to treat fibrotic disease.



<span id="page-13-0"></span>Frontiers in

[Immunology](https://www.frontiersin.org/journals/immunology)

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Frontiers in

[Immunology](https://www.frontiersin.org/journals/immunology)









Clinical trials in Phases 1-3 targeting TNFSF members or their receptors to treat diseases presenting with fibrosis. Due to the successful results and FDA approval of anti-TNFα therapies, please note that all clinical tri

1), whose downstream signaling events promote inflammation through inhibition of protein phosphatase 2A (PP2A) activity. TRAIL deficient mice treated with MID-1 targeted small interfering RNA (siRNA) displayed reduced esophageal eosinophil and mast cell counts along with protection against esophageal circumference enlargement and collagen deposition. Additionally, TRAIL was found to be necessary for the upregulation of four key cytokines implicated in EoE pathogenesis: CCL11, CCL24, TGFß, and TSLP. It was also discovered that the production of IL-5, which is the major driver of allergen induced-EoE, and IL-13, which plays a supporting role to IL-5, are TRAIL dependent. Histological findings also demonstrated that TRAIL expression is required for esophageal remodeling in this model of EoE.

TRAIL exemplifies the diversity of functions found within the TNF superfamily and shows great promise as a potential therapy for several fibrotic diseases because of it. Engineered TRAIL has demonstrated excellent selectivity and efficacy in killing target cell types in multiple fibrotic diseases, leading to amelioration and sometimes even reversal of fibrosis in animal models. Notably, TRAIL can induce apoptosis in cell types which are known to be particularly resistant, such as aHSCs and MFBs. TRAIL is therefore an excellent therapeutic candidate in fibrotic diseases where the primary driver of fibrosis is TRAIL sensitive or could reasonably be induced to become TRAIL sensitive. However, there is a need for further investigation into screening potential target cell types for TRAIL sensitivity and signaling pathways which affect TRAIL, DR4, and DR5 expression. Finally, the recent findings showing TRAIL's involved role in the various inflammatory processes leading to EoE highlights the need explore TRAIL signaling beyond the canonical apoptotic paradigm with emphasis on non-canonical TRAIL signaling.

# 11 Concluding remarks

Although TNFSF members were first identified as mediators of inflammation, apoptosis, and cell survival, our lab and others have recently implicated these members as drivers and regulators of fibrosis and tissue remodeling in many diseases and across numerous organs. Based on the growing literature, select TNFSF members are up regulated in fibrotic disease states in humans. These TNFSF members represent potential therapeutic targets for improving fibrotic disease outcomes and novel biomarkers for tracking disease progression in minimally invasive manners. TNF inhibitors are already approved and efficacious for treatment of diseases presenting in end stage fibrosis, including UC, rheumatoid arthritis, psoriatic arthritis, ankylosing spondylitis, juvenile idiopathic arthritis, Crohn's disease, plaque psoriasis, juvenile idiopathic arthritis, and non-radiographic axial spondyloarthritis. Currently ongoing clinical trials at many stages of development for other TNFSF inhibitors, described in [Table 2](#page-13-0), indicate a potential for targeting additional members in fibrotic disorders. Given current research on TNFSF members and fibrosis, in patients with scarring and tissue remodeling, blocking select TNFSF members by either neutralizing reagents or by antibodies to their receptors may represent a therapeutic benefit compared to presently available treatments which only slow disease progression as opposed to reversing fibrosis.

# Author contributions

HS, RH, VT, JC, AW, GD, JB, EC, and AG all contributed to writing this manuscript. HS made the Figures and Tables. HS and RH edited the manuscript. All authors contributed to the article and approved the submitted version.

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# Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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