REVIEW



Cellular mechanisms and molecular pathways linking bitter taste receptor signalling to cardiac inflammation, oxidative stress, arrhythmia and contractile dysfunction in heart diseases

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Abstract

Heart diseases and related complications constitute a leading cause of death and socioeconomic threat worldwide. Despite intense efforts and research on the pathogenetic mechanisms of these diseases, the underlying cellular and molecular mechanisms are yet to be completely understood. Several lines of evidence indicate a critical role of inflammatory and oxidative stress responses in the development and progression of heart diseases. Nevertheless, the molecular machinery that drives cardiac inflammation and oxidative stress is not completely known. Recent data suggest an important role of cardiac bitter taste receptors (TAS2Rs) in the pathogenetic mechanism of heart diseases. Independent groups of researchers have demonstrated a central role of TAS2Rs in mediating inflammatory, oxidative stress responses, autophagy, impulse generation/ propagation and contractile activities in the heart, suggesting that dysfunctional TAS2R signalling may predispose to cardiac inflammatory and oxidative stress disorders, characterised by contractile dysfunction and arrhythmia. Moreover, cardiac TAS2Rs act as gateway surveillance units that monitor and detect toxigenic or pathogenic molecules, including microbial components, and initiate responses that ultimately culminate in protection of the host against the aggression. Unfortunately, however, the molecular mechanisms that link TAS2R sensing of the cardiac milieu to inflammatory and oxidative stress responses are not clearly known. Therefore, we sought to review the possible role of TAS2R signalling in the pathophysiology of cardiac inflammation, oxidative stress, arrhythmia and contractile dysfunction in heart diseases. Potential therapeutic significance of targeting TAS2R or its downstream signalling molecules in cardiac inflammation, oxidative stress, arrhythmia and contractile dysfunction is also discussed.

Keywords Cardiac bitter taste receptors · Cardiac inflammation · Contractile dysfunction · Arrhythmia · Novel therapeutics

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Introduction

Heart diseases are a global epidemic (Gianluigi Savarese 2017; Khan et al. 2020) that pose an immense public health concern with a prevalence of over 500 million, affecting all age groups (Ahern et al. 2011), including children (Musa et al. 2017). Heart diseases are the leading cause of death worldwide (Ahern et al. 2011; Roth et al. 2017). In 2015 alone, mortality due to heart diseases was estimated at about 18 million, representing 32% of all deaths in the world (Roth et al. 2017). Alas, billions of dollars are spent in the management of heart diseases, causing a huge burden to the sufferers, relatives, caregivers and the health care system (Muka et al. 2015; Gheorghe et al. 2018; Roth et al. 2020). Though scientific advances, preventive measures and campaigns against heart diseases (Khan et al. 2020) as well as health care system reforms in the cardiovascular setting (Obama

2016; Weintraub and Boden 2017; León-Cortés et al. 2019) may have brought about higher quality healthcare (Clarke et al. 2017), regrettably, the incidence and mortality of heart diseases have constantly increased over the past years (Gianluigi Savarese 2017; Khan et al. 2020; Emmons-Bell and Johnson 2022). Even so, the prevalence and mortality of heart diseases are projected to rise substantially in the next decades, if adequate measures are not taken to address the growing menace of these diseases on the society (Kelly and Donovan 1995).

Over the past few years, accumulating data have consistently implicated cardiac inflammation in etiopathogenetic mechanism of a range of heart diseases, including myocarditis (Lu et al. 2015; Tschöpe et al. 2021), pericarditis, Kawasaki syndrome (Jui et al. 2021), cardiac vessel endotheliitis (Maccio et al. 2021), infective endocarditis (Jui et al. 2021), myocardial infarction/ischaemic heart disease (Moreira et al. 2015), cardiomyopathies (Meraviglia et al. 2021; Tschöpe et al. 2021), angina pectoris (Lu et al. 2015), coronary artery disease/atherosclerotic heart disease (Moreira et al. 2015), cardiac arrhythmias (Shenasa and Shenasa 2017), congestive heart failure (Murphy et al. 2020), hypertensive heart disease (Shenasa and Shenasa 2017), rheumatic and nonrheumatic heart valve disease (Lars et al. 2007; Lee and Choi 2018; Passos et al. 2021), cardiac amyloidosis (Siegismund et al. 2018; McVeigh and Tennyson 2020), and human heart senescence (de Arellano et al. 2019). In addition, inflammatory response plays a pivotal role in the pathogenic mechanism that drives cardiac involvement in systemic diseases (Knockaert 2007; Veinot 2010). Cardiac inflammation is a cellular and tissue response to adverse stimuli due to the activation of signalling cascades that control the secretion of inflammatory mediators in resident immunocytes and cardiac cells as well as recruitment of inflammatory cells, triggered by microbial agents, toxins, cellular debris or toxigenic metabolites. Though inflammatory response constitutes a key defence mechanism against pathogenic aggression or adverse environmental stimuli (Furman et al. 2019), inadequate or chronic inflammatory response can potentially lead to harmful consequences resulting in the development of diseases (Williams et al. 2019; Tsampasian et al. 2021). Despite intense efforts and research investigation directed towards the identification of the pathogenetic basis of cardiac inflammation, the underlying cellular and molecular mechanisms responsible for triggering the inflammatory responses in the cells and tissues of the heart are yet to be fully understood.

Interestingly, inflammatory responses usually occur concurrently with oxidative stress in several pathophysiological conditions, including heart diseases (Neri et al. 2015; Dludla et al. 2019). Oxidative stress is an adverse cellular and tissue response due to dysbalance between the production of reactive species and the endogenous antioxidant defence system (Pizzino et al. 2017) resulting in cell and tissue damage (van der Pol et al. 2019). Indeed, independent research groups have demonstrated an association between proinflammatory responses and the generation of reactive species that promotes oxidative stress (Ji and Li 2016; Dludla et al. 2019). Correspondingly, progress in cardiac research has identified oxidative stress cascades as fundamental pathophysiological pathways in the development and progression of heart diseases (van der Pol et al. 2019). In the heart, oxidative stress induces cardiomyocyte hypertrophy, apoptosis and Ca²⁺ overload via oxidation of membrane phospholipids, proteins and DNA molecules (Shibata et al. 2021). Regrettably, however, the mechanisms of development of oxidative stress in heart diseases are not completely known, thereby substantiating the need to step up research investigation against this global epidemic and search for new frontiers that may lead to the development of novel therapeutics for some heart diseases.

The relatively recent finding that bitter taste receptor (TAS2R)-expressing cells play a critical role as innate immune sentinels (Lee and Cohen 2013a) has sparked research interest on the functional role and the molecular mechanisms of these nodal signalling units of the plasma membrane (Welcome 2020a; Welcome and Mastorakis 2021; Welcome et al. 2021). TAS2Rs are transmembrane proteins of the G-protein-coupled receptors that sense "bitter" molecules to initiate intracellular signalling downstream multiple cytoplasmic acceptors, mediating cellular responses that ultimately lead to elimination of the aggression or protection of the cell or tissue from damage (Welcome 2020a). So far, 25 TAS2Rs have been discovered in humans (Meyerhof et al. 2010), 35 TAS2Rs in rat and mice (Wu et al. 2005), 3 TAS2Rs in chicken and 50 TAS2Rs in frog (Di Pizio and Niv 2015). The amino acid sequence of TAS2Rs from different species share a similarity of about 23-86% (Chandrashekar et al. 2000; Shi et al. 2003; Wu et al. 2005). TAS2Rs are activated by hundreds of different substances, including denatonium, amarogentin, caffeine, chloroquine, quinine (Bayer et al. 2021), N-phenylthiourea, phenylthiocarbamide, cycloheximide (Meyerhof et al. 2010; Gradinaru et al. 2022), xanthohumol, dextromethorphan, methimazole, and glimepiride (D'Urso and Drago 2021). These taste receptors are ubiquitously expressed in many cells and tissues of the body. TAS2Rs were first identified in taste bud cells of the oral cavity and were thought to only detect and prevent the ingestion of potentially poisonous "bitter" molecules (Adler et al. 2000; Chandrashekar et al. 2000). Thereafter, TAS2Rs were discovered in other regions of the gut-stomach, ileum and colon (Rozengurt 2006; Vegezzi et al. 2014), which suggested that these nodal signalling units may play a number of essential roles other than detecting poisonous "bitter" molecules (Rozengurt 2006). TAS2Rs were also discovered in the upper respiratory tract,

where they were shown to sense toxigenic and microbial molecules to mediate responses that ultimately lead to elimination of the pathogenic molecules (Gulbransen et al. 2008; Tizzano et al. 2011), in part, by activating the innate immune system to confer protection on the respiratory epithelium (Kinnamon and Finger 2019). TAS2Rs are expressed in blood monocytes or monocyte-derived macrophages (Grassin-Delyle et al. 2019), neutrophils (Maurer et al. 2015), keratinocytes (Wölfle et al. 2015), thymus (Panneck et al. 2014; Soultanova et al. 2015), vascular smooth muscles (Lund et al. 2013), pancreas (Gaida et al. 2016), brain (Singh et al. 2011), thyroid gland (Clark et al. 2015), testis (Xu et al. 2013), spermatozoa (Governini et al. 2020), prostate (Dupre and Martin 2017; Martin et al. 2019), vagina, cervix, endometrium, myometrium, placenta, ovary (Dupre and Martin 2017; Welcome 2020a), urethra, ureter, bladder (Welcome 2020a; Welcome et al. 2021), and kidney (Liu et al. 2015b). Relatively more recently, independent groups of researchers have identified the expression of TAS2Rs in cells and tissues of the heart (Foster et al. 2013, 2014; Manson et al. 2014), indicating that these receptors may be involved in mediating the inflammatory, oxidative stress responses, autophagy (Hamdard et al. 2019b), cardiac rhythm (Yuan et al. 2020) and contractile activities (Manson et al. 2014; Bloxham et al. 2020; Yuan et al. 2020) in this vital organ.

Indeed, several lines of evidence suggest that cardiac TAS2Rs may play a role in both cardiac and vascular diseases (Foster et al. 2015; D'Urso and Drago 2021; Kamila and Agnieszka 2021). The role of cardiac TAS2Rs in mediating reduction in spontaneous beating rate of the sinoatrial node and left ventricular relaxation (Yuan et al. 2020) indicates that dysfunction in cardiac TAS2Rs may necessarily affect impulse generation or propagation and mechanical efficiency of the heart, thereby predisposing to contractile dysfunction and arrhythmia. Comparable data have also been reported by Manson et al. (2014). Moreover, cardiac TAS2Rs can act as gateway surveillance units that detect pathogenic components, including the microbial quorumsensing signal molecules. Thus, under normal condition, stimulation of TAS2R by microbial molecules results in downstream signalling that activates the intracellular acceptors responsible for protecting the cell via secretion of anti-inflammatory and -microbial mediators. However, dysfunctional cardiac TAS2R signalling or excessive action of the pathogenic or danger molecules can result in collateral tissue damage, predisposing to disease development (Foster et al. 2015; D'Urso and Drago 2021; Kamila and Agnieszka 2021).

