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Regulators of G protein signalling: a spotlight on emerging functions in the cardiovascular system

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Regulator of G protein signalling (RGS) proteins are GTPase-activating proteins for heterotrimeric G protein α subunits, and are therefore physiologically and pathophysiologically important negative regulators of G-protein-coupled receptor signalling in the cardiovascular system. Owing to the functional redundancy of many of the 20 RGS, and more than 20 RGS-like, proteins even within a single cell, animal models shedding light on the functions of individual RGS proteins are often missing. Nevertheless, RGS2 is a member of this protein family, for which specific functions in the vasculature and the heart are now emerging. Recent data show that the 519-amino acid RGS3, the only RGS protein with an additional G protein $\beta\gamma$ dimer binding domain, largely alters the signalling of G_i proteins to the monomeric GTPases Rac1 and RhoA in cardiomyocytes. In addition, an alternative approach using transgenic animals expressing RGS-resistant G protein α subunits now highlights the contributions of RGS proteins to distinct signalling pathways in the heart.

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Introduction

G-protein-coupled receptors (GPCRs) are involved in the regulation of virtually every physiological process. They catalyse GDP/GTP exchange at a coupled heterotrimeric G protein ($G\alpha\beta\gamma$), thereby promoting dissociation of the heterotrimer into a free, GTP-liganded $G\alpha$ -subunit and a $G\beta\gamma$ dimer. Both $G\alpha$ and the $G\beta\gamma$ dimer then regulate the activity of various effectors. Regulator of G protein signalling (RGS) proteins were first identified as GTPase-activating proteins (GAPs), which accelerate the intrinsic GTPase activity of $G\alpha$ proteins. As the duration of the

G protein activation cycle is primarily controlled by GTP hydrolysis, RGS proteins are important regulators for GPCR-induced signalling. All RGS proteins share a 120-amino-acid RGS homology domain, which mediates the GTPase-accelerating activity at $G\alpha$ subunits. In mammals, 20 distinct genes for ‘classical’ RGS proteins have been identified and divided into four subfamilies (RZ/A: RGS17, 19 and 20; R4/B: RGS1–5, 8, 13, 16 and 21; R7/C: RGS6, 7, 9 and 11; R12/D: RGS10, 12 and 14). All RGS proteins are GAPs for $G\alpha_{i/o}$ family members and many also act on $G\alpha_{q/11}$ proteins, but none affect the GTPase rates of either $G\alpha_{12/13}$ or $G\alpha_s$ family members [1–3]. Most R7/C and R12/D proteins have additional functional domains, whereas the RZ/A and R4/B proteins do not. R7/C family members contain a $G\alpha$ -like domain and form requisite dimers with the atypical $G\beta$ subunit $G\beta_5$. RGS12 and RGS14 contain a GoLoco motif [4], which binds to isolated $G\alpha_i$ and impedes GDP dissociation in solution, although it could also confer other activities [5]. One splice variant of the atypical R4/B family member RGS3 is able to bind free $G\beta\gamma$ dimers [6]. In addition, there are also approximately 20 related ‘RGS-like’ proteins, of which some have GAP activity [1–3]. Notably, the three members of the p115RhoGEF Rho guanine nucleotide exchange factor subfamily are the only RGS-like proteins with GAP activity for $G_{12/13}$ proteins.

Is there functional redundancy of RGS proteins in the cardiovascular system?

