



Tumor Necrosis Factor- α in Heart Failure: an Updated Review

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Abstract

Purpose of the Review Proinflammatory cytokines are consistently elevated in congestive heart failure. In the current review, we provide an overview on the current understanding of how tumor necrosis factor- α (TNF α), a key proinflammatory cytokine, potentiates heart failure by overwhelming the anti-inflammatory responses disrupting the homeostasis.

Recent Findings Studies have shown co-relationship between severity of heart failure and levels of the proinflammatory cytokine TNF α and one of its secondary mediators interleukin-6 (IL-6), suggesting their potential as biomarkers. Recent efforts have focused on understanding the mechanisms of how proinflammatory cytokines contribute towards cardiac dysfunction and failure. In addition, how unchecked proinflammatory cytokines and their cross-talk with sympathetic system overrides the anti-inflammatory response underlying failure.

Summary The review offers insights on how TNF α and IL-6 contribute to cardiac dysfunction and failure. Furthermore, this provides a forum to begin the discussion on the cross-talk between sympathetic drive and proinflammatory cytokines and its determinant role in deleterious outcomes.

Keywords Heart failure · Beta-adrenergic receptor · G-protein coupled receptor kinases · Tumor necrosis factor alpha · Interleukins · Cardiac hypertrophy and dilation

Introduction

Heart failure is a complex progressive pathology, a phenotype reflective of an end organ damage as a consequence of insults/injuries, including hypertension, dyslipidemia, diabetes, ischemic heart disease, post-partum cardiomyopathy, and congenital disorders [1–4]. In response to the tissue injury from the diverse array of insults, the heart initiates tissue repair mechanisms by engaging the innate immune system. Consistent with the engagement of innate immunity, significant increase in the repertoire of proinflammatory cytokines is observed following cardiac insult [5, 6, 7•]. Tumor necrosis

factor- α (TNF α), transforming growth factor β (TGF β), and family of interleukins, including IL-1, -12, -8 and -18 are among the most common proinflammatory cytokines observed following cardiac stress [8, 9•]. The increase in the proinflammatory cytokine profile is a responsive tissue repair mechanism that is considered to provide beneficial effects by mediating cardiac remodeling. Accumulating evidence indicates that the acute proinflammatory stage is classically followed by the anti-inflammatory response to resolve the injury [10, 11]. However, given the diverse and unique nature of cardiac stress, the proinflammatory response is accentuated due to localized smooth muscle injury associated with increased extravasation of leukocytes that prolongs the proinflammatory cycle [7•, 12, 13]. The prolonged proinflammatory process if unchecked by the anti-inflammatory mechanisms transitions to chronic inflammation, aided in part by the constant cardiac stress mediated by co-morbid conditions like hypertension, diabetes, etc. [6, 14]. A key component in sustaining chronic inflammation is the infiltration of cardiac tissue by macrophages, which forms the nucleating site for generation of proinflammatory cytokines. Thus, there is excessive production and release of these cytokines into circulation, which in turn could have adverse effects on remote organs [15, 16•]. Consistent with their deleterious effects,

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multiple studies have suggested the use of TNF α and IL-6 as potential markers for heart failure [16••, 17–19]. Furthermore, high levels of proinflammatory cytokines like TNF α can impact cardiac function by mediating signals that underlie deleterious cardiac remodeling and negative inotropic effects [20–22]. In addition to the negative inotropic influence on the heart, there is also growing evidence of dynamic cross-regulation between sympathetic system and immune response [23]. Understanding the cross-talk and regulation becomes important given that cardiac function is tightly regulated by sympathetic signaling mechanisms [24]. In this context, we hope that our succinct review provides critical insights into immune responses focusing on integrating the cross-regulation between sympathetic systems and inflammation that mediate cardiac function/dysfunction and failure.