Therefore, defects in cardiac TAS2R signalling can initiate inflammatory and oxidative stress responses, as well as disorder of cardiac rhythm and contractile force of the heart in cardiac diseases. Unfortunately, the molecular mechanisms that link TAS2R sensing of the cardiac milieu to inflammatory and oxidative stress responses are not clearly known. Hence, we sought to review the possible role of TAS2R signalling in the pathophysiology of cardiac inflammation, oxidative stress, arrhythmia and contractile dysfunction in heart diseases. First, we discuss the contemporary view of the mechanisms of inflammation and oxidative stress and their roles in the development of heart diseases. Second, we discuss the expression of TAS2R, its ligands, functional roles and signal transduction mechanism in the heart. Third, we describe the role of dysfunctional TAS2R signalling in cardiac inflammation, oxidative stress, arrhythmia and contractile dysfunction in heart diseases. Further, we attempt to delineate the molecular pathways, linking TAS2R sensing of microbial and toxigenic molecules with inflammatory, oxidative stress responses, arrhythmia and contractile dysfunction in heart diseases. Potential therapeutic significance of targeting TAS2R or its downstream signalling molecules in cardiac inflammation, oxidative stress, arrhythmia and contractile dysfunction is also discussed.

Contemporary view of the mechanisms of cardiac inflammation and oxidative stress and their roles in disruption of cardiac rhythm and contractility in heart diseases

Cardiac inflammatory and oxidative stress responses are triggered by multiple pathogenetic factors

The inflammatory and oxidative stress responses in the heart are triggered by multiple factors, which include pathogens (bacteria, viruses, fungi, parasites) (Zhang et al. 2020), gut microbiota disorder (Mesquita et al. 2021), tissue injury (Chen et al. 2018), acute emotional and chronic psychological stress (Wirtz 2017), toxins and irritants (Lu et al. 2015; Chen et al. 2018). These factors mediate the release of pathogenic and danger molecules that stimulate the pattern-recognition receptors on local and distant immunocytes (macrophages, leukocytes, natural killer and cytotoxic CD8⁺ T cells (Jui et al. 2021)) as well as cardiac cells to initiate the inflammatory and oxidative stress response (Mesquita et al. 2021). Therefore, gut microbiota disorder, for example, causes gut epithelial barrier leakage with corresponding increase in circulating microbial particles that promote chronic low-grade inflammatory response, which is considered as a central player in cardiac failure, diastolic dysfunction, arrhythmia, ageing, and fibrotic heart disease (Mesquita et al. 2021). Interestingly, multiple pathogenetic factors have been reportedly shown to trigger cardiac pathology via gut microbiota disorder (Mesquita et al. 2021).

Indeed, cardiac diseases are associated with numerous inflammatory mediators, including interleukin (IL)-1 β , IL-6,

tumour necrosis factor- α (TNF- α) (Lu et al. 2015; Chen et al. 2018), macrophage chemoattractant protein-1 (MCP-1), and C-reactive protein (Jui et al. 2021). Similarly, reactive species play a crucial role in the development and progression of many heart diseases (Pashkow 2011). In addition, secretion of alarmins such as matrix metalloprotease (MMP)-2, -9 (Jui et al. 2021), high-mobility group box 1 (HMGB-1), cardiac myosin, heat shock protein (HSP)-60, HSP-70, hyaluronic acid, fibronectin-extra domain A, extracellular adenosine triphosphate (ATP), circulating RNA, nuclear and mitochondrial DNA (Silvis et al. 2020), Ca²⁺-binding S100 proteins (S100A7, S100A8, S100A9 and S100A12) (Yan 2014; Lu et al. 2019; Silvis et al. 2020) also contribute to the signalling cascades that promote the development of heart diseases. Accordingly, Zhang et al. (2020) showed that these factors promote aberrant cardiac metabolism and mitochondrial dysfunction that further worsen the abnormalities of cardiac rhythm and contractility in heart diseases (Zhang et al. 2020). Thus, the inflammatory mediators, reactive species, and alarmins represent fundamental drivers of the pathogenetic processes in cardiac pathology (Wadley et al. 2013; Zhang et al. 2017a; Papaconstantinou 2019).

Though the mechanisms are not exactly clear, cardiac inflammatory signalling is closely associated with oxidative stress response in the heart (Ooi et al. 2017; Zhang et al. 2017a; Wu et al. 2021b). Recent investigation has implicated reactive isolevuglandin, a toxic lipid peroxidation byproduct and γ -ketoaldehyde, as a possible molecular switch, connecting cardiac inflammation to oxidative stress. Ngwenyama et al. (2021) showed that myocardial oxidative stress triggers the generation of reactive isolevuglandin molecules that act as cardiac antigens to stimulate the T cell receptor (Ngwenyama et al. 2021) to promote the development of heart failure (May-Zhang et al. 2018), cardiac senescence, atherosclerotic and hypertensive heart disorders (Aschner et al. 2021), including high salt-induced heart disease (Ruggeri Barbaro et al. 2021). Data from both animal and human research (Ruggeri Barbaro et al. 2021) have revealed that reactive isolevuglandin formation due to high salt diet (Ruggeri Barbaro et al. 2021), myocardial oxidative stress (Ngwenyama et al. 2021), pressure overload (Shang et al. 2019), and lipopolysaccharide (LPS)-induced inflammation in mice (Mayorov et al. 2019) can initiate the activation of monocytes, dendritic cell, and secretion of the proinflammatory cytokines TNF-α, IL-1β, IL-6, IL-17A (Dikalova et al. 2020; Ruggeri Barbaro et al. 2021), and reactive species (superoxide anions, and reactive nitrogen species) (Dikalova et al. 2020). Thus, isolevuglandin may serve as a therapeutic target in the treatment of certain heart diseases. Indeed, the isolevuglandin scavengers, 2-hydroxybenzylamine (Shang et al. 2019; Ngwenyama et al. 2021) and (4-(4-aminomethyl)-3-hydroxyphenoxy)butyl)-triphenylphosphonium (Mayorov et al. 2019; Dikalova et al. 2020) have been shown to attenuate the pathological sequelae of left ventricular hypertrophy and heart failure in both animal and human cell lines.

Pathological activation and phenotype switching of resident cardiac immunocytes are critical to inflammatory and oxidative stress responses in the heart

Macrophages are primary resident immunocytes involved in both inflammatory and oxidative stress responses in several disorders, including heart diseases (Hu et al. 2020). These resident immunocytes play a central role in initiating, maintaining, and resolving the inflammatory and oxidative stress responses through the secretion of cytokines, chemokines and growth factors (Liu et al. 2021). The pathogenic factors that initiate inflammatory and oxidative stress responses in the heart concomitantly cause pathological activation of the cardiac immunocytes, initiating the phenotype switching of non-activated macrophage (M0) to the proinflammatory subtype M1 that propagates the inflammatory processes (Orekhov et al. 2019). Research data have shown that generation of M1 macrophage is triggered by LPS or interferon-gamma (IFN- γ), whereas IL-4 and IL-13 mediate the polarisation of M2 macrophage (Liu et al. 2021). Investigators have reported that the proinflammatory cytokines/chemokines released in the heart following the action of pathological factors activate the cell surface receptors of the resting resident macrophages with increased generation of the M1 proinflammatory over the M2 anti-inflammatory phenotype (Hu et al. 2019). The activated M1 macrophage secretes proinflammatory factors such as IL-1β, IL-6, IL-12, IL-23, TNF- α , nitric oxide (NO), inducible NO synthase (iNOS), MCP-1, IFN γ , prostaglandins (PGE₂), and MMPs to promote inflammation (Aimo et al. 2020; Liu et al. 2021). However, the M2 phenotype expresses the cluster of differentiation (CD) 14, CD80, CD163, CD200, and CD206 receptors and secretes anti-inflammatory factors, including IL-10, C-C motif chemokine ligand 17 (CCL17), CCL22, and CCL24 to blunt the inflammatory reactions, thereby enhancing tissue repair (Aimo et al. 2020; Kishore and Petrek 2021). Moreover, the macrophage precursors-monocytes can directly polarise into M1- or M2-like phenotypes or their respective isoforms to control inflammatory response (Orekhov et al. 2019; Lu et al. 2020).

Therefore, data from both animal (Hu et al. 2019) and human (Dai et al. 2021) studies have revealed that pathological processes resulting in heart diseases are associated with M1 macrophage polarisation, concomitantly with inhibition of M2 macrophage recruitment in the heart. For instance, Liu et al. (2015a, b) demonstrated M1 polarisation in a rat model of myocardial infarction along with disordered Ca²⁺ waves, which stimulated the extracellular Ca²⁺ receptor, CaSR,

which in turn activated the NLRP3 (nucleotide-binding oligomerisation domain, leucine-rich repeats, pyrin domaincontaining protein 3) inflammasome via phospholipase C (PLC)—inositol 1,4,5-triphosphate (IP3) pathway (Liu et al. 2015a). The authors also reported the secretion of collagen, α -SMA (alpha smooth muscle actin) and MMP-2/-9 (Liu et al. 2015a), which are implicated in cardiac fibrosis-a crucial process in the pathogenetic mechanism of myocardial infarction (Talman and Ruskoaho 2016; CHEN et al. 2021). In contrast, TIMP-2 (tissue inhibitor of matrix metalloproteinase) expression was downregulated in cardiac fibroblasts via IL-1 β /IL-1 receptor (Liu et al. 2015a). TIMP-2 is highly expressed in the myocardium, and required for pro-MMP-2 activation and MMP-2 inhibition. TIMP-2 plays multiple roles in cardiac physiology, including electrical coupling among myocardial cells. For instance, Givvimani et al. (2013) showed decreased expression of myocardial connexin (Cx) 37 and 43 in TIMP-2 knockout mice compared with control animals (Givvimani et al. 2013). ((Cx43 is required for the maintenance of electrical and mechanical synchrony in the heart (vide infra)). In addition, MMP-2 and TIMP-2 dysbalance plays an important role in the development of cardiomyopathy (Li et al. 2010) and heart failure (Kobusiak-Prokopowicz et al. 2018) in both animals and humans. Thus, TIMP-2/MMP-2 axis may serve as an important molecular target in the treatment of some cardiac diseases.

