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Non-canonical roles of GRKs in cardiovascular signaling

Sarah M. Schumacher, Ph.D.^{1,2} and Walter J. Koch, Ph.D.^{1,2,*}

¹Center for Translational Medicine, Lewis Katz School of Medicine at Temple University, Philadelphia, PA 19140, USA

²Department of Pharmacology, Lewis Katz School of Medicine at Temple University, Philadelphia, PA 19140, USA

Abstract

G protein-coupled receptor kinases (GRKs) are classically known for their role in regulating the activity of the largest known class of membrane receptors, which influence diverse biological processes in every cell type in the human body. As researchers have tried to uncover how this family of kinases, containing only 7 members, achieves selective and coordinated control of receptors, they have uncovered a growing number of non-canonical activities for these kinases. These activities include phosphorylation of non-receptor targets and kinase-independent molecular interactions. In particular, GRK2, GRK3, and GRK5 are the predominant members expressed in the heart. Their canonical and non-canonical actions within cardiac and other tissues have significant implications for cardiovascular function in healthy animals and for the development and progression of disease. This review summarizes what is currently known regarding the activity of these kinases, and particularly the role of GRK2 and GRK5 in the molecular alterations that occur during heart failure. This review further highlights areas of GRK regulation that remain poorly understood and how they may represent novel targets for therapeutic development.

Keywords

GPCR; GRK; cardiovascular

Introduction to GPCR Signaling and GRK Regulation

G protein-coupled receptors (GPCRs) comprise a large family of diverse membrane receptors that translate the binding of extracellular stimuli such as photons, neurohormones, chemokines, or ions into complex intracellular signaling cascades that regulate the function of all eukaryotic cells (1, 2). This occurs through ligand binding to the receptor, inducing a conformational change that stimulates the activation and dissociation of the associated heterotrimeric G protein subunits, G α and G $\beta\gamma$, which then bind effector proteins to alter cellular activity (3–5). Given the importance of GPCR signaling in determining cellular homeostasis and function, it is not surprising that receptor signaling is tightly controlled, and

*Walter J. Koch, PhD, FAHA, W. W. Smith Chair in Cardiovascular Medicine, Chairperson, Department of Pharmacology, Director, Center for Translational Medicine, 3500 North Broad Street, 942 MERB, Temple University School of Medicine, Philadelphia, PA 19140, walter.koch@temple.edu, Telephone: (215) 707-9820, Fax: (215) 707-9890.

that this control is through the phosphorylation of ligand-bound receptors via GPCR kinases (GRKs) (6). Phosphorylation of receptors by GRKs triggers desensitization via binding of β -arrestin, sterically blocking further G protein activation and attenuating downstream effector signaling (3–6). β -arrestins not only induce receptor desensitization and internalization, but downstream of GRK actions they can initiate intracellular signaling through kinase scaffolding functions, independent of G protein activity (7). In fact, endogenous GPCR ligands stimulate both G protein and arrestin signaling that can be biased by the GRK involved, while synthetic ligands may be designed to show bias for a particular pathway (8, 9). Thus, β -arrestin 1 and 2 in the heart may undergo GRK-arrestin signaling and play an important role in regulating normal and compromised cardiomyocyte function. This exemplifies the historically classical function of GRKs in regulating GPCR activity.