Innate Immune Response in Cardiac Remodeling and Heart Failure

The heart maintains cardiac tissue homeostasis like any other organ/tissue systems by engaging the innate and adaptive inflammatory responses. Traditionally, the innate immune response is associated with infections [25], and thus, difficult to envision its role as a part of initial inflammatory response [26]. However, it has come to be recognized that heart also encodes the classical germ-line encoded pattern recognition receptors that initiate repair upon detecting pathogen-associated molecular patterns (PAMPs or damage-associated molecular patterns (DAMPs) [6, 27, 28]. There is increasing appreciation that the pattern recognition receptors can detect molecules of self-origin like DAMPs providing the link between cardiac tissue injury/damage to the initial proinflammatory response [7••, 29]. In the context of cardiac injury, the DAMPs could include mitochondrial components, dsRNA, heart shock proteins released from damaged/necrotic cardiomyocytes, or degraded extracellular matrix components like Hyaluronan fragments [6, 30, 31]. These molecules engage the recognition pattern receptors to mediate a robust inflammatory response with infiltration of neutrophils and monocytes that initiate tissue repair. Given the robustness of the inflammatory response “sans,” the pathogenic infection in the cardiac tissue, it has been referred to as “sterile infection.” Thus, the innate inflammatory response is mediated by an ensemble of components involving macrophages, dendritic cells, and poly-morphonuclear granulocytes through cytokines, chemokines, and activation of complement system [32–34].

A key determinant in the robust innate inflammatory response is the pattern recognition receptors that are activated by DAMPs or PAMPs, which are primarily represented by Toll-like receptors (TLRs) and C-type lectin receptors (CLRs) [35–37]. In addition to these classical pattern recognition receptors, there are also intercellular receptors like retinoic acid-

inducible gene-1-like receptors (RLRs) and nucleotide-binding oligomerization domain-like receptors (NLRs) [34, 38, 39]. Together, this repertoire of pattern recognition receptors senses the DAMPs and/or PAMPs to mediate the initial repair response to resolve the damage. Although the roles of pattern recognition receptors are well described in immune cells, less is known about their roles in cardiac systems, especially in cardiomyocytes. In this context, it is important to note intense studies are in progress defining the roles of pattern recognition receptors in human hearts and in conditions of failure. It is known that human hearts express the ensemble of pattern recognition receptors, including TLRs, CLRs, and NLRs [38, 40, 41]. Thus, expression of these set of receptors in human heart may provide a quick and robust inflammatory repair response to cardiac stressors, including injury to cardiac tissue or infection [34, 37, 42].

The primary purpose of this response is to resolve the source underlying disruption of homeostasis with aim to restore cardiac function. However, given that co-morbidities like hypertension, dyslipidemia, and diabetes are sustained cardiac stressors, in turn, ensues in prolonged inflammatory response leading to persistent low-grade inflammation. This low-grade inflammation that occurs in the absence of any identifiable infection is termed “parainflammation” [43]. Occurrence of this low-grade inflammation suggests that the heart is not able to restore homeostasis by resolving the initial inflammatory response [44]. Consistent with this idea, human heart failure has long been known to be associated with elevated levels proinflammatory cytokines (TNF α and IL-6) [19, 45] and reduced level of circulating regulatory T cells (Tregs, known to suppress immune response) [46–48]. In addition, Tregs from heart failure patients have innately reduced functional capability to suppress cytokines production [46, 47]. Accordingly, rodent studies have shown that transfer of Tregs from healthy to hypertension-induced cardiac hypertrophic rats results in reverse remodeling and amelioration in cardiac function [48]. This supports the idea that resolution of the inflammatory response may not occur efficiently paving the way for a low-grade inflammation that could transition into a sustained low-grade pathological proinflammatory response.