Furthermore, the M1 phenotype within the myocardium can mediate inflammatory processes by internalising and accumulating oxidised low-density lipoprotein, leading to the formation of "foam cells" in atherosclerotic plaques of the coronary vessels, which in turn may cause myocardial ischaemia and necrosis (Bonetti et al. 2021). However, phenotype conversion between M1 and M2 has been documented and depends on the activity of the dominant signalling molecules. For instance, M1 conversion to M2 occurs by selective apoptosis of M1 macrophages and maybe induced by iNOS/NO (Albina et al. 1989; Mills 2012; Lu et al. 2020), TNF/TNF receptor 1, and phosphoinositide 3-kinase (PI3K)/protein kinase B (Akt) pathways (Lu et al. 2020). Interestingly, some pharmacological agents can attenuate cardiac inflammation and oxidative stress by promoting the polarisation of M2 over M1 phenotype or conversion of M1 to M2 phenotype. Correspondingly, Zhou et al. (2020) demonstrated specific inhibition of M1 polarisation by attenuating CD11c, iNOS, IL-6 and MCP-1 and augmenting CD206 and IL-10 expression in M2 via suppression of the nuclear factor κB (NF- κB) and Notch1 signalling upon treatment with recombinant human IL-37 in LPS- and IFNy-stimulated THP-1 monocytes (Zhou et al. 2020). Comparable results have been reported for other pharmacological agents (Zhou et al. 2015; Saqib et al. 2018; Davoodvandi et al. 2019), including drugs currently used in the clinic (He and Marneros 2014; He et al. 2021). For example, both preclinical (Garcia et al. 2007; Spaulding et al. 2018) and clinical (Cerisano et al. 2014) studies have shown that acute administration of the tetracycline-class antibiotic, doxycycline in myocardial infarction considerably ameliorates cardiac dysfunction by inhibiting the proinflammatory macrophage and mediators. In an open-label, randomised, phase II trial (ClinicalTrials.gov: NCT00469261), doxycycline (100 mg b.i.d. for 7 days) in addition to standard therapy substantially enhanced left ventricular function and reduced the infarct size in patients with acute ST-segment elevation myocardial infarction and low (<40%) left ventricular ejection fraction (Cerisano et al. 2014). Several investigators have consistently shown that the beneficial effects of doxycycline on the heart are mainly due to the suppression of intracellular matrix metalloproteinase (MMP)-2 (Fan et al. 2014; Berry et al. 2015), MMP-9 (Fan et al. 2014), secretory phospholipase A2 activity (Berry et al. 2015), and M2-type macrophage polarisation (He and Marneros 2014b), while also upregulating and normalising the distribution of Cx43 in the infarct zone (Fan et al. 2014). (The role of Cx43 in cardiac physiology is discussed below). These data corroborate the essential role of this broad-spectrum antibiotic in abrogating the proinflammatory stress responses of the heart (Kandasamy et al. 2010).

Inflammatory and oxidative stress responses in the heart are responsible for disruption of cardiac rhythm and contractility via connexon and calcium signalling defects

Emerging data indicate that the detrimental effects of inflammation and oxidative stress in the heart are mediated via dysfunctional connexon, a major type of gap junction protein expressed in the heart. Research investigation has consistently shown that C×40, C×43, and C×45 are expressed in relative and distinct combination in different regions of the heart (Severs 2002; Severs et al. 2008). However, C×43 is the best characterised cardiac gap junction connexon protein with the most important role in cardiac physiology. In the myocardium of a healthy heart, the expression of C×43 is very high (Eckardt et al. 2004; Takanari et al. 2016), whereas in the cardiac conduction system, its expression is low (Eckardt et al. 2004). The myocardial Cx43 not only forms the gap junction that constitutes a critical component of the intercalated disc (Palatinus et al. 2012; Takanari et al. 2016), but also forms hemichannels, which represent crucial players in cardiac ionic homeostasis (Hirschhäuser et al. 2021). Therefore, myocardial Cx43 are required for direct cell-to-cell contact, movement of ions and signalling molecules to maintain cardiac electrical coupling (Takanari et al. 2016) and synchrony (Palatinus et al. 2012) that ensure a regulated contractile activity of the heart (Severs 2002).

Concomitantly with decreased C×43 protein expression in high glucose-stimulated AC16 human cardiomyocytes, Thakur et al. (2021) demonstrated upregulation of troponin-I, HSP-60, RAGE (receptor for advanced glycation endproducts), HMGB-1, toll-like receptor (TLR)-4, and CXC chemokine receptor (CXCR)-4 (Thakur et al. 2021). The reduction of Cx43 expression in left ventricular hypertrophy induced by type-2 diabetes mellitus in rats was associated with reduced expression of heme-oxygenase 1 (HO-1) and increased level of TNF α and asymmetric dimethylarginine (ADMA) (Leffler and Abdel-Rahman 2019, 2020). ADMA is a cardiac biomarker and risk factor for heart diseases that acts as an endogenous competitive inhibitor of NOS (Böger 2005; Hou et al. 2018), formed during proteolysis by protein methyl transferases via methylation of L-arginine sites of protein molecules (Bulau et al. 2007). ADMA has been demonstrated to inhibit the expression and heterogeneous localisation of C×43 (Jia et al. 2009; Tsang et al. 2013). Under normal condition, 10% of ADMA is formed daily and subsequently excreted in the urine. The remaining 90% is metabolised by dimethylarginine dimethylaminohydrolase (DDAH) to dimethylamine and L-citrulline (Tsikas 2020). Deficiency of DDAH due to cardiomyocyte injury or apoptosis is the primary cause of elevated circulating ADMA (Tsikas 2020). Interestingly, DDAH has been shown to attenuate left ventricular dysfunction after myocardial infarction by inhibiting oxidative stress and apoptotic biomarkers (Hou et al. 2018).

The secretion of inflammatory, oxidative stress and profibrotic mediators due to C×43 dysfunction can trigger dysregulation of spontaneous generation of excitation by the cardiac pacemakers and impulse conduction via disruption of ionic homeostasis and redox potential, thereby predisposing to disorders of cardiac rhythm and contraction (Palatinus et al. 2012; Li et al. 2013; Andelova et al. 2021). Consistent with previous data (Takanari et al. 2016), several pieces of evidence have shown that C×43 breakdown, modification or remodelling in heart diseases essentially impairs the gap junction function through disruption of its charge, size, organisation and distribution-representing a distinct feature of cardiac arrhythmia in many heart diseases (Severs et al. 2008; Palatinus et al. 2012). Truly, several dysfunctions of the heart, including cardiac electrical instability have been associated with C×43 dysfunction in animal models of cardiac specific C×43 knockout (Gutstein et al. 2001; Eckardt et al. 2004). Similarly, a marked reduction in the expression of C×43 mRNA and protein levels in the left ventricle of ischaemic cardiomyopathy and idiopathic dilated cardiomyopathy was reported (Dupont et al. 2001). Though the mechanisms underlying connexon-induced elevation of proinflammatory, oxidative stress and pro-fibrotic molecules that subsequently results in cardiac pathology are not fully understood, researchers have previously demonstrated the association of endothelial C×43 knockout with hypotension, bradycardia, and elevation of angiotensin I and II in experimental animals (Liao et al. 2001). Indeed, the involvement of regional (organ-specific) angiotensin system in inflammatory and oxidative responses is extensively been discussed in the literature (Leung 2007; Rodriguez-Pallares et al. 2008; Labandeira-Garcia et al. 2017; Tsai et al. 2018; Milanesi et al. 2019). Regrettably, however, little is known about the role of intrinsic angiotensin system of the heart in cardiac inflammation, oxidative stress and fibrosis.

The cardiac C×43 also interacts with several ions, including Na⁺ (Delmar and Liang 2012) and Ca²⁺ (Takanari et al. 2016) to control cardiac rhythm via cross-talks in the ventricular cardiomyocytes. Thus, disorders in C×43 function can directly affect Na⁺ and Ca²⁺ transport across the sarcolemma (Delmar and Liang 2012; Takanari et al. 2016). Accordingly, dysfunctional Ca²⁺ signalling has been shown to mediate the detrimental effects of inflammatory and oxidative stress responses in the heart. Research data indicate that increased activity of Ca²⁺ signalling via calmodulin/ Ca²⁺-calmodulin protein kinase II (CaM/CaMKII) regulates C×43 expression and impulse conduction in a diseased heart (Takanari et al. 2016). Dries et al. (2021) demonstrated CaMKII involvement in susceptibility to arrhythmia, via spontaneous Ca²⁺ release, in cryoinjured subendocardium of experimental rats (Dries et al. 2021). Therefore, investigators have reliably established that inhibition of CaMKII results in decreased tissue excitability (Procida et al. 2009) and susceptibility to arrhythmia (Dries et al. 2021). Similar findings were revealed by Takanari et al. (2016) who demonstrated augmentation of conduction velocity and C×43 expression in the intercalated disc of CaMKII knockout AC3-I mice subjected to pressure overload (Takanari et al. 2016). Researchers have demonstrated a heightened predisposition to inflammatory responses in the heart following experimental CaMKII activation. Thus, Suetomi et al. (2018) reported that CaMKIIδ actively participates in detection and transduction of pressure overload to trigger the activation of NF-kB and NLRP3 inflammasome (Suetomi et al. 2018). These molecular sensors of inflammation mediate an increased secretion of pro-fibrotic molecules, proinflammatory cytokines and chemokines in cardiomyocytes, along with macrophage activation, which predispose to arrhythmia and contractile dysfunction in heart diseases, including myocardial infarction (Suetomi et al. 2019). Similar findings are reported elsewhere (Ling et al. 2013; Willeford et al. 2018). As a matter of fact, inhibition of CaMKII reportedly attenuated the expression of proinflammatory and profibrotic molecules (Suetomi et al. 2019). Likewise, Jiang et al. (2020) demonstrated attenuation of myocardial injury via inhibition of CaMKII by tilianin, a TAS2R agonist (Jiang et al. 2020). Though the role of CaMKII in cardiac pathology is not exactly clear, Gray and co-workers (2017) have

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previously demonstrated a differential regulation of CaM-KII isoforms—CaMKII $\delta_{\rm R}$ and CaMKII $\delta_{\rm C}$ in the development of myocardial ischaemia or infarction via NF-κB signalling (Gray et al. 2017). Further research on the role of specific isoforms of CaMKII in cardiac inflammation, oxidative stress, fibrosis and apoptotic cell death is important for understanding the underlying molecular mechanisms in some heart diseases.

Phosphorylation reactions at specific sites of the C×43 are also critical to the changes in its expression and functions in heart diseases (Procida et al. 2009). These reactions may be triggered by CaMKII (Procida et al. 2009), mitogen-activated protein kinase (MAPK) (Yang et al. 2019; Hirschhäuser et al. 2021), and protein kinase C (PKC) (Lampe et al. 2000; Hirschhäuser et al. 2021). Although certain phosphorylation of cardiac connexon may be protective, abnormal connexon phosphorylation can lead to serious abnormalities in electrical coupling and synchrony (Hirschhäuser et al. 2021). Thus, research on identification of novel pharmacological agents that can mediate favourable phosphorylation reactions of connexon in a region-dependent manner may provide important information for identification of new therapeutic options for some heart diseases. Correspondingly, a novel class of pharmacological agents-known as C×43 mimetic peptides, which stimulate favourable connexon phosphorylation are currently been developed for potential treatment of heart diseases. For instance, Jiang et al. (2019) reported a marked attenuation of left ventricular dysfunction and arrhythmia, accompanied by increased phosphorylation of C×43 at serine 368 by PKC_ε, following treatment with 25–amino acid α -carboxyl terminus 1 peptide (C×43) mimetic peptide α CT1) or a variant of α CT1 (known as α CT11) in a mouse model of myocardial ischaemia-reperfusion injury (Jiang et al. 2019).

Bitter taste receptors of the heart and their signal transduction mechanism

Cardiac bitter taste receptors: subtypes, ligands and functions

TAS2Rs were discovered in cardiomyocytes and fibroblasts of the rat and human heart by Foster and co-workers (Foster et al. 2013). The following year, same group of researchers established the expression of TAS2R subtypes 108, 137, and 143 in the mouse heart (Foster et al. 2014). Several subtypes of these receptors have been identified in the cells and tissues of both murine and human heart (Table 1).

The cardiac TAS2R mediates the sensation of bitter tasting (i.e. bitter tastants or bitterants), toxigenic or pathogenic molecules. There are thousands of TAS2R ligands. All currently known bitterants are available on the "database of bitter molecules": BitterDB (http://bitterdb.agri.huji.ac.il) and PlantMolecularTasteDB (www.plantmoleculartastedb.org).