GRKs represent a subgroup of the AGC protein kinase family of serine/threonine kinases, which includes PKA, PKG, and PKC, due to the sequence similarity within their kinase domains (10). A thorough review of the known literature regarding GRK structure, localization, GPCR activity, cardiac function, and regulation has recently been published (11). The GRK family is composed of 7 known members that have been classified into 3 subfamilies based on their sequence and structural similarities. One subfamily is the rhodopsin kinases including GRK1 and GRK7, that are solely expressed in the retina and regulate opsin signaling (12). Additionally, there is the β -adrenergic receptor kinase (β ARK) subfamily with GRK2 and GRK3, and the GRK4-like subfamily that includes GRK4, GRK5, and GRK6 (6). While GRK4 is predominantly expressed in the testes (13), GRK2, 3, 5, and 6 are ubiquitously expressed with GRK2 and GRK5 being the predominant GRKs in the heart (14). GRK2, GRK3, GRK5, GRK6, and particularly GRK4 have also been shown to play important roles in regulating blood pressure and hypertension through activities in the heart, vasculature and kidneys. These important contributions to overall cardiovascular function are outside the scope of this article, but have recently been reviewed in detail (15). All GRKs have a tri-domain structure with a central catalytic domain flanked by amino (N) and carboxyl (C) terminal domains containing elements involved in GRK regulation and key binding elements for effectors and protein-protein interactions (3). Importantly, the N-terminal 30 amino acids that are critical for recognition of the activated receptor are highly conserved, while the C-terminus that is necessary for membrane localization is rather divergent between GRK subfamilies (16, 17).

The retinal GRK1 and GRK7 contain sequences that can be targeted for prenylation, and this hydrophobic moiety may act as a lipid anchor to facilitate their association with the plasma membrane (18, 19). Similarly, GRK4 and GRK6 contain palmitoylation sites, and these C-terminal cysteine modifications tether the GRKs to the membrane (20–22). GRK5 is unique in this subfamily in that it does not contain this palmitoylation site. Instead, GRK5 contains a positively charged amphipathic helix (N-terminal residues 25–31) that acts as a lipid-binding element, tethering it to phosphatidylinositol 4, 5 bisphosphate (PIP₂) such that GRK5 is constitutively membrane bound (23, 24). Unlike the GRK4 subfamily, GRK2 and GRK3 are not independently capable of membrane association and rely upon binding to the heterotrimeric G-protein subunit G $\beta\gamma$. G-protein γ subunits are isoprenylated through a covalent cysteine modification that mediates the membrane association of G $\beta\gamma$ subunits (25). Following receptor activation and dissociation of the heterotrimeric G-proteins, GRK2 and

GRK3 associate with membrane bound $G_{\beta\gamma}$ through their C-terminal pleckstrin homology domain, thereby facilitating their membrane translocation (26–28). The pleckstrin homology domain then further orients GRK2 at the site of GPCR action via association with membrane phospholipids such as PIP2 (29, 30). The critical interaction of GRK2 and GRK3 with $G_{\beta\gamma}$ subunits is further affected by the expression and localization of different β and γ subunit isoforms (31–33) that may partially account for the receptor selectivity of these GRKs. No matter the method, membrane localization is critical for the classical function of GRKs, where close proximity to the receptors facilitates GRK activation and subsequent phosphorylation of the agonist bound receptors. The details regarding activation of GRKs and the mechanism by which they phosphorylate receptors is outside the scope of this article, but the current understanding of these processes and how they are being further investigated has been recently described (24, 34).

Of the many functions of GRKs, the best characterized is this classical phosphorylation of agonist-bound GPCRs to regulate their signaling. GRKs mediate homologous desensitization of GPCRs via phosphorylation of agonist-occupied receptors that in turn promotes the binding of β -arrestin, sterically blocking further G protein activation and attenuating downstream effector signaling (3–5). β -arrestin binding then serves as a scaffold for association of the internalization machinery, and following internalization receptors may be targeted to lysosomes for degradation or recycled through early endosomal compartments back to the plasma membrane (35). Receptor recycling plays a critical role in determining the active pool of receptors at the membrane, since receptor de-phosphorylation and dissociation of β -arrestin occurs within these endosomal compartments (5). Therefore, through this classical function, GRKs contribute significantly to controlling the duration and capacity for GPCR signaling in the cell. In addition to the classical activity of these enzymes, ongoing research has demonstrated a great diversity in the function of GRKs, including phosphorylation of non-GPCR substrates and numerous phosphorylation-independent regulatory binding partners. These studies suggest that such alternate or non-canonical activities of GRKs are more prevalent than expected. Further, that they embody significant, functional interactions that alter cardiac physiology and disease progression. These non-canonical activities of GRKs and the role they play specifically in cardiovascular function in healthy tissue and during disease will be the focus of this review article.