An integral part of the inflammatory response with progression of heart failure is the simultaneous observation of graded increase in the proinflammatory cytokine profile. However, due to the complexity of the immune response, a key question that remains to be addressed is whether proinflammatory cytokines are the “cause” or “effect” of HF. Thus, despite evidence that inflammatory cytokines are associated with heart failure, anti-cytokine therapies have not achieved significant success [49, 50], in part, due to incomplete understanding of the beneficial vs. deleterious role these play in cardiac remodeling [51]. It is known that proinflammatory cytokines bind to their cognate receptors to mediate their effects through a key transcription factor—nuclear factor kappa B (NF- κ B) [52,

53]. NF- κ B is engaged by both the innate immune response as well as by the proinflammatory cytokines [6, 54]. Increasing evidence shows that NF- κ B can be activated by canonical and non-canonical pathways reviewed in-depth in Bartekova et al. [9••]. Canonical activation of NF- κ B involves the activation of I κ B kinase that predominantly mediates p65/p50 dimer to be translocated to the nucleus to initiate transcription [9••, 55, 56]. Non-canonical activation involves IKK α kinase complex predominantly mediating p52/RelB complex translocation to the nucleus [57, 58]. Despite these complexities in activation, NF- κ B is well-known to mediate both beneficial and deleterious effects reflecting the beneficial vs. deleterious role of inflammation in cardiac remodeling and failure.

Given that human heart failure is associated with an elevated proinflammatory cytokine milieu, a key question studies have been focused are on determining whether biological effects of proinflammatory cytokines are adequate to provoke a phenotype of heart failure in experimental animals and in humans [7••]. However, increasing evidence supports the prevailing idea that heart failure progression occurs as a result of deleterious signaling exerted by proinflammatory cytokines secreted by the hearts in addition to the secondary effects accruing from circulating cytokines [59]. Thus, chronic sustained inflammation contributes to worsening of heart failure phenotype reminiscent of the sustained neurohormonal activation in heart failure. In this context, pathological effects of chronic proinflammatory cytokines have been extensively reviewed [23, 51], including their role in cardiomyocyte function [23] and ventricular remodeling [7••, 60]. Studies have shown that proinflammatory cytokines directly modulate cardiac contractile output, wherein this modulation can be mediated by immediate and delayed effects. The early immediate outcomes encompass effects on EC coupling [19, 28–40], NOS leading to nitric oxide generation [61–78], sphingomyelinase signaling [67, 70, 72, 77–92], and phospholipase A2 (PLA2) and arachidonic acid (AA) activation [81, 93–99]. In contrast, the delayed effects also play a role in modulating contractile function by altering β AR signaling, wherein loss of β AR responsiveness to β AR agonists like isoproterenol underlies the reduction in contractile responses [22, 67, 100, 101].

Tumor Necrosis Factor- α (TNF α)

TNF α belongs to a large family of proinflammatory cytokine TNF ligands (Table 1) that play a key role in immune responses and are altered primarily in autoimmune diseases [102]. Although analysis has shown that some of the TNF family of ligands are elevated in heart failure [103, 104] (Table 1), less is understood about their role in heart failure. Among these TNF superfamily of ligands (TNFSF), one of the key members that has been extensively studied, including

Table 1 Changes in expression of the tumor necrosis factor (TNF) superfamily of ligands (TNFSF) in heart failure [103, 104]

Member of TNF family	Ligand	Expression in heart failure
TNFSF1	LT α	NA
TNFSF2	TNF α	Elevated
TNFSF3	LT β	Unchanged
TNFSF4	OX40L/CD252/gp34	Unchanged
TNFSF5	CD40L/CD154/gp39	Elevated
TNFSF6	FasL/CD95/Apo1	Elevated
TNFSF7	CD27L/CD70	Elevated
TNFSF8	CD30L	Unchanged
TNFSF9	4-1 BBL	Unchanged
TNFSF10	TRAIL	Elevated
TNFSF11	RANKL/TRANCE	Elevated
TNFSF12	TWEAK	Unchanged
TNFSF13	BAFF/APRIL	Elevated
TNFSF14	LT γ /LIGHT	Elevated
TNFSF15	TL1	NA
TNFSF16	GITRL/TL6	NA