Reference

Comments

Table 1 Summary of bitter taste receptor expression in the heart Model

Cells and tissues of the

heart Whole heart tissue Mice TAS2R108, TAS2R137, (Foster et al. 2014) Concentration-dependent **TAS2R143** decrease in contraction Left ventricle, sinoatrial TAS2R108 (Yuan et al. 2020) Rat Concentration-dependent node and cardiomyocytes decrease in contraction Aorta and pulmonary Guinea-pig, mice, human TAS2R3, TAS2R4, Strong endothelium-inde-(Manson et al. 2014) TAS2R10, TAS2R14 pendent relaxation arteries Aortic smooth muscle Rat TAS2R and gustducin Increased muscle tone (Manson et al. 2014) tissue Whole heart tissue Chinese Fast Yellow TAS2R (Hamdard et al. 2019a) Chicken Whole heart tissue Chinese fast yellow chicken TAS2R1, 2, 7, α-gustducin ↑PLC62, IP3R3, TRPM5, (Hamdard et al. 2019b) CALPN1, dyanin, GPX1, CAT, SOD1; ↓CASP, Bcl-2 (Bcl-2l1, Mcl, BID, NOXA), beclin-1* Rat and human TAS2R Cardiac myocytes and (Foster et al. 2013) fibroblasts TAS2R (Foster et al. 2015) Whole heart tissue Human and mice Whole heart tissue Rodent TAS2R14 (D'Urso and Drago 2021)

Types of taste receptors

Note: *in acute administration at low-moderate doses (5 and 20 mg/kg), but not in chronic and large dose, Bcl-2 B cell lymphoma 2, Bcl-211 Bcl-2 like 1, BID—BH3-interacting domain death agonist, CALPNI calpain 1, CASP caspase, CAT catalase, GPx1 glutathione peroxidase, Mcl Mantle cell lymphoma, NOXA NADPH (nicotinamide adenine dinucleotide phosphate) oxidase activator, SOD superoxide dismutase

Similar to other extra-oral tissues, cardiac TAS2Rs may play multiple physiological roles, including immune defence against pathogens (D'Urso and Drago 2021) and local metabolic regulation, at least in part, by regulating cytoplasmic protein kinases and cyclic AMP levels (Manson et al. 2014; D'Urso and Drago 2021). TAS2Rs are also involved in the maintenance of endothelial homeostasis (D'Urso and Drago 2021).

Data also indicate a role of TAS2Rs in cardiac contractility (Foster et al. 2014; Bloxham et al. 2020) and vascular tone (Manson et al. 2014; Bloxham et al. 2020). Yuan et al. (2020) investigated the effect of the TAS2R agonists, quinine and chloroquine on Langendorff-perfused hearts in adult rat and demonstrated increased expression of TAS2R mRNA and α -gustducin in the left ventricle (Yuan et al. 2020). Furthermore, the researchers showed that stimulation of TAS2R with either quinine or chloroquine resulted in increased R-R interval and QRS duration (Yuan et al. 2020). Foster et al. (2014) demonstrated the involvement of mouse cardiac TAS2R 108, 137, and 143 in decreased force of ventricular contraction (Foster et al. 2014). Interestingly, previous investigation revealed this relaxation effect of TAS2R agonists in the two major arteries connecting the heart-aorta and pulmonary arteries (Manson et al. 2014). These results suggest that TAS2Rs may play an important role in the pathophysiology of cardiac and vascular diseases, including disorders of the coronary arteries (Manson et al. 2014; Foster et al. 2014).

Yuan et al. (2020) demonstrated increased expression of TAS2R and *a*-gustducin and reduced spontaneous beating rate in the sinoatrial node following treatment with the TAS2R agonists, quinine and chloroquine in Langendorffperfused hearts of adult rats (Yuan et al. 2020), suggesting that cardiac TAS2R may play a crucial role in the regulation of cardiac rhythm. Furthermore, the involvement of cardiac TAS2R in the regulation of cardiac rhythm may be essential for the prevention of arrhythmia, in part, via regulation of C×43 activity (see "Bitter taste receptors, cardiac contractility and rhythm: bitter taste receptor agonists modulate cardiac contractility and pacemaker activity via Ca2+-, cyclic AMP- and PDE-dependent mechanisms" and "Molecular signalling pathways, linking bitter taste receptor sensing of pathogenic and toxigenic molecules with inflammatory, oxidative stress responses, arrhythmia and contractile dysfunction in heart diseases").

The expression of TAS2Rs in the heart suggests that these nodal signalling units of the plasma membrane are critical for evaluating the chemical composition of blood and tissue fluid, serving as gateway surveillance units that sense and mobilise protective mechanisms against the transport of noxious or toxigenic molecules into the cells and tissues of the heart (D'Urso and Drago 2021). Thus, pharmacological agents that act on cardiac TAS2Rs can be harnessed for potential therapeutics in some cardiac diseases (Foster et al. 2015). Indeed, some phytochemicals and their derivatives acting as TAS2R agonists have been identified as promising therapeutic agents for potential treatment of several disorders, including heart diseases (vide infra) (Kamila and Agnieszka 2021). Therefore, research has revealed that denatonium benzoate, an agonist of TAS2R1, 2, 7, and α -gustducin, at low dose (5 mg/kg) and short period of treatment (i.e. 7 days) causes a decrease in the expression of apoptosis and autophagy-related genes-caspase (Casp) 2, Casp3, Casp7, Casp9, Bcl-2l1 (B cell lymphoma 2 like 1), Mcl (mantle cell lymphoma), Bid (BH3-interacting domain death agonist), and Noxa (NADPH oxidase activator), along with increased expression of antioxidant enzymes or mediators such as glutathione peroxidase 1 (Gpx1), catalase (CAT), superoxide dismutase 1 (SOD1) and calpain-1 in whole heart tissues of experimental animals (Hamdard et al. 2019b). However, at higher doses and chronic treatment with denatonium benzoate, Hamdard et al. (2019a, b) demonstrated increased expression of the apoptosis and autophagy-related genes, suggesting that TAS2R activation may be beneficial at low doses and acute treatment period (Hamdard et al. 2019b).

Furthermore, Burt and coauthors demonstrated that treatment of HL-1 mouse cardiac myocytes with flufenamic acid (10 μ M) decreases Ca²⁺ oscillations followed by an overall increase in intracellular Ca²⁺ level as well as depolarisation of the mitochondrial membrane (Burt et al. 2013). Flufenamic acid is a TAS2R14 agonist (Meyerhof et al. 2010) and a member of the anthranilic acid derivative class of nonsteroidal anti-inflammatory drugs (Chi et al. 2011). Though it is not exactly clear whether the anti-inflammatory effect of flufenamic acid is due to its stimulatory action on TAS2R, available data suggest that this TAS2R14 agonist can modulate the expression of COX-2 gene via interaction with the NF-kB pathway (vide infra) or NADH oxidase signalling (Hamdard et al. 2019b). Indeed, activation of TAS2R1, 8, 10, 13, 14, and 38 by the human gut microbiota-derived quorum-sensing signal molecule, 3-oxo-C12:2-HSL in LPS- and IFNy-stimulated RAW264.7 macrophages reportedly resulted in decreased expression of the proinflammatory cytokines IL-1ß and TNFa via modulation of the NF-kB, Janus kinases/Signal transducer and activator of transcription (JAK/STAT) and TNF signalling pathways (Coquant et al. 2022). Similar cardioprotective effects have been reported for the TAS2R agonists genistein in preclinical studies (Bai and Wang 2019; Chen et al. 2019) and clinical trial (ClinicalTrials.gov: NCT00287690), and epigallocatechin-3-gallate in preclinical studies (Xuan and Jian 2016; Reddy et al. 2020), and clinical trials (Clinical-Trials.gov: NCT02015312; aus dem Siepen et al. 2015). However, it is not exactly clear how these agonists exert their protective effects on the heart via TAS2R-activated intracellular signalling.

Besides the TAS2R agonists, a few molecules have been identified to act as TAS2R antagonists in taste receptor-expressing cells. Probenecid ((p-(dipropylsulfamoyl) benzoic acid)) is an inhibitor of the multidrug resistance protein 1 transporter, approved by the United States Food and Drug Administration, and clinically used for the treatment of gout in humans. Probenecid was identified to inhibit the human type TAS2R16, -38, and -43 through an allosteric mechanism of action (Greene et al. 2011). Roland et al. (2014) demonstrated that 6,3'-dimethoxyflavanone, 4'-fluoro-6-methoxyflavanone, and 6-methoxyflavanone inhibit denatonium benzoate- and epigallocatechin-3-gallate-mediated activation of TAS2R14 and -39 by reversible insurmountable antagonism (Roland et al. 2014). Antagonists of TAS2Rs also include homoeriodictyol (TAS2R14, 39 and 43) (Tiroch et al. 2021), eriodictyol (TAS2R14, 39) (Ley et al. 2006), enterodiol (TAS2R10) (Ley et al. 2006, 2012), 2,4-dihydroxybenzoic acid vanillylamide (unknown TAS2R subtype) (Ley et al. 2006), [2]-gingerdione and its homologue [3]-gingerdione (unknown TAS2R subtype) (Lev et al. 2008), sakuranetin, 6-methoxysakuranetin, and jaceosidin (TAS2R31) (Fletcher et al. 2011). Research is required to explore and clarify the mechanisms of TAS2R antagonism, its implication on cellular signalling, the clinical significance and potential therapeutic effects of TAS2R antagonists in cardiac diseases.

It should be mentioned that the mechanism of TAS2R-ligand interactions is yet to be fully elucidated and the pharmacology of TAS2R is poorly defined (Devillier et al. 2015; Jaggupilli et al. 2016; Medapati et al. 2022). There is severe lack of data on the mechanism of deactivation of TAS2R after it has been activated by a noxious stimulant. Notwithstanding, available data indicate that the activation of TAS2R causes a conformational change in the receptor (Jaggupilli et al. 2016), which may lead to its deactivation, thereby preventing its continued stimulation. It is currently not clear whether the activation of this taste receptor causes it to subsequently undergo proteolysis or other mechanisms of deactivation. It is also not clear whether a feedback mechanism is involved in the control of TAS2R activity. Therefore, further research is required to unravel the pharmacology of TAS2R-ligand interactions.

Signal transduction mechanism of cardiac bitter taste receptors

Upon activation by certain metabolites, toxigenic or microbial molecules, TAS2Rs relay their signal downstream the cytoplasm (Fig. 1), which under normal condition, is required to resolve cellular or tissue injury (Welcome 2020a; Welcome and Mastorakis 2021). However, disordered signalling or excessive activation of TAS2Rs by pathological molecules can initiate cellular or tissue damage, characterised by proinflammatory and oxidative stress responses (Welcome 2020a; Welcome and Mastorakis 2021; Welcome et al. 2021). Notwithstanding, however, there are peculiarities in the responses or mechanisms of signal transduction of TAS2Rs in some regions of the body. Therefore, in addition to activation and recruitment of macrophages and other immunocytes in the heart, the cardiac TAS2Rs respond to stimuli via transduction cascades involving the activation of phosphodiesterase (PDE)-dependent pathways and downregulation of cyclic AMP. The pathways of signal transduction of cardiac TAS2Rs are summarised in Fig. 1.