GRK2

GRK2 was the first GRK identified in the heart and was originally named β -adrenergic receptor (β AR) kinase 1 (β ARK1) due to phosphorylation of activated β ARs and other GPCRs (Figure 1-1) (36). Further, GRK2 has been shown to be intimately involved in heart failure (HF) progression. GRK2 is the most abundant GRK isoform in the heart and its mRNA, protein and activity is elevated (3–4 fold) in failing human hearts (37) and animal models of HF (38–41). Several mouse models support a critical and facilitative role for GRK2 in HF development. The role of GRK2 in the regulation of β AR signaling in the healthy and diseased myocardium and the pursuit for therapeutic inhibition of GRK2 has recently been reviewed in detail (42).

In addition to the canonical function of this enzyme, ongoing research has demonstrated great diversity in the functional roles of GRK2 (7, 43). GRK2 is ubiquitously expressed and participates in diverse biological functions including cell migration, inflammation, insulin sensitivity and vascular biology (44–48); however, the mechanisms by which GRK2 participates in these cellular functions remain to be determined. An underlying mechanism for these diverse functions may be the phosphorylation-independent desensitization of diverse GPCRs, including endothelin, α and β adrenergic, muscarinic cholinergic, angiotensin, and thyrotropin releasing hormone (TRK) receptors, among others, in distinct cellular populations. Further, GRK2 has emerged as a complex regulator of cellular migration, acting through classical GPCR desensitization during chemotaxis in addition to numerous non-canonical substrates and protein interactions. For example, GRK2 dynamically binds to and phosphorylates histone deacetylase 6 (HDAC6), activating deacetylase activity at α -tubulin subunits within the leading edge of migrating cells to promote cell motility (Figure 1-2) (49). In addition, phosphorylation of non-receptor substrates including tubulin, synucleins, and ezrin may underlie GRK2 function in endocytosis and cytoskeletal rearrangements for cell migration (48). A recent review thoroughly outlined the role of GRK2 in chemotaxis and gradient sensing, cell polarization and migration, and cell adhesion and the implications of these diverse functional roles of GRK2 for cellular function and pathophysiology (50). In addition, GRK2 has been identified as an important negative regulator of insulin-dependent glucose uptake and insulin signaling (Figure 1-3). Heterozygous KO of GRK2 improves glucose transport, whole-body glucose and insulin tolerance, and insulin signaling pathways in relevant animal models of insulin resistance (51–54); however the underlying mechanism has not been elucidated. These studies indicate that the overall impact of GRK2 levels and activity on diverse cellular functions depends significantly on the particular stimuli and cell type in consideration. More importantly, these studies indicate that a complete understanding of the role of GRK2 in immune cell migration and infiltration will expand our knowledge of this enzyme in regulating scar formation and fibrosis in the heart following cardiac injury. Further, GRK2 regulation of insulin signaling and cardiac metabolism will provide a more encompassing view of the importance of this enzyme in cardiac metabolism and function during disease progression.

GRK2 has also been shown *in vitro* to interact with numerous cell signaling and trafficking proteins (55–58). For many of the GRK2 interacting partners, such as the Raf kinase inhibitor protein RKIP, GIT proteins, and mitogen activated protein kinases (MAPK), the functional consequences on GRK2 activity have been described, while the specific amino acid binding domain on GRK2 is not yet known (Figure 1-4) (59, 60). Similarly, phosphoinositide 3-kinase (PI3K) has been shown to interact with GRK2 through its 197 amino acid PIK domain, resulting in GRK2-mediated recruitment of PI3K to the membrane and enhanced internalization of agonist bound β ARs (Figure 1-4) (61). These cellular proteins may interact with GRK2 directly or in complex, potentially as members of scaffolded nodal signaling systems. In contrast, the binding domain of proteins such as Akt have been defined, amino acids 492–689 in the C-terminus of GRK2; however, this interaction inhibits Akt by an unknown mechanism (59). Some GRK2 binding partners have presumed binding domains within the N-terminus and the C-terminal pleckstrin homology