NA data not available

Ligand: LT α lymphotoxin α , TNF α tumor necrosis factor- α , LT β lymphotoxin β , Apo1 apoptosis 1, TRAIL TNF α -related apoptosis inducing ligand, RANKL receptor activator of NF- κ B ligand, TRANCE TNF α -related activation induced cytokine, TWEAK TNF-like weak inducer of apoptosis, BAFF B cell activating factor, APRIL a proliferation inducing ligand, LT γ lymphotoxin γ ; LIGHT lymphotoxin-related inducible ligand that competes for glycoprotein D binding to herpes simplex virus entry mediator on T cells; TL1 TNF-like 1, GITRL glucocorticoid-induced TNF receptor ligand, TL6 TNF-like 6

its use for therapeutic strategies and as a potential biomarker associated with heart failure is TNF α [19, 45, 49, 50]. One of the key mediators of TNF α signaling in the cells is through NF- κ B, which again is reflective of the dual role TNF α plays in cardiac physiology and pathology [105]. The downstream cellular effects of TNF α are mediated by two cognate receptors, TNF receptor 1 or 2 (TNFR1 or 2) [106]. Classically, it is considered that TNF α activation of TNFR1 is deleterious, while TNFR2 is beneficial and the relative ratio of their expression in a given tissue system would potentially drive the phenotypes [106–108]. In addition to the divergent roles the receptors play in TNF α signaling, it is known that these receptors can be shed from various cells to generate soluble TNFR1 or 2 (sTNFRs). Circulating TNF α may bind to these receptors depleting the available pool of TNF α to bind and activate membrane TNFRs on cells [85, 109]. However, it is important to note that the role of these sTNFRs is not yet well understood in the overall cardiac pathophysiology [51]. Furthermore, TNF α as an inflammatory ligand has two forms: (a) the membrane bound form and (b) the secreted form [110, 111], adding another layer of complexity in the overall development of pathophysiology. Despite the complexities of

TNF α signaling, multiple studies have shown that cardiomyocyte-specific expression of TNF α results in depressed cardiac function that is gene dosage dependent [112, 113]. Consistently, studies have shown that TNF α per se mediates negative inotropic effects in vitro and in vivo [114–116] and is discussed later in the review. Such findings indicate that the proinflammatory cytokine TNF α could cross-talk with the beta-adrenergic receptor (β AR) system, and thereby, underlie the negative inotropic phenotype observed in heart failure.

Cross-Talk Between Inflammatory Cytokines and Sympathetic System

Sympathetic overdrive and elevated levels of proinflammatory cytokines underlie the progression of heart failure and a key concern has been whether these parallel pathways cross-talk and contribute to the pathology. In this regard, many studies have consistently shown that an increase in proinflammatory cytokine TNF α leads to negative inotropy both in “in vitro” and “in vivo” settings [115, 116]. Given that β ARs are key regulators of cardiac inotropic responses, these observations show that proinflammatory cytokines like TNF α could directly alter β AR function to induce negative inotropy. Similarly, chronic activation of β ARs by sympathetic system results in induction of proinflammatory response characterized by increased expression of TNF α , IL-1 β , and IL-6 in the hearts [117–120]. Consistently, antagonizing β ARs using the β -blockers markedly reduces myocardial TNF α and IL-1 β expression in the hearts [121] indicating a “quid-pro-quo” relationship between the sympathetic β AR activation and induction of inflammatory responses. As discussed in the earlier part of the review, upregulation of TNF α , IL-1 β , and IL-6 in the myocardium occurs through the NF- κ B dependent mechanisms [122, 123]. In addition, studies have shown an increase in the proinflammatory cytokine profile following sympathetic β -agonist is markedly blunted by epidermal growth factor receptor (EGFR) blocker gefitinib [124] indicating another layer of complexity in the dynamic cross-talk between inflammatory cytokines and sympathetic systems. Thus, accumulating evidence from multiple studies portrays the existence of a dynamic cross-talk between sympathetic activation and proinflammatory responses that determines the ultimate cardiac phenotype.