Emerging role of cardiac bitter taste receptors in cardiac inflammation, oxidative stress, arrhythmia and contractile dysfunction: cellular and molecular mechanisms

Data have consistently shown that TAS2Rs can act as immune sensors by detecting not only the danger-associated molecular patterns, but also microbial components to mobilise protective measures against the pathogenic invasion or aggression (Manson et al. 2014; Hamdard et al. 2019b; Welcome 2020a; D'Urso and Drago 2021; Welcome and Mastorakis 2021). Accordingly, TAS2Rs are now considered as integral components of the sensory (Palmer 2007; Barham et al. 2013) and innate immune system (Gulbransen et al. 2008; Tizzano et al. 2011). Therefore, cardiac TAS2Rs may function as immune cystocytes or sentinels that effectively monitor and maintain the cardiac immediate environment to ensure uninterrupted functioning of the heart. Furthermore, previous studies have revealed a potential role of these receptors as critical mediators of inflammatory and oxidative stress responses (Hamdard et al. 2019b; Welcome 2020a; Welcome and Mastorakis 2021). Very recent data suggest a possible role of cardiac TAS2Rs in the pathophysiology of arrhythmia and contractile dysfunction in heart diseases (vide infra).

Cardiac bitter taste receptors sense the "quorum" to mobilise defensive mechanisms against pathogenic aggression

Research has shown that TAS2Rs can sense the "quorum" to regulate the activities of pathogens by detecting the quorum-sensing signal molecules (Gulbransen et al. 2008; Tizzano et al. 2011). Quorum-sensing signal molecules are substances produced by pathogens that enable them communicate with each other, share information about cell density and adjust to gene expression until sufficient quantity



Fig. 1 Signal transduction mechanisms of cardiac bitter taste receptors (TAS2R). The pathogenic or toxigenic molecules activate TAS2R (Freund et al. 2018) to trigger the dissociation of α-gustducin from the $\beta\gamma$ subunit. The former stimulates the membrane bound enzyme, adenylate cyclase (AC). This enzyme produces cyclic adenosine monophosphate (AMP) in the presence of adenosine triphosphate (ATP) (Jeon et al. 2011; Workman et al. 2018; Xie et al. 2018). Cyclic AMP activates some ion channels and intracellular enzymes, including protein kinase A (PKA), which phosphorylates its downstream targets. However, cyclic AMP is hydrolysed by phosphodiesterases (PDE3, -4) to form 5'AMP, thereby decreasing the level of activated PKA (Foster et al. 2014). The $\beta\gamma$ subunit stimulates phospholipase C β (PLC β), which mediate the formation of diacylglycerol (DAG) and 1,4,5-inositol trisphosphate (IP3) from phosphatidylino-

sitol 4,5-bisphosphate (PIP2). IP3 stimulates IP3 receptor (IP3R) to mediate cytosolic release of Ca²⁺. The increase in cytosolic Ca²⁺ activates transient receptor potential cation channel, subfamily M, member 5 (TRPM5), calcium homeostasis modulator 1 (CALHM1), and ryanodine receptor 2 (RyR2) of the sarcoplasmic reticulum (SR) (Chandrashekar et al. 2000; Jeon et al. 2011; Workman et al. 2018; Xie et al. 2018). Elevation of cytosolic Ca²⁺ may cause ATP secretion via P2XY channel (Welcome et al. 2015). However, increase in Ca²⁺ level is only transient and not able to cause contraction of the muscle cell. DAG activates protein kinase C (PKC), which phosphorylates other intracellular proteins and membrane receptors such as Ca²⁺-calmodulin protein kinase II (CaMKII), angiotensin II receptor (Ang IIR), connexins (Cx) (Manson et al. 2014; Welcome et al. 2015)

of the pathogens is available to counteract the host defence mechanisms (Rajput et al. 2016). Quorum-sensing signal molecules are essential in secretion of virulence factors, biofilm formation, motility, etc. (Rajput et al. 2016). As a matter of fact, the virulence of pathogens, in part, depends on the quantity of quorum-sensing signal molecules synthesised in the host (Wu et al. 2021a). All currently identified quorum-sensing signal molecules are available in specialised repositories, namely SigMol Database (http://bioinfo. imtech.res.in/manojk/sigmol), which harbours about 1380 molecules (Rajput et al. 2016), and QSIdb (http://qsidb.lbci. net/), a quorum-sensing interference (QSI) database with several hundreds of quorum-sensing signal molecules (Wu et al. 2021a). Table 2 shows some quorum-sensing signal molecules produced by cardiotrophic pathogens. Under normal condition, the quorum-sensing signal molecules activate the TAS2Rs to initiate intracellular signalling that culminate in protection of the host against microbial invasion, at least in part, by suppressing the host immune responses (Grassin-Delyle et al. 2019; Kinnamon and Finger 2019). Though the mechanisms of suppression of the host immune system is not completely known, Lee et al. (2018) showed that quorum-sensing signal molecules subvert the host anti-viral, -bacteria and -fungi defences mainly by abrogating interferon (IFN)- β production via pathogen interaction with the activation of retinoic-acid-inducible gene-I (Lee et al. 2018). More so, evidence indicates that pathogens use quorum-sensing signal molecules to actively suppress the production of inflammatory cytokines, reactive species, including NO via inhibition of κB (I κB) kinase

Dothoron	Conombination 1	Oursense sizes aires and south	Dridanna af introduzament in aandina infration
raurugen	Octicial types	Quotum-sensing signal morecure	
Gram-positive bacteria	Bacillus sp. (e.g. Bacillus cereus), Listeria sp., Enterococcus sp., Streptococcus pordonii, and Staphylococcus sp. (e.g. S. aureus)	Oligopeptides, thiolactone, PlcR, Npr, and PapR (autoinduc- ing peptides) [166,167, 168]	Endocarditis (Fernández Guerrero et al. 2007; Guerrero et al. 2009; Thomas et al. 2012; Ferrand et al. 2013; Lamond et al. 2021); myocarditis (McGee et al. 2018; Strmadel et al. 2018)
Gram-negative bacteria	Escherichia coli	Autoinducer (AI)-3 (Zhou et al. 2016)	Endocarditis (Quiring and Burke 2021)
	Stenotrophomonas Maltophilia (Xanthomonas maltophilia and Pseudomonas maltophilia), X. campestris	Homologue of farmesoic acid: cis-11-methyl-2-dodecenoic acid, α,β unsaturated fatty acid (diffusible signal factor, DSF) [178,179]	Endocarditis (Mehta et al. 2000)
	Acinetobacter sp. (A. baumannii). Aeromonas hydrophyla, Pseudomonas sp., Serratia marcescens, and Yersinia sp.	N-acyl-L-homoserine lactone, N-(3-oxoacyl)-L-homoserine lactone, N-(3-hydroxyacyl)-L-homoserine lactone; AI-1 (Deep et al. 2011; Zhou et al. 2016)	Endocarditis (Suri et al. 1971; Rodríguez-Hernández et al. 2004; Pugliese et al. 2016; Gürtler et al. 2019; Joannou et al. 2021), myocarditis (Del-Pozo et al. 2011; Ranjani et al. 2015)
	Pseudomonas aeruginosa	Butyryl-homoserine lactone; AI-1(Deep et al. 2011; Zhou et al. 2016)	Endocarditis (Gürtler et al. 2019), myocarditis (Ranjani et al. 2015)
	Escherichia coli	Furanosyl borate diester (AI-2) (Li et al. 2007; Zhou et al. 2016)	Endocarditis (Quiring and Burke 2021)
	Escherichia coli, Salmonella enterica, and Shigella flexneri	2-Methy-2,3,3,4-tetrahydroxytetrahydrofuran (AI-2) (Li et al. 2007; Zhou et al. 2016)	Endocarditis (Fernández Guerrero et al. 2004; Quiring and Burke 2021), pericarditis (Fernández Guerrero et al. 2004), myocarditis (Chehab et al. 2020), pancarditis (Guerrero Ortiz et al. 2003)
	Pseudomonas aeruginosa	2-heptyl-3-hydroxy-4 quinolone, 3-oxododecanoyl-1- homoserine lactone (Rennemeier et al. 2009)	Vide supra
	Neisseria gonorrhoeae	NgAI-2 (AI) (Anderson et al. 2016; Edwards et al. 2016)	Endocarditis (Olayemi et al. 2017)
	Treponema pallidum	TpAI-2 (AI) (Babb et al. 2005; von Lackum et al. 2006; Arnold et al. 2015)	Endocarditis (Hijikata et al. 2019), septic cardiomyopathy (Guo and Guo 2021)
	Chlamydia trachomatis	CtAI, certain fatty acids (AI) (Bergsson et al. 1998; Barczak and Hung 2009; Rabin et al. 2015; Simon et al. 2015)	Endocarditis (Brearley and Hutchinson 1981), myocarditis (Ringel et al. 1982)
	Legionella sp. (e.g. <i>Legionella pneumophila</i>)	LAI-1 (Legionella autoinducer) (3-hydroxypentadecane- 4-one—an α -hydroxyketone) (Tiaden and Hilbi 2012; Simon et al. 2015)	Endocarditis (Pearce et al. 2011), pericarditis, myocarditis (Burke et al. 2009)
	Vibrio vulnificus	cyclo-(l-Phe-l-Pro) (Kim et al. 2018)	Endocarditis (Truwit et al. 1987)
Parasites	Candida albicans, C. auris, Aspergillus fumigatus, Crypto- coccus	Farnesol, tyrosol, 3(R)-hydroxy-tetradecaenoic acid (β-oxidation metabolite of linoleic acid), phenylethanol, tryptophol (Rennemeier et al. 2009; Deep et al. 2011; Nigam et al. 2011)	Pacemaker site infection, cardiac failure (COHEN et al. 1991; Mullick et al. 2006)
Viruses	Coronaviruses (e.g. SARS-CoV-2), coxsackievirus, par- vovirus B19, Epstein-Barr virus, cytomegalovirus, and varicella-zoster virus, human herpesvirus 6, etc	Rap-Phr, AimR-AimP, AimR-AimP-like, etc. (Bernard et al. 2021)	Endocarditis (Ouarradi et al. 2021), myocarditis (Martens and Accornero 2021)
Note: QSS quorum-sen inducing peptides	sing signal, SARS-CoV-2 severe acute respiratory syndror	me coronavirus 2, Gram-negative bacteria are called auto	inducers, whereas Gram-positive bacteria produce auto-

(IKK) phosphorylation, IkBa degradation, and nuclear translocation of NF- κ B (Kim et al. 2015). In addition to activation of NF-kB, cardiotrophic quorum-sensing signal molecules (including those of the severe acute respiratory syndrome coronavirus 2) (Freeman and Swartz 2020; Kandasamy 2021) initiate intracellular signalling via TAS2Rs (Barham et al. 2021; Parsa et al. 2021; Sharma et al. 2021) to activate the cytoplasmic sensor of inflammatory signal-NLRP3 inflammasome (Freeman and Swartz 2020; Kandasamy 2021). However, under normal condition, cardiac TAS2Rs counteract these quorum-sensing signal molecules by binding to them and mediating responses that eventually result in the prevention of the pathogenic aggression, suggesting that TAS2Rs may serve as a novel type of patternrecognition receptors (Lee et al. 2018; Zhou et al. 2021). Interestingly, recent data showed that TAS2R16 activation effectively suppresses LPS-induced secretion of proinflammatory cytokines (Zhou et al. 2021). Therefore, cardiac TAS2Rs detect quorum-sensing signal molecules to initiate microbicidal and other responses that lead to elimination of the pathogens. Nevertheless, dysfunctional signalling of TAS2Rs can predispose to pathologies (Welcome 2020a). Thus, investigating the mechanisms of detection of quorumsensing signal molecules or other pathogenic molecules by TAS2Rs and their signal transduction cascades in health and disease can provide useful information for identification of novel frontiers in the treatment of some heart diseases.