(PH) domain such as caveolin (residues 63–71 and 567–584) (62) and calmodulin (residues 18–37 and 593–689) (63). Caveolins are known scaffolding proteins that serve to inhibit or enhance signaling through compartmentalization of GPCRs and kinases within distinct membrane microdomains (64–68), and caveolin 1 or 3 binding to GRK2 has been shown to inhibit GRK2-mediated phosphorylation (62, 64, 69). Similarly, calmodulin binding directly inhibits GRK2 activity (63). Overall, though, little is known regarding what distinct signaling complexes GRK2 participates in at any given time, the localization of the complexes within the cell, and the full consequences of these regulatory binding interactions for cardiomyocyte or other cell type function *in vivo*.

A domain of interest for determining the mechanism of action of GRK2 is the Regulator of G protein signaling (RGS) - like domain identified within the N-terminus (amino acids 51–173) of GRK2. This domain has been shown to bind to and regulate Gαq activity *in vitro* (70–73), an interaction that could prove an interesting therapeutic target as Gαq represents the final common trigger of maladaptive cardiac hypertrophy (Figure 1-5). Transgenic (Tg) mice with cardiac-specific overexpression of Gαq have a phenotype of decompensated cardiac hypertrophy (74–76), but this Gαq-mediated hypertrophy and HF is blocked by cardiac overexpression of RGS4 (77). Furthermore, studies in a Tg mouse line with αMHC-targeted cardiac expression of a Gαq inhibitor (GqI), the last 50 amino acids of murine Gαq that targets the Gαq-coupled GPCR (GqPCR) interface, have demonstrated significantly lessened ventricular hypertrophy and ventricular dysfunction after pressure overload (78–80). Classically, RGS proteins bind to Gα proteins, allosterically increasing their rate of GTP hydrolysis and thereby inhibiting their activity (72, 77). The RGS domain of GRK2 appears to directly interact with Gαq and inhibit signaling without altering its GTPase activity (73). Rather Gαq was found to adopt an effector binding structure with GRK2 (81), and the domain of GRK2 responsible for Gαq binding is distinct from known binding sites for RGS4 and RGS9 (72, 82). Together, these data suggest potential distinct functions of the RGS domain of GRK2, such that a selective interaction of the GRK2 RGS domain with Gαq may alter cardiac hypertrophic responses.

The potential impact of an interaction between the GRK2 RGS domain and Gαq was recently investigated in a mouse model of pressure overload-induced hypertrophy and HF in transgenic mice with αMHC-targeted cardiac expression of this domain (residues 45–185, βARKrgs) (83). In this study, the βARKrgs mice were not only resistant to hypertrophic growth after trans-aortic constriction, providing the same anti-hypertrophic effect as inhibition of Gαq association with GPCRs, but the reduction in fibrosis and molecular remodeling prevented the transition to HF during chronic pressure overload (83). This occurred through an association of βARKrgs, but not full-length GRK2, selectively with Gαq in the heart in a manner that inhibited the activity of the Gαq effector phospholipase C beta (PLCβ) (Figure 1-5). This interaction was enhanced after pressure overload, presumably through Gαq-coupled GPCR activation driving the association of βARKrgs with dissociated Gαq (83). Importantly, unlike βARKrgs, this study revealed that cardiac restricted overexpression (TgGRK2) or peptide inhibition (TgβARKct) of GRK2 did not alter cardiac hypertrophy, demonstrating that loss or gain of function of the full-length enzyme does not alter cardiac hypertrophic responses. In contrast to previous *in vitro* studies, these data are consistent with βARKrgs inhibiting pressure-overload induced

hypertrophy via altered G α q-mediated signaling in manner independent of kinase activity and encompassing and interaction that is not observed for full-length GRK2.