Proinflammatory milieu (TNF α) modulates cardiac sympathetic response TNF α is a known negative cardiac depressant and thought to mediate these effects through β ARs [114, 115]. As discussed, TNF α is thought to mediate these effects by engaging immediate and delayed signaling mediators. The immediate effects include alterations in Ca²⁺ [93], sphingolipid mediators [75] and nitric oxide synthase [74]. However, the mechanistic underpinnings of the delayed signaling mediators are still an area of intense study. Despite the knowledge that

TNF α drives negative inotropy through β ARs, less has been known on whether traditional pathways that mediate β AR dysfunction are engaged by the TNF α -driven mechanisms. Sympathetic hormones (catecholamines) mediate cardiac contractility through β ARs [24, 125]. Diminution in β AR signaling to catecholamines occurs through β AR desensitization contributing to the pathogenesis of heart failure. β AR desensitization is mediated by phosphorylation of the receptor by G-protein coupled receptor kinases (GRK 2, 3, 5, and 6), protein kinase C (PKC), and protein kinase A (PKA). Among them, GRK2 is a predominant player [126–128] as blocking recruitment of GRK2 to the β ARs through a strategy of deploying C-terminal of GRK2 (GRK2-Ct) results in beneficial cardiac remodeling [127]. In this context, GRK2 is consistently upregulated in response to proinflammatory cytokine TNF α in various tissues [129], and our studies identified that cardiac GRK2 is upregulated in mice with cardiac overexpression of TNF α , which occurs before cardiac dysfunction [22].

GRK2 upregulation in response to TNF α in these hearts indicates that GRK2 could be the proximal link in mediating cardio-depressant effects of TNF α through β AR dysfunction [113–115]. Studies showed that GRK2 is key in mediating β 2AR desensitization following TNF α as cardiomyocyte conditional GRK2 knockout mice had preserved β 2AR function despite elevated TNF α . In contrast to the known benefits afforded by cardiomyocyte-specific expression of GRK2-Ct, expression of GRK2-Ct expression was not able to ameliorate cardiac dysfunction in response to TNF α . This indicates the presence of a yet unknown mechanism by which GRK2 can be recruited to phosphorylate β AR instead of the traditional G-protein beta-gamma (G $\beta\gamma$) subunits [126, 130, 131]. Furthermore, recruitment of GRK2 to the β AR complex is mediated by TNFR2 as there was marked reduction in GRK2 recruitment to β ARs in TNFR2 knockout cells [22], potentially indicating mechanisms that could be independent of G $\beta\gamma$ subunits. However, such a role for TNFR2 is counter-intuitive as TNFR2 is considered to play a beneficial role compared to TNFR1 signaling [22]. In conditions of heart failure with significant pre-existing sympathetic overdrive, TNFR2 signaling could provide beneficial effects by dampening cardiac function in presence of TNF α by mediating non-canonical β AR desensitization. Such mechanisms could underlie the beneficial role TNFR2 may play in presence of chronic β AR agonist as studies have shown that absence of TNFR2 (TNFR2 knockout mice) results in deleterious cardiac remodeling to β -agonist isoproterenol [21, 132]. These observations indicate a dynamic relationship exists between the sympathetic β AR activation and proinflammatory cytokine TNF α .

Sympathetic signals modulate immune response Given the dynamic “quid-pro-quo” relationship, wherein TNF α mediates β AR dysfunction, thereby reducing the ability of β ARs to respond to sympathetic stimulation. While, simultaneously,

sympathetic overdrive in turn elevates inflammatory cytokine TNF α setting up a deleterious feed-forward and feed-back loop. A biochemical feature observed in many pathologies including obesity, rheumatoid arthritis, myocardial infarction, and kidney renal injury [60, 133, 134]. The sympathetic nervous system (SNS) is integral to the overdrive that mediates increased proinflammatory cytokines profile. SNS innervates both primary organs and lymphoids like bone marrow, thymus, and secondary lymphoid tissues, including the spleen and lymph nodes [135–139]. This innervation of noradrenergic fibers provide direct communication between the nervous system and cells of the immune system through catecholamine neurotransmission. In addition, circulating catecholamines released from the adrenal medulla also influences immunocompetent cell activity [140–142]. In this context, it is important to note that the functional response displayed by the immune cells in part is mediated by the β ARs on these cells in response to catecholamines [139, 143–146].