Nitric oxide secretion contributes to the anti-inflammatory effects of cardiac bitter taste receptor activation

The synthesis and secretion of NO is a key mechanism involved in the anti-inflammatory effects of TAS2R activation. Kim et al. (2015) showed that pathogens use quorumsensing signal molecules to actively suppress the production of NO (Kim et al. 2015). Indeed, NO has been repeatedly shown to exhibit a microbicidal effect on cardiotropic pathogens (Akaike and Maeda 2000; Uehara et al. 2015). TAS2Rs of the endocardium or cardiac vessel endothelium respond to quorum-sensing signal molecules, potentially dangerous microbial metabolites, toxins, pharmacological agents such as acetaminophen, chloramphenicol, chloroquine, quinine, noscapine (Tables 1 and 2) [BitterDB (http://bitterdb. agri.huji.ac.il)], and phytochemicals such as genistein and polyphenols (Gradinaru et al. 2022) to trigger NO secretion via the canonical pathway of taste receptor transduction (Gopallawa et al. 2021; Carey et al. 2021). Accordingly, in the canonical pathway, the microbicidal effects of activation of cardiac endothelial TAS2Rs are largely due to the rise in intracellular Ca²⁺, which forms complexes with CaM, and in turn activates CaM-dependent protein kinases to stimulate eNOS (endothelial NOS). eNOS is the enzyme that catalyses

the formation of L-citrulline and NO from L-arginine (Welcome 2020a). Upon stimulation of α -gustducin by a higher concentration of bitterants or microbial quorum-sensing signal molecules in TAS2R-expressing endothelial cells, a rise in cytosolic Ca²⁺ activates a greater NO generation in a dose-dependent manner, thereby inducing substantial microbicidal effects on the pathogens (Gopallawa et al. 2021). Consistently, Grekov et al. (2017) reported significant destruction of *Leishmania promastigotes*, the parasite that causes leishmaniasis, following treatment with calcimycin (a calcium ionophore) via activation of NO secretion (Grekov et al. 2017). Comparable data are discussed elsewhere (Jeandroz et al. 2013).

Bitter taste receptors, cardiac contractility and rhythm: bitter taste receptor agonists modulate cardiac contractility and pacemaker activity via Ca²⁺-, cyclic AMP- and PDE-dependent mechanisms

Since TAS2R signalling is associated with changes in cardiomyocyte cytosolic Ca²⁺ and cyclic AMP along with other signalling molecules (Manson et al. 2014; D'Urso and Drago 2021), activation of TAS2Rs will elicit corresponding changes in cardiac mechanics and pacemaking. Accordingly, administration of TAS2R108 and 137 agonists in Langendorff-perfused heart of C57BL/6 mice revealed a ~40% decrease in left ventricular pressure and increase in the aortic pressure, respectively (Foster et al. 2014). However, these responses were abolished in the presence of pertussis toxin and gallein, which are, respectively, inhibitors of G α i and G $\beta\gamma$ subunits of the G-protein, indicating a negative inotropic effect of TAS2R agonists on the heart (Foster et al. 2014). Thus, activation of cardiac TAS2Rs leads to negative ionotropy (Fig. 2).

In a relatively recent study, Yuan et al. (2020) demonstrated a negative chronotropic effect of quinine and chloroquine on the sinoatrial node, which was abrogated via inhibition of TAS2R108 with abscisic acid. In addition, both TAS2R agonists suppressed the isoprenaline-induced tachycardia on the sinoatrial node (Yuan et al. 2020). In the same study, the authors showed that inhibition of phosphodiesterases (PDE3 and PDE4) with 3-isobutyl-1-methylxanthine resulted in a negative chronotropic effect on the sinoatrial node (Yuan et al. 2020). Thus, TAS2R agonists suppress the pacemaker activity of the sinoatrial node via PDE-induced cyclic AMP reduction (Fig. 3), suggesting that dysfunctional signalling of TAS2R may play a role in the development of cardiac arrhythmia via disordered generation of impulse.



Fig. 2 The negative ionotropic effect of TAS2R activation in cardiac muscle cell. TAS2R activation initiates downstream signaling that culminates in reduced formation of cyclic AMP (adenosine monophosphate) in a PDE-dependent manner. This reduces the activity of protein kinase A (PKA) along with deregulated activity of protein kinase C (PKC) resulting in decreased phosphorylation of its targets (Foster et al. 2014; Manson et al. 2014; Welcome et al. 2015). These protein kinases reduce their stimulatory effect of Ca²⁺-calmodulin protein kinase II (CaMKII), thereby decreasing the

Molecular signalling pathways, linking bitter taste receptor sensing of pathogenic and toxigenic molecules with inflammatory, oxidative stress responses, arrhythmia and contractile dysfunction in heart diseases

Accumulating research data have consistently shown that TAS2Rs participate in inflammatory and oxidative stress responses (Hamdard et al. 2019b; Welcome 2020a; Welcome et al. 2021; Welcome and Mastorakis 2021). Furthermore, available data indicate that TAS2Rs are involved in modulation of cardiac excitability and contractile activities, suggesting that disorders in TAS2R signalling might predispose to cardiac diseases, which are characterised by inflammation, oxidative stress, contractile dysfunction and possibly arrhythmia (Manson et al. 2014; Hamdard et al. 2019b; Yuan et al. 2020). Data also indicate a critical role of NLRP3 and NF- κ B in mediating and establishing a molecular bridge

activity of ion channels/receptors such as 1,4,5-inositol trisphosphate receptor (IP3R), transient receptor potential cation channel, subfamily M, member 5 (TRPM5), ryanodine receptor 2 (RyR2), CaATPase, angiotensin II receptor (AngIIR), adrenoreceptor (AR), etc. (Chandrashekar et al. 2000; Jeon et al. 2011; Workman et al. 2018; Xie et al. 2018). The resultant effect is reduced cytosolic calcium waves, decreased phosphorylation of the motor proteins that promote relaxation of the cardiac muscles (negative inotropy). Other abbreviations are similar to those in Fig. 1

between the immune-inflammatory system and TAS2R dysfunction (Welcome 2020a; Welcome and Mastorakis 2021). These molecular sensors of the immune system and inflammatory responses are responsible for cardiac inflammation due to defective TAS2R signalling.

The NF- κ B and NLRP3 inflammasome are the primary regulators of inflammatory responses (Welcome 2020a; Welcome and Mastorakis 2021) and have been widely implicated in cardiac inflammation (Lu et al. 2015; Chen et al. 2018; Jui et al. 2021) and taste receptor signalling defects (Zhou et al. 2018; Welcome 2020a). In addition, it is widely acknowledged that the master oxidative stress sensor, Nrf-2 (nuclear factor erythroid 2-like 2) connects the inflammatory signalling cascades to oxidative stress responses and vice versa (Jui et al. 2021). Indeed, the Nrf-2 has been consistently implicated in the pathogenic mechanism of cardiac disorders (Jui et al. 2021). Thus, Nrf-2 may be responsible for mediating the signalling cascades that link oxi-inflammatory stress



Fig. 3 The negative chronotropic effect of TAS2R activation on the sinoatrial node. The reduced activity of protein kinase A (PKA) and protein kinase C (PKC) leads to downregulation of the activity of Ca²⁺-calmodulin protein kinase II (CaMKII), funny (f) channel, L-type Ca channel, T-type Ca channel, 1,4,5-inositol trisphosphate receptor (IP3R), transient receptor potential cation channel, subfamily M, member 5 (TRPM5), ryanodine receptor 2 (RyR2), CaATPase, angiotensin II receptor (AngIIR), glucagon-like peptide 1 receptor

(GLP1-R), adrenoreceptor (AR), etc. However, certain phosphorylation may increase channel activity (e.g. K channel). The overall effect is associated with increase in the slow depolarising (pacemaker) potential (negative chronotropic effect) mainly due to reduced i_f current, reduced Ca²⁺ waves, and increased K⁺ current (Foster et al. 2014; Manson et al. 2014; Welcome et al. 2015). Other abbreviations are similar to those in Fig. 1

with taste receptor dysfunction (Hamdard et al. 2019b). Hence, an extensive cross-talk occurs between the inflammatory sensors (NLRP3 and NF- κ B) and Nrf-2 to regulate the homeostasis of the immune system, inflammatory and oxidative stress profiles of the cells and tissues of the heart.

NF-κB signalling

The NF- κ B is a transcription factor that regulates the expression of over 550 genes (nf-kb.org) involved in immune, inflammatory, oxidative stress responses, cell proliferation, differentiation, growth, survival, apoptosis and other cellular processes (Collins et al. 2016). The mammalian proteins of the NF- κ B family consist of p105 (precursor protein of p50), p100 (precursor of p52), RelA (p65), RelB and c-Rel (Thu and Richmond 2010). The NF- κ B signalling pathway is stimulated by pathogenic factors, cytokines, ROS, and reactive nitrogen species. Therefore, oxidative stress molecules such as ROS or the proinflammatory cytokine, IL-1 β , produced by dysfunctional taste receptors (Zhou et al. 2018; Welcome and Mastorakis 2021) can activate the NF- κ B signalling through the I κ B kinase or TLR, respectively. In

addition, abnormal stimulation of TAS2R by pathogenic components or quorum-sensing signal molecules can also activate the NF- κ B (Welcome 2020a).

The NF- κ B is abundantly expressed in cardiac endothelial cells, fibroblasts and cardiomyocytes (Sangeetha et al. 2011; Yin et al. 2021). This molecular sensor of inflammation is present in the cytosol of cardiac cells as an inactive protein bound to IkB to form the NF-kB/IkB complex. Upon activation by pathological stimuli, the IkB kinase phosphorylates the inhibitory kappa B ($I\kappa Bs$) protein of the cytoplasmic complex NF-KB/IKB to cause degradation of IKB and release of NF-kB protein heterodimers to translocate into the nucleus to activate gene transcription (Fig. 4). The IkB kinase is a primary target of reactive species, proinflammatory mediators such as IL-1 β , TNF α and other pathogenic signals (Gloire and Legrand-Poels 2006; Thu and Richmond 2010; Collins et al. 2016; Jimi et al. 2019). Even so, a non-classical (non-canonical) or alternative pathway exists for the activation of NF-kB. The pathway involves activation of the NF-κB-inducing kinase (NIK) (Jimi et al. 2019; Pflug and Sitcheran 2020). In the alternative pathway, NIK is stimulated by ligands such as TNF receptor superfamily



Fig. 4 NF-κB/IκB and NLRP3 signaling in TAS2R dysfunction in cardiac cell. Dysfunctional signaling or pathological activation of TAS2R can trigger the activation of NLRP3 (NLR Family Pyrin Domain Containing 3) (Murakami et al. 2012; Zhong et al. 2016; Welcome and Mastorakis 2021) and nuclear factor κB (NF-κB) signaling, which mediate the production of proinflammatory cytokines and alarmins that cause inflammation, pyroptosis and fibrosis—constitute critical pathological processes in several heart diseases (Zhong et al. 2016; Chen et al.2017; Li et al. 2018). NF-κB/IκB and NLRP3 signaling in TAS2R dysfunction is also accompanied by Ca²⁺ over-

member 5 (CD40) ligand and TNF-related weak inducer of apoptosis (Thu and Richmond 2010) resulting in cleavage of the p100 to produce p52 with subsequent dimerisation of the latter with RelB. The complex formed translocates into the nucleus to initiate gene transcription (Thu and Richmond 2010). Recent evidence indicates that the NIK protein can interact with the canonical NF- κ B pathway by activating the I κ B kinase (Woronicz et al. 1997; Thu and Richmond 2010). The activated NF- κ B induces the expression of caspase-1, IL-1 β and NLRP3 (Welcome and Mastorakis 2021). NLRP3 is discussed in the next subsection.