In addition to mapping the distinct functional domains of GRK2 and their relevant protein interactions, the diverse cellular functions of this enzyme are also due to non-canonical targeting and localization of GRK2. In addition to the classical membrane translocation, GRK2 has been shown to localize to the mitochondrial outer membrane, where phosphorylation of non-GPCR targets causes significant alterations in mitochondrial biogenesis and cell survival (Figure 1-6) (84–86). In a mouse model of ischemia/reperfusion (I/R), mice overexpressing GRK2 exhibited increased infarct size and apoptosis post-injury due to reduced induction of vital cell survival pathways such as Akt and nitric oxide (NO) generation(87). The opposite was observed in mice expressing the β ARKct (87). In contrast, GRK2 KO resulted in cardioprotection, wherein mice exhibited reduced mitochondrial-mediated apoptosis and infarct size (88). GRK2 exerts these detrimental effects via translocation to mitochondria, an event dependent on both extracellular-regulated kinase (ERK)-mediated phosphorylation at serine 670 and heat shock protein 90 (Hsp90) chaperone function (89, 90). Elevated mitochondrial GRK2 increased Ca²⁺-induced opening of the mitochondrial transition pore and was an absolute requirement for stress-induced, mitochondrial-dependent pro-death signaling, while β ARKct led to cardioprotection (Figure 1-6) (89). In fibroblasts, GRK2 can localize to the mitochondrial outer membrane through binding sites within its RGS homology and kinase domain (85). This localization is enhanced during ischemic stress, and was found to elevate cellular ATP content by promoting mitochondrial respiration (85). In cardiomyocytes, GRK2 overexpression impaired fatty acid oxidation and increased mitochondrial-based superoxide production, while GRK2 inhibition increased oxygen consumption rates and ATP production (Figure 1-6) (91). These effects were dependent upon GRK2 kinase activity and demonstrated that independent of cardiac injury, GRK2 localization to the mitochondria altered substrate utilization and impaired mitochondrial biogenesis (91). Future studies will be needed to elucidate the protein substrates for GRK2 kinase activity, or GRK2 binding interactions that mediate the clear role of this enzyme in regulating mitochondrial function, as well as how mitochondrial GRK2 activity is regulated.

In addition to regulatory protein-protein binding interactions, GRK activity is controlled by multiple phosphorylation sites within both the N- and C-termini. PKC-mediated phosphorylation of GRK2 alleviates the inhibition induced by calmodulin binding (92). c-Src-mediated phosphorylation of GRK2 at select N-terminal Tyrosine residues (amino acids 13, 86, and 92) enhances its kinase activity (92, 93) and selectively increases binding of GRK2 to G α q as demonstrated by the use of phospho-tyrosine defective and mimic GRK2 mutants (94). Furthermore, increased tyrosine phosphorylation on GRK2 occurs in parallel with both increased co-immunoprecipitation of GRK2 and G α q post activation of the G α q-coupled M1 muscarinic receptor and inhibition of G α q-mediated activation of phospholipase C β signaling in vitro, supporting a physiological role for this GRK2 regulatory mechanism (94). GRK2 is also differentially regulated by phosphorylation at distinct serine residues. MAP kinase phosphorylation at C-terminal residue Ser670 reduces binding with G $\beta\gamma$, thereby inhibiting GRK2 activity (95), while protein kinase A (PKA)-mediated phosphorylation at Ser685 increases G $\beta\gamma$ association (55), enhancing GRK2