The SNS driven catecholamine effects are mediated by the most commonly expressed member of adrenergic receptor family (composed of α 1, α 2, β 1, β 2, and β 3 [147]), the β 2ARs, that are found in the majority of immune cells except T-helper 2 cells [148–151]. However, studies have shown that the expression of the repertoire of the adrenergic receptor members can be altered in pathology, like upregulation of α 1- and α 2ARs in certain lymphoid compartments [152]. Though a speculation, the differences in receptor subtype expression in various immune cells may underlie the apparent controversial effects of catecholamines with regard to their pro- and anti-inflammatory effects that could be dependent on cell type, activation state, and other circumstances [151–153]. For example, α AR stimulation enhances, while β AR stimulation inhibits lymphocyte proliferation, antibody secretion, and proinflammatory cytokine production [148–150]. Further, β 2AR activation is known to increase NK cell number and activity [142], whereas α AR drives bone marrow-derived lymphocyte production [154, 155] mimicking acute psychological stress and exercise [142, 154, 155]. In contrast to acute catecholamine release, chronic elevation of catecholamine levels decreases lymphocyte and NK cell numbers in the peripheral blood without altering immune cell distribution [156]. Despite these differential effects, accumulating evidence indicates that sympathetic overdrive leads to an increase in proinflammatory cytokine response resulting in neuroinflammation and pain in fibromyalgia [157], while causing negative inotropy in heart leading to heart failure.

An important aspect that needs recognition is the parallels observed between the sympathetic and immune systems. It is well-known that the “fight-or-flight” response triggers SNS and hypothalamic-pituitary-adrenal (HPA) axis activation in an attempt to overcome the effects of the stressors with an aim to return homeostasis [154, 155]. Similarly, during acute stress the innate immune system is activated to release

proinflammatory cytokines that prepares the body to fight infections or limit injury [158]. However, in the context of inflammation, chronic stress is believed to induce a shift from an adaptive response to immunosuppression, potentially through receptor desensitization or downregulation, with detrimental outcomes for the host [159] that are associated with low-grade inflammation. This low-grade inflammation due to chronic stress has a negative impact in the context of cardiac function, as evidenced in the co-morbidities of numerous pathologies like cardiovascular disease, metabolic syndrome, and arthritis among others [160, 161]. Given the dynamic cross-talk between SNS and inflammatory response, it is possible that the stress-induced immunomodulation is mediated by the SNS activation, which maintains a low-grade inflammation. This in turn causes negative inotropy, leading to increase in epinephrine/norepinephrine levels and keeping this SNS-inflammatory cytokine cycle active. At a cellular level, epinephrine/norepinephrine released from the nerve endings or adrenal medulla results in adrenergic activation and GRK2 upregulation in lymphocytes, leukocytes, and other immune cells [162], which in turn underlies the chronic immune response that seems to occur in the absence of active infection. However, it is important to note that the immunomodulatory effects by epinephrine/norepinephrine could be different depending on pathology like rheumatoid arthritis and multiple sclerosis, which are associated with decreased PBMC GRK2 levels [163, 164] in contrast to heart failure [165].

In conditions of heart failure, it is well-known that sympathetic overdrive is coupled with elevated proinflammatory cytokine profile. Studies have found a persistent relationship between circulating TNF α and soluble TNF receptors and mortality in patients with heart failure [51]. Given the evidence, it is perhaps easy to speculate that sympathetic overdrive induces TNF α , which mediates cellular/physiological responses that initially may be beneficial but becomes deleterious with time. In terms of the molecular signaling, TNF α produced in response to β AR activation is synthesized as a 26 kDa transmembrane protein, which can also be cleaved into a soluble 17 kDa TNF α by TNF α -converting enzyme (TACE) [133, 166]. As detailed previously, TNF α mediates its effects through TNFR1 or R2 via NF- κ B “fine-tuning” the cellular response. TNFR1- and R2-mediated responses are complex as they engage multiple pathways like TNFR1 interaction with the death domain TNFR1 protein (TRADD) and TRAF2 activates NF- κ B, while its engagement with TRADD-death domain containing Fas protein complex mediates apoptosis [133, 167]. While TNFR2 activation leads to beneficial effects through its interaction with TRAF2 that activates NF- κ B, MAPK, and protein kinase B (AKT) that are pro-survival signals [133, 168, 169]. TRAF2 is the nodal molecule that mediates beneficial signals downstream of both TNFR1 and R2, and thus, its expression could be a key determinant of TNF α response in conditions of heart failure. Interestingly,