All mammalian cells (e.g. cardiomyocytes [7]) express at least a few different RGS proteins with GAP activity for $G_{i/o}$ and $G_{q/11}$. Given that RGS proteins tend to produce their effects over comparable concentration ranges (generally mid-to-high nanomolar *in vitro* [1–3]), the abundance of an RGS protein should correlate with its contribution to the total GAP activity within a cell. Therefore, questions regarding promiscuous and redundant functions of RGS proteins have been raised in the past. Nowadays, there is increasing evidence that specific interactions occur between certain signalling systems and RGS proteins. RGS proteins are able to bind to GPCRs, effector molecules, scaffold proteins and regulators that govern their availability and or activity [8,9]. Taking into account that the expression of several RGS proteins (e.g. RGS2, RGS4 and RGS16) can be rapidly induced by different stimuli [10–12], further specific actions of RGS proteins can be anticipated. Nevertheless, only two viable knockout mice for RGS proteins with specific phenotypes have been published. The first protein, RGS9-1 [13], has a specific function in regulating photoreceptor signal transduction;

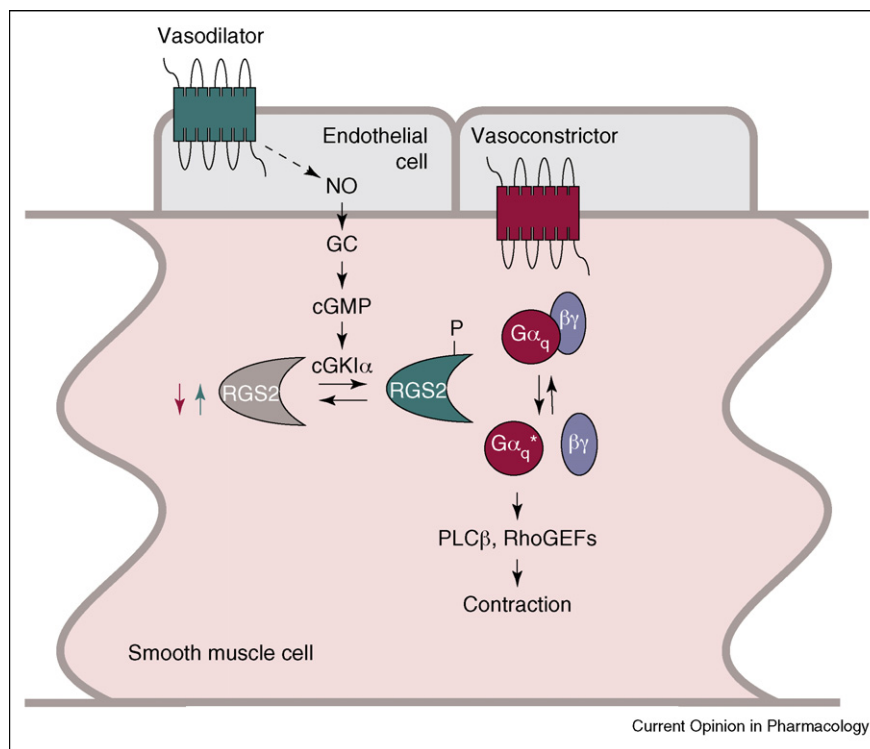
the second, RGS2 [14], is of interest in the cardiovascular system and will be discussed below.

The lack of further reported phenotypes of knockout mice argues for considerable redundancy among RGS protein family members. Furthermore, in contrast to the rapid induction of RGS proteins mentioned above, antidromic regulation might occur if the respective stimuli persists for longer periods of time (e.g. downregulation of RGS2 in cardiac hypertrophy [15^{*}], and upregulation of RGS4 in cardiac hypertrophy [16] and human heart failure [17,18]). Therefore, the physiological and pathophysiological role of a specific RGS protein in cardiovascular tissues is often obscure. This short review highlights, firstly, the role of RGS2 and RGS3 (see also Update) in the cardiovascular system and, secondly, an interesting model that has recently been developed as a result of transgenic mice carrying $G\alpha_{i2}$ subunits resistant to the GAP function of RGS proteins [19^{**},20^{**}]. This method is ingenious at circumventing methodological problems caused by the tandem arrangement of many RGS genes on one chromosome [21], which makes it difficult to create mice carrying more than one depletion of closely related RGS genes.