kinase activity at the membrane. In addition to regulatory phosphorylation of GRKs, GRK2 has also been recently shown to undergo post-translational modification in the form of S-nitrosylation at cysteine (Cys) 340 (96). The physiological consequence of this modification is that when endothelial nitric oxide synthase (eNOS)-NO bioavailability is high, S-nitrosylation of GRK Cys340 inhibits GRK2 kinase activity (96, 97). Further, in mice with heterozygous KO of GRK2, de-repression of eNOS led to a preservation of NO bioavailability, supporting resistance to vascular remodeling in response to angiotensin II-induced hypertension (98). Thus, NO can be considered an endogenous GRK2 inhibitor. Together, these data suggest that distinct GRK interactions and their effect on cellular signaling processes may be tightly controlled by post-translational modification of these kinases. This may provide an additional level of regulation beyond the capability for diverse intermolecular interactions by fine-tuning the affinity of these interactions and/or the resulting activity of GRKs at specific targets within the cell. Future studies are needed to fully elucidate in what signaling complexes GRKs participate in at any given time, their localization within the cell, and the full functional consequences of regulatory binding interactions and post-translational modifications on cardiovascular signaling and function.

Based on these canonical and non-canonical activities of GRK2 in the heart and other cells types, GRK2 has emerged as a target of interest for therapeutic intervention in numerous disorders. In fact, the role of GRK2 in diverse pathologies including vascular, immune, cancer, and neurological disorders, and methods targeting GRK2 inhibition have been reviewed in detail (99). Recently, a high-throughput screen for small molecule inhibitors of GRK2 was developed using an RNA aptamer to elucidate compounds that would selectively and potently inhibit GRK2 kinase activity (100). This screen uncovered the FDA approved selective serotonin reuptake inhibitor (SSRI) paroxetine that effectively inhibited GRK2-mediated phosphorylation of cytosolic and membrane receptor targets *in vitro*, and enhanced contractility and relaxation during *in vivo* hemodynamics, unlike the chemically unrelated SSRI fluoxetine (100). In a mouse model of myocardial infarction, initiation of paroxetine, but not fluoxetine, treatment after HF development significantly improved left ventricular (LV) structure and function, inhibiting or reversing several hallmarks of HF progression, with beneficial effects greater than β -blocker therapy alone (101). Importantly, no adverse effects on cardiovascular function or gross phenotypic effects were observed in paroxetine treated Sham mice in this study, lending support to the therapeutic potential for moderate, global GRK2 inhibition. While significant limitations exist for the use of paroxetine as such a therapy, this compound served as a starting point for the development of rationally designed analogs with increased efficacy and selectivity for GRK2 and reduced central nervous system activity (102, 103). While it remains to be seen whether these or related compounds will progress through clinical trials to provide a significant advance in the treatment of human HF, these compounds will serve as useful research tools to look at various aspects of GRK2 kinase function in cell culture and animals models of disease. Furthermore, the crystal structure of GRK2 will offer a template on which to not only investigate kinase domain inhibitors, but perhaps target and disrupt protein-protein interactions that represent key aspects of cardiovascular signaling and function or are sources of dysregulation during disease (16, 99, 103).