Though the exact mechanisms are not known, emerging data suggest that NF- κ B activation is linked to TAS2R signalling. As a matter of fact, increased expression of taste

load, which worsens cardiac functions. The secreted interleukins can trigger proinflammatory responses in neighbouring cardiac cells and immunocytes. (See further explanation in text). *TLR* toll-like receptor, *IL* interleukin, *MMPs* Matrix metalloproteinases, *TIMP* tissue inhibitor of metalloproteinases, *PYD* pyrin domain, *CARD* caspase activation and recruitment domains, *LRR* leucine-rich repeat, *ASC* apoptosis-associated speck-like protein containing a caspase activation and recruitment domain—CARD, *NACHT* domain present in NAIP, CIITA, HETE and TP1. Other abbreviations are similar to those in Figs. 1 and 2

receptors has been reported in inflammatory conditions (Shin et al. 2010), suggesting that taste receptor dysfunction can predispose to inflammatory conditions. Consistent with these findings, independent groups of researchers (Cui et al. 2019; Wu et al. 2020) have demonstrated the involvement of disorders of the bitter taste sensor, TRPM5 (transient receptor potential cation channel subfamily M member 5) in hypertensive heart disease. Zhou et al. (2021) reported that TAS2R16 activation by salicin effectively suppressed the release of LPS-induced proinflammatory cytokines, in part, by inhibiting the increase in cytosolic cyclic AMP and nuclear translocation of NF- κ B p65 in human fibroblasts (Zhou et al. 2021). Though NF- κ B p65 activation can mediate the secretion of alarmins and pore-forming proteins, which result in pyroptosis (a form of cell death ensuing from the formation of pores in the plasma membrane), evidence indicates that under normal condition, taste receptor signalling also leads to inhibition of autophagy in the heart through the activation of the mammalian rapamycin complex 1 (mTORC1) (Kokabu et al. 2015). In fact, rodents lacking taste receptors displayed increased rate of autophagy in the heart (Kokabu et al. 2015). Apparently, NF-kB activation provides a critical molecular nexus between inflammatory cascades and mTORC1 activity via interaction with IκBα. Moreover, the activation of mTORC1 is considered as a downstream event of NF-kB activation in immortalised NPE cells (Zhu et al. 2016). Therefore, NF-kB and mTORC1 exhibit an extensive cross-talk with each other (Li et al. 2019) and are both involved in regulating the inflammatory and host defence system against pathogenic aggression (Bao et al. 2015; Li et al. 2019).

Several pharmacological compounds activate the TAS2Rs to mediate downstream signalling that leads to the inhibition of NF-kB. For instance, the anti-microbial, -inflammatory and immunomodulatory activities of flavones are mediated via TA2R14 activation, which suppresses the release of proinflammatory cytokines (Hariri et al. 2017). Flavoneinduced taste receptor activation also increases the TA2R14driven Ca²⁺ flux that subsequently stimulate NO production in response to multiple inflammatory stimuli, in part, through inhibition of PKC, receptor tyrosine kinase (Hariri et al. 2017) and NF-κB (Panche et al. 2016; Yahfoufi et al. 2018; Choy et al. 2019). Some flavones may also activate a functional TA2R38 isoform, which closely co-localises with TA2R14 to mediate the anti-inflammatory effects of this class of phytochemicals (Hariri et al. 2017). Consistent with the findings of previous authors (Hariri et al. 2017), a recent investigation by Tiroch et al. (2021) revealed that the anti-inflammatory effect of trans-resveratrol was mediated via the activation of TAS2R50 as treatment with the TAS2R antagonist homoeriodictyol or small interfering RNA-mediated TAS2R50 knockdown completely abolished the antiinflammatory effect of trans-resveratrol in LPS-induced IL-6 secretion in an in vitro model of human fibroblasts (Tiroch et al. 2021). Interestingly, the flavone and stilbenoid subclasses of polyphenolic compounds possess cardioprotective properties, which highlight a possible adjunct therapeutic role of these phytochemicals in heart diseases (Akinwumi et al. 2017; Khan et al. 2021).

NLRP3 signalling

The NLRP3 is a cytoplasmic sensor that detects pathogenic (Swanson et al. 2019; Ciążyńska et al. 2020) and endogenous danger molecules as well as environmental toxins, including ultraviolet radiation (Liu et al. 2014; Ciążyńska et al. 2020) resulting in the formation of the NLRP3 inflammasome

(Swanson et al. 2019). The NLRP3 is also activated by metabolic toxins, extracellular ATP, reactive species, K^+ efflux (Liu et al. 2014; Swanson et al. 2019; Wang et al. 2020) and disordered gut microbiota (Henao-Mejia et al. 2013).

Inflammasomes are cytosolic oligomeric multiprotein complexes of the innate immune system that assemble in response to pathogenic signals to mediate inflammatory responses via the activation of caspase-1, resulting in proteolytic cleavage of pro-IL-1β, -IL-18 and gasdermin-D into their active forms with corresponding initiation of proinflammatory responses and pyroptosis (Mariathasan et al. 2004; de Zoete et al. 2014; Broz and Dixit 2016). Out of the 22 proteins of the NLR ((nucleotide-binding oligomerisation domain (NOD) like receptor)) family currently discovered in humans, only 8 have been reported to form an inflammasome: NLRP-1, -2, -3, -6, -7, -12, NLRC4 (Nod-like receptor Card domain-containing protein 4), and AIM2 (Absent In Melanoma 2) (de Zoete et al. 2014). However, the NLRP3 is the most widely studied and best characterised inflammasome (Swanson et al. 2019).

The NLRP3 is normally autoinhibited in the absence of danger or pathogenic signals (Sharma and De Alba 2021). The presence of pathogenic signal leads to the activation of NF-κB to promote the transcription of NLRP3, pro-IL1β, pro-IL-18, and a 53-kDa gasdermin-D through a process known as priming (Brownlee et al. 2020). The signal subsequently activates the NLRP3 (Brownlee et al. 2020) to promote the formation of active NLRP3 (i.e. NLRP3 inflammasome), involving the assembly or oligomerisation of the inactive upstream sensor (NLRP3), the adapter protein ASC (apoptosis-associated speck-like protein), and the downstream effector procaspase-1 (Henao-Mejia et al. 2013; Brownlee et al. 2020). The formation of the inflammasome triggers an autocleavage of procaspase-1 to caspase-1, which mediates the proteolytic cleavage, maturation and release of IL-1 β and IL-18 (Broz and Dixit 2016; Swanson et al. 2019). The downstream effector of the NLRP3 inflammasome also mediates the cleavage of gasdermin-D to produce a 22-kDa C-terminal and a 31-kDa N-terminal fragment. The latter mediates the formation of membrane pores resulting in a greater secretion of proinflammatory molecules and alarmins (Wang et al. 2020) and eventually, pyroptotic cell death (Broz and Dixit 2016; Swanson et al. 2019). Apart from caspase-1, other caspases (e.g. caspase-11 in rodents, caspase 4 and caspase 5 in humans) can cause the activation of inflammasome via the non-canonical pathway by direct sensing of microbial components (e.g. bacterial LPS) in the cytosol (Broz and Dixit 2016).

Under normal condition, the NLRP3 is expressed in the cytosol at low levels in healthy heart tissues (Huang et al. 2014; Ye et al. 2015). Liu et al. (2014) demonstrated sparse expression of NLRP3 in cardiomyocytes, but increased expression of the protein in cardiac microvascular endothelial cells, which may indicate a greater role of the cardiac endothelium in inflammatory and immune response (Liu et al. 2014). Correspondingly, the authors showed increased NLRP3 inflammasome activation in cardiac ischaemia/reperfusion injury in cardiac microvascular endothelial cells, but not in cardiomyocytes (Liu et al. 2014). New data indicate a fundamental role of the cardiac microvascular endothelial cells in triggering cardiomyocyte injury (Zhang et al. 2021). Consistent with these data, Mezzaroma et al. (2011), Sandanger et al. (2013), and Liu et al. (2014) previously showed high NLRP3 expression in myocardial leukocytes, fibroblasts, and endothelial cells in myocardial ischaemia. Similar findings have been reported in a recent investigation (Mesquita et al. 2021). Increased expression of NLRP3 has also been confirmed in heart failure and cardiomyopathy (Wang et al. 2020). This pathogenic sensor is believed to be a critical molecular target for some existing medications, including agents used for the treatment of cardiovascular diseases (Wang et al. 2020). The NLRP3 is also expressed in dendritic cells, monocytes, macrophages and neutrophils (Wang et al. 2018, 2020).