Role of RGS2 in cardiovascular function

RGS2 is unique owing to its preferential interaction with $G\alpha_{q/11}$ (and $G\alpha_s$) and its low affinity for $G\alpha_i$ [22,23]. RGS2 binds either directly (M_1 muscarinic receptor [24], or α_{1A} - [25,26] and β_2 -adrenoceptors [27]) or indirectly via interaction with a scaffold protein (e.g. at the α_{1B} -adrenoceptor [28^{*}]) to GPCRs. In addition, it has been shown that RGS2 directly binds to $G\alpha_s$ (without displaying GAP activity for this $G\alpha$ subunit [29]) and to different adenylyl cyclase (AC) isoforms [30,31]. Both might contribute to the reported inhibition of AC activity by RGS2 [27,29–31]. Through its unique G protein selectivity for $G\alpha_{q/11}$, RGS2 appears to play a key role in cardiovascular pathophysiology, in which deleterious processes are often initiated via $G_{q/11}$ -coupled GPCRs; for example, in blood vessels, many contractile responses are mediated via $G\alpha_q$ (Figure 1). Furthermore, the expression of RGS2 is upregulated in response to angiotensin II stimulation in vascular smooth muscle cells [11,32]. Furthermore, the GAP activity of RGS2 is increased in the vasculature by the nitric oxide–cGMP pathway via phosphorylation by cGMP-dependent kinase I α (cGKI α) [18,33^{*},34^{*}]. A vascular role for RGS2 is also implied by