high levels of myocyte-specific overexpression of TRAF2 lead to deleterious cardiac remodeling [20], while lower levels of TRAF2 provides beneficial remodeling in ischemia reperfusion injury [105]. Thus, expression levels of TRAF2 in cells may produce counterintuitive phenotypes in pathology. This is critical as sympathetic overdrive leads to β AR stimulation, increasing TNF α whose downstream effects would be determined by the ratio of TNFR1 and R2 expression and driven by levels of TRAF2 in various cells. In addition to this paradigm of cross-talk mediated by SNS, the pathophysiological phenotype is also further determined by whether TNF α is membrane bound or is in the soluble format. It is thought that membrane bound TNF α activates TNFR2 [106, 170, 171] initiating beneficial responses to TNF α . Correspondingly, studies show that cardiomyocyte-specific expression of non-cleavable TNF α leads to concentric hypertrophy, while expression of secreted TNF α results in dilated cardiomyopathy [110, 111]. More importantly, the key role of TNF α in cardiac pathophysiology is documented by findings showing reduction in apoptosis and amelioration in deleterious cardiac remodeling in TNF α knockout mice (TNF KO) upon myocardial infarction (MI) [172]. It is known that MI is associated with upregulation of sympathetic hormones elevating TNF α , and thus, the absence of TNF α in TNF α KO mice ameliorates the major β AR agonist epinephrine driven deleterious signals via TNF α . These exciting observations led to the idea of targeting elevated

TNF α in humans with a premise to sequester the circulating TNF α , thus reducing the deleterious effects in heart failure. To accomplish the sequestration of elevated TNF α two approaches were employed, wherein (a) genetically engineered TNF receptor was used as decoy to bind and potentially clear circulating TNF α and (b) to use a chimeric monoclonal antibody that would bind and neutralize TNF α . The clinical trial using the genetically engineered humanized TNF receptor etanercept named RENAISSANCE and RECOVER were terminated prematurely due lack of accrued benefits [50]. Critically, a greater portion of patients on etanercept had worsened prognosis compared to placebos [7••, 50]. Similar to the observation with etanercept, use of monoclonal antibody infliximab neutralizing TNF α also resulted in early termination of the clinical trial due worsening heart failure [49]. The failure of the clinical trial resulted in significant sojourn of studies pertaining to this area. However, given that the underlying mechanisms for worsening in heart failure following anti-TNF α treatment is not well understood, it is imperative that more effort and resources need to be dedicated to gain insights as elevated TNF α is consistently associated with heart failure. This is all the more important given that anti-TNF α antibody infliximab provides beneficial effects in Crohn's disease and rheumatoid arthritis [7••] reflecting the complexity of the disease etiologies. Finally, it argues to the idea that unique engagement of the certain pathways could