On the basis of available evidence, indicating that taste receptors are crucial components of the innate immune system, inflammatory (Gulbransen et al. 2008; Tizzano et al. 2011; Lee and Cohen 2013b) and oxidative stress (Hamdard et al. 2019b) responses, as well as data suggesting a critical role of taste receptor signalling in neuroinflammation (Welcome and Mastorakis 2021), respiratory tract infection (Lee and Cohen 2013b), gastrointestinal infection (Liszt et al. 2022) and urinary and reproductive tract inflammation (Welcome et al. 2021), we therefore suggest that activation of NLRP3 by reactive species and abnormal Ca^{2+} signal is involved in the proinflammatory and oxidative stress responses of dysfunctional taste receptor signalling in the heart (Fig. 4). The activation of NLRP3 contributes to several cardiac disorders, including atherosclerotic heart disease, hypertensive heart disease, myocardial infarction, cardiac infection, cardiomyopathy, heart failure (Wang et al. 2018), and ageing (Mesquita et al. 2021). Indeed, the NLRP3 inflammasome and elevated cytosolic ROS along with decreased intracellular Ca²⁺ level have been associated with taste receptor dysfunction involving downregulation of α -gustducin, TRPM5, and phospholipase C β 2 (Zhou et al. 2018). In mammals, TRPM5 is coexpressed with phospholipase C β 2 in taste receptor cells, and both molecules are essential elements in the signal transduction mechanism of TAS2R (Pérez et al. 2002). Again, disorders of these taste receptor components are involved in inflammation and cardiac disorders. For instance, it has been reported in animal and humans studies that TRPM5 dysfunction is associated with cardiac inflammation (Koc et al. 2022; Virginio et al. 2022) and conduction disorders (Syam et al. 2014), suggesting that specific cardiac isoforms of TRPM may serve as useful therapeutic targets in heart diseases. Accordingly, there is a growing interest on the use of pharmacological agents for targeting the TRPM in pathological conditions (Virginio et al. 2022). Therefore, Simard et al. (2012) demonstrated that 9-phenanthrol, an aromatic alcohol derived from phenanthrene and an inhibitor of TRPM4, substantially reduces the frequency of early afterdepolarisations in a mouse model of cardiac hypoxia/re-oxygenation injury (a model of cardiac ischaemia/arrhythmia), suggesting that 9-phenanthrol can act as an anti-arrhythmogenic agent (Simard et al. 2012). (Early afterdepolarisations are essential cause of life-threatening ventricular arrhythmias, which are associated with sudden cardiac death. The limited efficacy of current antiarrhythmic therapy and the associated toxicity Bhat et al. 2022; Zeppenfeld et al. 2022) substantiates the need to search for novel therapeutic agents for the treatment of ventricular arrhythmias). Furthermore, the phenanthrenederived TRPM4 inhibitor has been demonstrated to abrogate cardiac contractile dysfunction and oxidative stress in preclinical studies. Wang et al. (2013) showed that treatment of isolated Langendorff-perfused rat hearts with 9-phenanthrol resulted in a dramatic recovery of contractile function, significant decrease in infarct size and ischaemia-reperfusion injury (Wang et al. 2013). The authors also revealed that 9-phenanthrol substantially reduced the activity of lactate dehydrogenase (LDH) (Wang et al. 2013), an important oxidative stress marker implicated in a range of cardiac diseases (Lin et al. 1991; Kopel et al. 2012; Dai et al. 2020). In contrast, control hearts had reduced contractile function, increased size of the infarct area and LDH activity (Wang et al. 2013). Piao et al. (2015) also reported that prior treatment with 9-phenanthrol or TRPM4 silencing substantially decreased the level of reactive species in ROS-induced injury in H9c2 cardiomyocytes subjected to hydrogen peroxide treatment (Piao et al. 2015). Flufenamic acid can also inhibit the TRPM4. Using a mouse model of cardiac hypoxia/re-oxygenation injury, Simard et al. (2012) showed that administration of flufenamic acid abolished cardiac arrhythmias and significantly improved cardiac contractility (Simard et al. 2012). The sulfonylurea antidiabetic drug, glibenclamide at a concentration of 100 µM completely inhibited TRPM4 activity in sinoatrial node cells (Demion et al. 2007). Interestingly, both flufenamic acid (Chi et al. 2011; Hamdard et al. 2019b) and glibenclamide (Zhang et al. 2017b; Hou et al. 2020) possess anti-inflammatory and antioxidative properties. However, only 9-phenanthrol specifically inhibits TRPM4 activity (Grand et al. 2008; Burris et al. 2015) as flufenamic acid and glibenclamide can also inhibit Ca²⁺ and ATP-dependent K⁺ channels, respectively (Ozhathil et al. 2018).

Research investigation with animal models has demonstrated cross-signalling between the NLRP3 inflammasome and cytosolic Ca^{2+} level, suggesting that Ca^{2+} is a critical modulator of inflammasome activity (Lee et al. 2012). Interestingly, the activation of TAS2Rs elicits a brief rise in cvtosolic Ca²⁺ level (Tomás et al. 2016; Duarte et al. 2020), followed by a fall (Suetomi et al. 2018) in cardiac muscle cells. Notwithstanding, however, dysfunctional taste receptor signalling may result in an excessive increase in cytosolic Ca²⁺ level with associated cytotoxicity due to Ca²⁺-induced activation of inflammatory and apoptotic signalling cascades. Recent investigations have shown that the Ca²⁺-dependent protein kinase, CaMKIIS plays a central role in initiating inflammatory responses through its interaction with the NLRP3 inflammasome in cardiomyocytes in response to pressure overload, thereby upregulating NLRP3, caspase-1, IL-1 β , IL-18, and MCP-1 to trigger macrophage recruitment (Suetomi et al. 2018). These pathological processes are associated with cardiac fibrosis, apoptosis, necrosis along with ventricular dilation and contractile dysfunction in heart diseases (Suetomi et al. 2018). Thus, CaMKIIS acts as an intracellular molecular switch that controls cardiac Ca^{2+} flux, contractility, and inflammation via interaction with NLRP3 (Suetomi et al. 2018) and NF-kB (Martin et al. 2018).

Moreover, ROS (Suetomi et al. 2018) and toxigenic metabolites formed during taste receptor disorder (Hamdard et al. 2019b) can activate the NLRP3 signalling pathway (Kong et al. 2016). Data obtained from animal experiment have shown that toxigenic metabolites induce the expression and release of peri- and intracellular degrading enzymes such as MMP-1, -3, -8, and -9 (Lee et al. 2012). Interestingly, MMP-3, -8, or -9 reportedly increased the cytosolic levels of ROS, NO, IL-1β, TNF-α, expression of NF-κB and protease-activated receptor-1 (Lee et al. 2010). Notably, MMPs have been shown to degrade cellular components by targeting proteinases, cell adhesion molecules, extracellular matrix proteins and cell surface receptors, including TAS2Rs (Sternlicht and Werb 2001). The secreted proinflammatory molecules promote inflammatory responses, oxidative stress, and downregulate the expression of connexon gap junction, anti-inflammatory mediators, pro-oxidants and antioxidant enzymes (Welcome 2020b; Welcome and Mastorakis 2020).

Fig. 5 Nrf-2 and TAS2R signalling in cardiac cell. TAS2R dysfunction triggers the formation of intracellular molecules that inhibit the nuclear translocation of Nrf-2 to downregulate the synthesis and secretion of protective and detoxifying enzymes (see further explanation in text). Akt protein kinase B (PKB), ARE antioxidant response element, ERK extracellular signal-regulated kinase, Keap1 Kelch-like ECH-associated protein 1. Maf MAF transcription factor, Nrf-2 nuclear factor erythroid-derived 2-like 2, PI3K phosphoinositide 3-kinase, SOD superoxide dismutase, CAT catalase, GSH glutathione, GR glutathione reductase, GPx glutathione peroxidase, GSH-ST glutathione-S-transferase, NQO1 dehydrogenase quinone1, XOR xanthine oxidoreductase, TrxR thioredoxin reductase, IDD iodothyronine deiodinases, GCLC glutamate-cysteine ligase catalytic subunit. (See explanation in text)



Nrf-2 signalling

The Nrf-2 is a transcription factor that acts as an oxidative stress sensor, which upon activation, translocates into the nucleus to bind with the antioxidant response element, stimulating a battery of cytoprotective, detoxifying and antioxidant genes (Fig. 5) (Vomund et al. 2017). Nrf-2 activity is mainly controlled by Kelch-like ECH-associated protein 1 (Li and Jia 2019) and protein kinases such as glycogen synthase kinase 3 beta and PI3K (Wu et al. 2014; Li and Jia 2019).

The Nrf-2 transcription factor plays a major role in regulating the equilibrium between formation and removal of reactive species (Qin and Hou 2017). Nrf-2 interacts with inflammatory signalling pathways to increase the expression of anti-inflammatory mediators (Vomund et al. 2017). Thus, Nrf-2 activation is required to abrogate the progression of inflammatory and oxidative stress responses (Ahmed et al. 2017; Hennig et al. 2018). Truly, the Nrf-2 exhibits cross-talks with the NLRP3 (Ahmed et al. 2017; Hennig et al. 2018) and NF-KB signalling pathways (Lampiasi and Montana 2018). The IkB kinase mediates the molecular interaction between Nrf-2 and the proinflammatory NLRP3 and NF-kB. As an integration point, activation of the IkB kinase stimulates both Nrf-2 and NLRP3, and also serves as a potential mechanism for the activation of antioxidant enzymes such as SOD, CAT, GPx, glutathione, glutathione reductase, glutathione-S-transferase, dehydrogenase quinone1 (Tinggi 2008; Lampiasi and Montana 2018; Cecerska-Heryć et al. 2021), xanthine oxidoreductase, thioredoxin reductase, iodothyronine deiodinases, and glutamate-cysteine ligase catalytic subunit (Tinggi 2008; Cecerska-Heryć et al. 2021).

Regrettably, however, there is a severe scarcity of data on the interaction between TAS2Rs and Nrf-2. Nevertheless, it can be suggested that TAS2R signalling may activate downstream cytoplasmic acceptors that interact with this transcription factor. Indeed, TAS2R signalling has been associated with several oxidative stress markers (Hamdard et al. 2019b). Furthermore, several activators of TAS2R have been shown to interact with the Nrf-2 to mediate downregulation of oxidative stress and proinflammatory mediators (Zhai et al. 2018; Hamdard et al. 2019b; Welcome and Mastorakis 2021). For instance, salicin activates TAS2R to exert its anti-inflammatory and anti-oxidant effects by promoting Nrf-2 nuclear translocation, HO-1 expression and inhibition of p65 phosphorylation to reduce ROS, IL-6, TNF- α , MMP-1, and -3 in animal model of inflammation (Zhai et al. 2018).

Conclusion

Cardiac inflammatory and oxidative stress responses represent central pathophysiological processes in several diseases of the heart and are associated with dysfunctional cardiac TAS2R signalling. Under normal condition, cardiac TAS2R is required for endocardial and myocardial homeostasis, including regulation of impulse generation and propagation, cardiac rhythm, and contractile functions of the heart primarily via the activities of PDE3, PDE4, protein kinases, and Cx43. However, defects in cardiac TAS2R signal transduction essentially activate the molecular switches that connect cardiac inflammation and oxidative stress to contractile dysfunction and arrhythmia via Ca²⁺-calmodulin protein kinase II, NLRP3, NF-KB, and Nrf-2 signalling cascades. These molecular signalling pathways mediate the secretion of inflammatory, oxidative stress, apoptotic and fibrotic mediators, activation and recruitment of immunocytes as well as monocyte/macrophage polarisation, which initiate the development of cardiac arrhythmia and contractile dysfunction in heart diseases. Cardiac TAS2Rs also act as gateway surveillance units that monitor and detect toxigenic or pathogenic molecules, including microbial components, and initiate responses that ultimately culminate in protection of the host against pathogenic aggression. Several pharmacological agents can act as TAS2R agonists to attenuate cardiac inflammation, oxidative stress responses, apoptosis and fibrosis, thereby abrogating cardiac arrhythmia and contractile dysfunction via activation of Nrf-2 and inhibition of NLRP3 and NF-kB signalling cascades.

Future directions

Since TAS2R signalling defects are involved in the pathophysiology of heart diseases, investigating the molecular switches that connect cardiac inflammation and oxidative stress to contractile dysfunction and arrhythmia may provide important information for identifying the molecular culprits of some heart diseases. In addition, investigation of specific molecular bridges that link cardiac TAS2R signalling defects to cardiac inflammation, oxidative stress, contractile dysfunction and arrhythmia in heart diseases may lead to identification of novel molecular targets for potential therapeutics of heart diseases. There is need to investigate the potential therapeutic roles of pharmaceuticals in cardiac TAS2R dysfunction, inflammation, oxidative stress, fibrosis, and pyroptotic cell death in heart diseases.

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Declarations

Conflict of interest None declared.

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