Figure 1

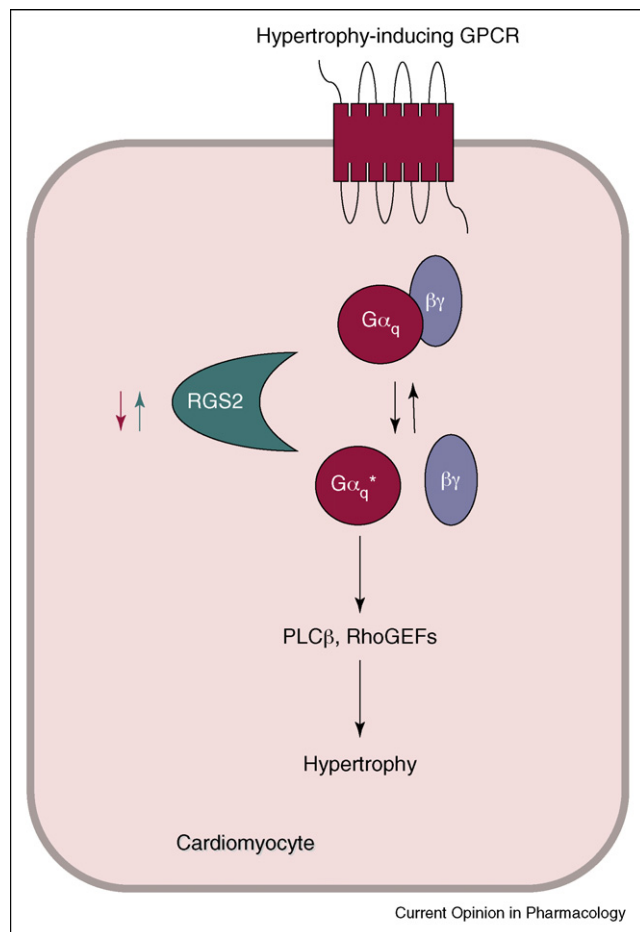


Role of RGS2 in regulation of vascular tone. RGS2 negatively regulates G_q -coupled receptors for vasoconstrictors (e.g. angiotensin II, vasopressin, noradrenaline) by accelerating the GTP hydrolysis of activated $G\alpha_q$ ($G\alpha_q^*$) in vascular smooth muscle cells. Thereby, the activity of the known $G\alpha_q$ effectors phospholipase C β (PLC β) and $G\alpha_q$ -regulated Rho guanine nucleotide exchange factors (RhoGEFs) is lowered. The activity of RGS2 appears to be controlled via phosphorylation by cGMP-dependent kinase I α (cGKI α). Thereby, RGS2 activity is under control of vasodilators (e.g. bradykinin, acetylcholine, endothelin-2) that induce nitric oxide (NO) production in endothelial cells and thus stimulation of soluble guanylyl cyclase (GC) in the smooth muscle cell. Enhanced RGS2 expression (↑) that increases negative regulation occurs in response to prolonged angiotensin II exposure and is observed in hypotensive patients. By contrast, decreased RGS2 expression occurs in hypertension (↓).

the observed correlation between the elevated and reduced expression of RGS2 and hypo- and hyper-tension, respectively, in humans [35,36^{*}]. Correspondingly, RGS2 knockout mice exhibit an elevation in mean arterial blood pressure, which could reflect enhanced and/or prolonged vascular contractile responses to α_1 -adrenoceptor and angiotensin II receptor stimulation [18,37]. RGS2 knockout animals also display moderate hypertrophy of the aorta and renal vessels in these studies [18,37].

Several studies have indicated that RGS2 might be important in cardiac hypertrophy initiated by $G_{q/11}$ -coupled receptors (Figure 2). RGS2 mRNA is selectively

Figure 2



Role of RGS2 in regulation of cardiac hypertrophy. In cardiomyocytes, RGS2 negatively regulates G_q -coupled receptors that induce cardiac hypertrophy (e.g. α_1 -adrenoceptors, endothelin receptors and protease-activated receptors) either by accelerating GTP hydrolysis or by scavenging activated G_{α_q} ($G_{\alpha_q}^*$). Again, the activity of the known G_{α_q} effectors phospholipase C β (PLC β) and G_{α_q} regulated Rho guanine nucleotide exchange factors (RhoGEFs) is lowered. Enhanced RGS2 expression (↑), which increases negative regulation, occurs in response to cardiomyocyte stimulation with hypertrophy-inducing GPCR agonists (e.g. phenylephrine). Animal models with persistent G_q activation (i.e. cardiac overexpression of $G_{\alpha_q}^*$) displayed reduced cardiac RGS2 expression (↓).

upregulated in neonatal rat cardiomyocytes by the α_1 -adrenoceptor agonist phenylephrine [11]. A recent report additionally demonstrates enhanced expression of RGS2 in response to sustained activation of the AC-cAMP system in osteoblasts [38^{*}], a response that might similarly occur in cardiomyocytes. The overexpression of RGS2 in cardiomyocytes essentially eliminated any increases in cell size and genetic markers of hypertrophy in response to α_1 -adrenoceptor stimulation [11,39]. However, the exact mechanisms through which RGS2 produces its observed protective effects in cardiomyocytes remain to be determined, as both GTPase acceleration and scavenging ('effector antagonism') of activated G_{α_q} has been observed with RGS2 [24,25]. Other GPCR signals associated with hypertrophy, including those mediated via endothelin-1, angiotensin II and protease-activated receptors, might also be blocked by RGS2, as these signals have all been shown to be inhibited by RGS2 in cardiomyocytes [39,40]. In contrast to the acute protective effects of RGS2 observed in isolated neonatal cardiomyocytes [11], a recent study found RGS2 to be selectively downregulated during the early onset of cardiac hypertrophy *in vivo* in two different models with enhanced $G_{q/11}$ signalling [15^{*}]. Corresponding experiments examining hypertrophy and G_{α_q} signalling in isolated neonatal rat cardiomyocytes showed that the small interfering RNA-mediated suppression of RGS2 expression increased both the hypertrophic effect and phospholipase C β stimulation induced by α_1 -adrenoceptors and endothelin-1 [15^{*}].