GRK3

GRK3 shares 85% sequence identity with GRK2, with nearly 95% identity in the catalytic domain, and has nearly the same tissue distribution although with lower expression levels (104). Unlike GRK2 or GRK5, myocardial levels of GRK3 are not regulated in HF (105), and cardiac restricted overexpression of GRK3 did not alter β AR signaling or downstream adenylyl cyclase activation (106, 107). In fact, no overt cardiac phenotype was observed in either transgenic mice with cardiac restricted overexpression of GRK3 or GRK3 KO mice (108, 109). While GRK3 overexpression had no effect on angiotensin II receptor activation and mitogen-activated protein (MAP) kinase signaling, it was found to significantly blunt responses to the thrombin receptor agonist SFLLRN (Figure 2-1) (108). This was confirmed in that both GRK3 overexpression and peptide inhibition of GRK3 through expression of the C-terminal pleckstrin homology domain of GRK3 (GRK3ct) were highly potent and efficient at reducing or enhancing endothelin receptor activity, respectively (Figure 2-1) (110). Further, GRK3 was highly potent at inhibiting α_1 -adrenergic receptor (α_1 AR) activity, whereas GRK2 was not effective at endothelin or α_1 ARs even at substantial overexpression levels (Figure 2-1) (110). This is consistent with a primary role for GRK2 in the regulation of cardiac contractility and chronotropy through β_1 ARs while GRK3 may regulate cardiac growth and hypertrophy through regulation of endothelin and α_1 ARs (110). Further, proto-oncogene tyrosine kinase Src (c-Src) phosphorylation of GRK3 has been shown to participate in the regulation of α_{1B} AR activity (111); however, the mechanism has not been uncovered. Interestingly, the highest degree of variance between these two GRKs occurs within the approximately 28 amino acid region critical for G $\beta\gamma$ binding (26, 28, 112). This may underlie differences in G $\beta\gamma$ subunit affinity and therefore the divergent receptor selectivity observed *in vivo* between the otherwise similar GRK2 and GRK3 (108, 113), particularly as G $\beta\gamma$ subunits have also show preferences for distinct GPCRs (114, 115).

Transgenic mice expressing the C-terminal pleckstrin homology domain of GRK3 (TgGRK3ct) demonstrated an increase in diastolic and systolic blood pressure compared to non-transgenic littermate controls (NLC), while heart rate (HR) and activity level were maintained (Figure 2-1) (116). *In vivo* hemodynamics demonstrated an increase in stroke work and stroke volume in the TgGRK3ct mice, supporting an increase in systolic function (116). Interestingly, this was accompanied by myocardial hyper-responsiveness to α_1 AR stimulation both *in vivo* and *in vitro*. This suggests that the loss of GRK3-mediated desensitization of the cardiac α_1 ARs in TgGRK3ct, a positive inotropic signaling pathway, may be the mechanism for increased contractility (Figure 2-1) (116). Similar to TgGRK3ct, mice with cardiac restricted overexpression of the α_{1A} AR exhibited hyper-contractile hearts without cardiac hypertrophy (117). More importantly, they demonstrated preserved cardiac function after chronic pressure overload and are protected from LV remodeling after myocardial infarction (118, 119). Consistent with these results, while cardiac hypertrophy was equivalent in TgGRK3ct and NLC hearts following aortic banding, *in vivo* hemodynamics revealed that the elevated end-diastolic pressure, reduced cardiac output, and reduced dP/dt maximum and minimum in NLC mice were all prevented in the GRK3ct mice (Figure 2-1) (120). Thus, phosphorylation of cardiac α_1 ARs by GRK3 may contribute to the detrimental molecular alterations that occur during cardiac disease, such that inhibition by

GRK3ct preserves cardiac function and prevents the transition to HF during chronic pressure overload.