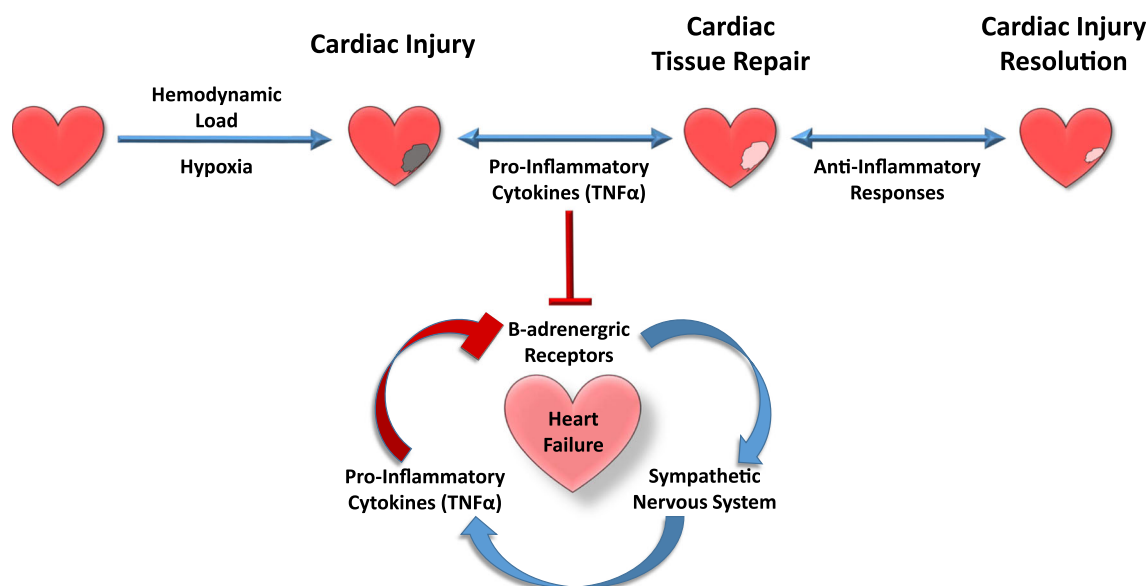


Fig. 1 The schematic illustration describes the current understanding on the cross-regulation of proinflammatory cytokines and the neurohormonal-beta-adrenergic receptor (β -adrenergic receptors) axis. Cardiac stressors like changes in hemodynamic load or hypoxia leads to cardiac injury and in response proinflammatory cytokines, including tumor necrosis factor- α (TNF α), are employed as first step in the defense mechanism. This is followed by cardiac tissue repair and injury resolution phase primarily mediated by anti-inflammatory cytokines. However, as TNF α inhibits β -adrenergic receptor function, it results in the inability of these receptors to respond to sympathetic drive

fundamentally impeding cardiac responses to changes in mechanical demand. Reduced β -adrenergic receptor response leads to a feed-back increase in sympathetic hormones that in turn results in feed-forward elevation in proinflammatory cytokine TNF α , which leads to self-perpetuating cycle that is now independent of pro- and anti-inflammatory response, which was initiated due to injury. This cycle of increased TNF α now inhibits β -adrenergic receptors, thereby leading to feed-back and feed-forward cycle resulting in deleterious signaling mechanisms that underlies cardiac hypertrophy, deleterious remodeling, and heart failure.

provide beneficial effects in certain pathologies, while resulting in deleterious outcomes in others. Such an observation with anti-TNF α treatment suggests that better understanding of the mechanisms would allow for selectively leveraging the beneficial components of the anti-TNF α treatment in the complex etiology of heart failure.

Conclusions

A key focus of our review was to bring-to-fore the current state of understanding regarding the dynamic cross-talk between the proinflammatory cytokines and SNS, which have independent and interdependent effects on cardiac function and pathology. Our discussion was to focus on how the active feed-forward and feed-back between SNS and inflammatory cytokines effects cardiac function and pathology (Fig. 1). This is all the more critical given the failure of anti-TNF α , therapy, indicating that an in-depth understanding of the complexity of TNF α activity in context of TNF α - β AR signaling axis may shed light on deleterious manifestations in heart failure. On the same note, it is also important to understand the conundrum of upregulation of proinflammatory pathways following sympathetic overdrive, a hallmark feature of heart failure. Thus, molecular delineation of these bi-directional pathways will pave the way for comprehensive understanding of the mechanism, while simultaneously providing insights into potentially novel therapeutic strategies/approaches.

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Compliance with Ethical Standards

Conflict of Interest Sarah M. Schumacher and Sathyamangla V. Naga Prasad declare that they have no conflict of interest.

Human and Animal Rights and Informed Consent This article does not contain any studies with human or animal subjects performed by any of the authors.

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