Somewhat surprisingly, no overt changes were seen in the cardiac function of RGS2 $^{-/-}$ mice up to 6 months of age [37]. Therefore, it seems likely that RGS2 knockout animals develop compensatory mechanisms in pathways that are normally repressed by this RGS protein in the myocardium. Consistent with this notion, a study on pancreatic acinar cells from RGS2 $^{-/-}$ mice showed G_{α_q} -mediated intracellular calcium transients to be largely normalized owing to decreased calcium influx into the cytosol from the ER and extracellular space, as well as increased calcium efflux through pumps in the ER membrane and plasma membrane [41]. Taken together, the available evidence implies a protective role for RGS2 against hypertrophy-associated GPCR signals in the heart, although clearly more studies are needed to elucidate the factors that control RGS2 expression during this disease process.

RGS-resistant G_{α} subunits to dissect cardiovascular signalling pathways

As mentioned above, several RGS proteins have overlapping specificities, and their role in distinct pathways is often difficult to dissect owing to their functional redundancy. Similarly, even without consideration of the influence of RGS proteins, the contribution of an individual

G protein α -subunit isoform to a specific physiological response is often difficult to analyse.

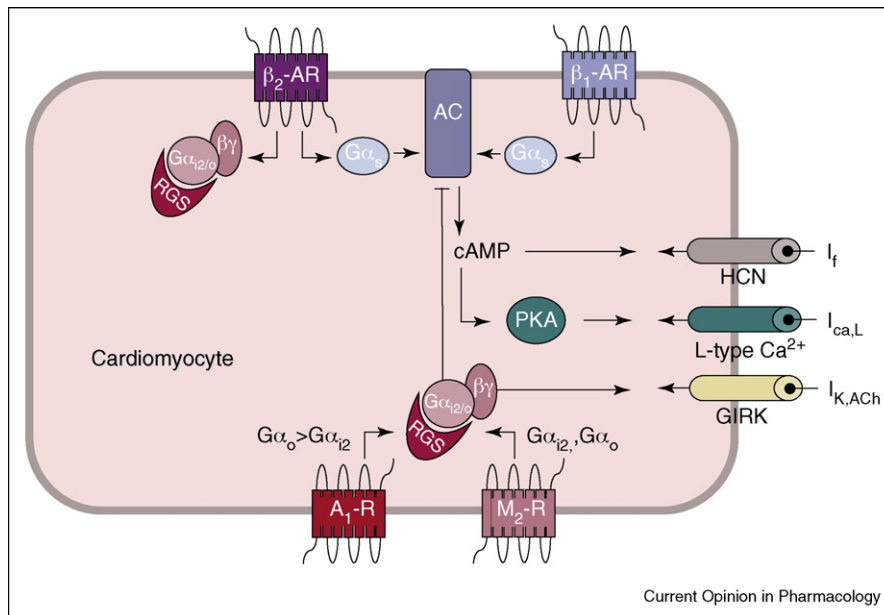
For example, it has been shown that the negative chronotropic effect of G_i -coupled receptors (e.g. M_2 muscarinic and A_1 adenosine receptors) involves several members of the $G_{i/o}$ subfamily (G_{i2} , G_{i3} and different splice variants of G_o [42–44]). In addition, at least three different ion currents ($I_{K, Ach}$, I_f and $I_{Ca,L}$) are regulated via this pathway. The $I_{K, Ach}$ current is caused by $G_{i/o}\beta\gamma$ -mediated activation of G-protein-regulated potassium channels (GIRKs) [45]. The inhibition of cardiac hyperpolarisation-activated cyclic nucleotide-regulated cation channels carrying the I_f current [46] depends upon the decrease of cAMP production, which also contributes to the inhibition of $I_{Ca,L}$ by lowering the protein kinase A (PKA)-dependent phosphorylation of L-type calcium channels.

A recent study [19^{••}] used the knock-in of RGS-insensitive mutants to analyse the individual contributions of $G\alpha_{i2}$ and $G\alpha_o$ to the negative chronotropic effects of M_2 muscarinic and A_1 adenosine receptors. The strength of this approach lies within the method, which mimics the natural arrangement and stoichiometry of signalling proteins. The concentration dependence of the agonist

effects confirmed that, under physiological conditions, there is an impartial overlap with respect to the coupling of the studied GPCRs to specific $G_{i/o}$ proteins. The authors demonstrated major sensitisation of the carbachol-induced negative chronotropy by elimination of RGS protein control on $G\alpha_{i2}$. As this sensitisation was entirely abolished by a blocker of GIRK, a preferential coupling of M_2 muscarinic receptors to GIRK via G_{i2} -derived $G\beta\gamma$ dimers can be assumed (Figure 3). Unexpectedly, A_1 adenosine receptors diminished heart rate largely through $G\alpha_o$ -dependent inhibition of AC and subsequent inhibition of I_f and $I_{Ca,L}$.

Furthermore, the authors provided new insights into the controversially discussed coupling of $G_{i/o}$ family members to β_2 -adrenoceptors. It is well-known that, in regular heart function, β_2 -adrenoceptor stimulation in concert with the more abundant β_1 adrenoceptors exerts positive chronotropic and inotropic effects through activation of the G_s -AC-PKA pathway. In heart failure, however, the potential coupling of β_2 -adrenoceptors to G_i proteins is assumed to be cardioprotective [47,48]. Surprisingly, the use of RGS-resistant mutants revealed profound coupling of the β_2 -adrenoceptors to $G\alpha_{i2}$ and $G\alpha_o$, even under physiological conditions. In the presence of the $G\alpha_{i2}$

Figure 3



RGS proteins control $G_{i/o}$ -mediated negative chronotropic responses in cardiomyocytes. In cardiomyocytes, three different currents, I_f , $I_{Ca,L}$ and $I_{K, Ach}$, which are carried by hyperpolarisation-activated cyclic nucleotide-regulated cation (HCN), L-type Ca^{2+} and G-protein-regulated inward rectifying potassium (GIRK) channels, respectively, contribute to negative chronotropic effects of $G_{i/o}$ -coupled receptors. The I_f is directly, whereas the $I_{Ca,L}$ is indirectly (via phosphorylation by PKA), regulated by cellular cAMP levels. AC activity is stimulated by G_s -coupled β_1 -adrenoceptors (β_1 -AR) and β_2 -adrenoceptors (β_2 -AR). The $G_{i/o}$ -coupled M_2 muscarinic acetylcholine (M_2 -R) and adenosine A_1 (A_1 -R) receptors exert negative chronotropic effects by inhibiting both AC and the activation of GIRK by $G_{i/o}$ -derived $G\beta\gamma$ dimers. A_1 -R-mediated negative chronotropic actions are largely dependent upon $G\alpha_o$ and minimally involve regulation of GIRK currents. By contrast, the M_2 -R utilizes $G\beta\gamma$ dimers released from both $G\alpha_{i2}$ and $G\alpha_o$ to activate GIRK, with this being the main mechanism mediating its negative chronotropic response. Both pathways are controlled by RGS proteins. Interestingly, the potential effects occurring via the coupling of β_2 -ARs to $G_{i/o}$ proteins appear to be completely suppressed by RGS proteins under physiological conditions.

mutant, β_2 -adrenoceptor stimulation primarily induced a negative chronotropic response, which was replaced by an increase in the heart rate at higher agonist concentrations. These data indicate that the naturally occurring coupling of β_2 -adrenoceptors to $G_{i/o}$ proteins under physiological conditions is blunted by RGS proteins, and thus $G\alpha_s$ -mediated activation of AC prevails. These data indicate a completely unanticipated function of cardiac RGS proteins that awaits further analysis.

The authors meanwhile analysed the transgenic $G\alpha_{i2}$ (G184S) mutant mice on a broader basis [20^{••}]. They demonstrated a complex phenotype affecting multiple organ systems (i.e. heart, myeloid, skeletal muscle and central nervous system). Even heterozygotes (with one intact $G\alpha_{i2}$ allele) exhibited reduced viability and decreased body weight. The transgenic animals showed stunted growth of long bones, a markedly enlarged spleen, elevated neutrophil counts, an enlarged heart, and behavioural hyperactivity. The authors therefore concluded that the loss of RGS action on a single $G\alpha$ subunit (i.e. $G\alpha_{i2}$) produces dramatic and pleiotropic alterations. This phenotype is much more severe than those typically seen for individual RGS protein knockouts.

In future studies, a thorough understanding of RGS protein function in the cardiovascular system and other organs might be achieved by a double-mutant approach, rescuing specifically one pair of RGS and $G\alpha$ species. Indeed, such a strategy has been reported for the interactions of RGS16 and RGS4 with $G\alpha_{i1}$ and $G\alpha_q$, respectively [49]. In this approach, a highly conserved Glu residue on the RGS protein, and a highly conserved Lys residue on $G\alpha$, are substituted by a Lys and a Glu, respectively. Whereas one of these substitutions yielded significantly reduced RGS– $G\alpha$ interactions with wild-type partners, the two complementary point mutations together form an interacting salt bridge at the RGS– $G\alpha$ interaction surface. Thereby, RGS and $G\alpha$ mutants were developed that exhibit significantly reduced interactions with their ‘natural’ counterparts, but which, together, form a fully functional RGS– $G\alpha$ pair as proven by *in vitro* GAP activity and functional inhibition at the cellular level. By applying such mutant pairs to transgenic animals [20^{••}], divergent functions of apparently redundant $G\alpha$ isoforms [48,50] and RGS proteins [51,52] can be addressed at a new level of scientific rigour and (patho)physiological significance.

Conclusions

A significant amount of work on RGS proteins has been performed in recent years that has clearly provided evidence for important functions of these molecules in signalling cascades in almost every cell-type. Certainly, RGS and RGS-like proteins are more than GAPs for $G\alpha$ subunits; they interact with GPCRs, effector molecules, scaffold proteins and additional regulators. Some of these

proteins (e.g. the p115RhoGEF family members) unify effector and GAP activities within same protein [1–3]. Despite all of the data on RGS proteins which have been accumulated so far, our knowledge of the specific function(s) of a distinct family member in the physiology and pathophysiology of the cardiovascular system is still limited. Owing to functional redundancies of several highly related RGS proteins and also experimental obstacles, new approaches have to be applied to future research on RGS proteins to indeed make them the ‘the next therapeutic target’, as anticipated in a recent review [3].

Update

RGS3 is an abundant RGS protein in the heart that exists in several splice variants. At least two of these variants exhibit an extended amino-terminal domain in addition to the RGS domain [53]. Out of these, the 519-amino acid isoform of RGS3 (RGS3L) binds $G\beta\gamma$ -dimers with a unique interaction domain located between amino acids 319 and 458 [6]. It thereby acts as a $G\beta\gamma$ scavenger and inhibits the $G\beta\gamma$ -induced effector activation independently of its GAP activity. A recent manuscript now reports that, by binding to $G\beta\gamma$, RGS3L acts as molecular switch regulating the activation of Rho GTPases by prototypical G_i -coupled receptors in cardiomyocytes [54^{••}]. At a low expression level of RGS3L, these receptors induce the activation of Rac1 using the canonical $G_i\beta\gamma$ - and phosphoinositide 3'-kinase-dependent pathway. In contrast, at increased expression levels of RGS3L, these receptors activate RhoA but not Rac1, apparently through the same signalling pathway. The expression of RGS3L in cardiomyocytes is under control of fibroblast growth factor 2, a known cardioprotective stimulus. Therefore, the differential activation of Rac1 and RhoA, depending upon RGS3L expression and the distinct downstream signalling pattern, might contribute to these cardioprotective effects.

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