In addition to an assessment of the classical activity of GRK3 in regulating GPCR signaling in the heart, a study of GRK3 KO mice observed an unexpected and potentially non-canonical effect of this GRK on the baroreceptor reflex (109). GRK2 and GRK3 have been demonstrated to phosphorylate and desensitize human M2 and M3 muscarinic acetylcholine receptors *in vitro*, and given their expression in airway smooth muscle and cardiac pacemaker cells, these GRKs may play a role in regulating airway narrowing and bradycardia (121–123). Unlike GRK2 heterozygous KO mice that displayed no alteration in the respiratory or cardiac parameters tested, GRK3 homozygous KO mice exhibited an increase in cholinergic airway responsiveness and an enhanced HR recovery from muscarinic acetylcholine-induced bradycardia (Figure 2-2 and 2-3) (109). Importantly, direct vagal nerve stimulation revealed no significant difference in the absolute decrease in HR or in the time course of HR recovery between GRK3 KO and wild-type mice, nor was any alteration observed in the dose-response to the selective M2 agonist gallamine during vagal stimulation, suggesting that GRK3 does not contribute to the regulation of cardiac M2 receptors (109). Further, treatment with the β AR antagonist propranolol had no effect on resting HR in the GRK3 KO mice, and normalized the HR recovery in these mice following vagal stimulation, suggesting that β AR regulation by GRK3 is also not the mechanism for enhanced HR recovery in the GRK3 KO mice. In combination with the lower resting HR in these mice, these data indicate that tonic sympathetic outflow may be diminished (109, 124). Data suggests that the HR recovery in GRK3 KO mice is not due to any adaptation of cardiac GPCR signaling, but rather that GRK3 may play a role in desensitization of the baroreceptor reflex response to the vasodilation induced changes in MAP kinase signaling following muscarinic acetylcholine injection (Figure 2-3) (109). Further, since the baroreceptor reflex response is mediated through multiple central nervous system structures, GRK3 may regulate the chronotropic component of the baroreceptor reflex in mice by altering activation of adrenergic neurons in this reflex pathway (Figure 2-3) (109, 125). Importantly, while the significance of alterations in GRK3 activity on human pathophysiological conditions remains to be elucidated, given these data regarding GPCR selectivity and the baroreflex, it is interesting to note that the GRK3 gene locus corresponds with a position on chromosome 22 that has been associated with hypertension (126). Ultimately, the mechanism by which GRK3 alters airway reactivity and the cardiac component of the baroreceptor reflex, and whether this occurs through regulation of GPCR signaling or alternative, non-canonical pathways, remains to be determined.

GRK5

GRK5 has been shown to be highly expressed in the heart and other muscle types, as well as the respiratory, nervous, and immune systems (12, 127, 128). While homozygous KO of GRK5 is not embryonic lethal (13), this enzyme is believed to play a role in cardiac development based upon studies in zebrafish, and it may be compensated for by GRK6 as double KO of GRK5 and GRK6 is embryonic lethal (129, 130). Similar to GRK2, GRK5 expression is elevated in patients with various cardiovascular diseases (131–134), and participates in desensitization of multiple GPCRs including β 1-adrenergic receptors (β 1AR)

(Figure 3-1) (107). PKC-mediated phosphorylation of GRK5 at Ser572 and either Ser566 or Ser568, or at the auto-regulatory sites Ser484 or Thr485, dramatically inhibits GRK5 affinity and activity at agonist-bound GPCRs (135). The role of GRK5 in the regulation cardiac signaling in the healthy and diseased myocardium and the pursuit for therapeutic inhibition of GRK5 has recently been reviewed in detail (136). Interestingly, mice with cardiac-restricted overexpression of GRK5 demonstrated increased sensitivity to pressure overload, marked by enhanced hypertrophy and a more rapid progression to HF (137). Further analysis demonstrated that this exaggerated hypertrophy was caused by a unique, non-canonical activity of GRK5 in the nucleus. This was facilitated by the presence of a nuclear localization sequence (NLS) and nuclear export sequence (NES), both within the catalytic domain, with the NLS sequence homologous to that of homeobox containing transcription factors (41, 138, 139). Following Gα_q-coupled receptor signaling, GRK5 translocated to the nucleus where it acted as a class II histone deacetylase (HDAC) kinase, phosphorylating HDAC5 and leading to de-repression of the hypertrophic gene transcription factor myocyte enhancer factor-2 (MEF2) (Figure 3-2a) (137, 140, 141). Activation of α₁-adrenergic and angiotensin II receptors, neither of which is desensitized by GRK5, induced this translocation through calmodulin binding to the N-terminus of GRK5 (140), and was dependent on the intact nuclear localization sequence (NLS) (Figure 3-2a). Calmodulin binding to GRK5 led to C-terminal auto-phosphorylation, reducing activity at GPCRs and enhancing phosphorylation of non-receptor substrates (Figure 3-2a) (142). In contrast, Gα_q-coupled endothelin receptor activation, a GPCR that is desensitized by GRK5, did not cause nuclear translocation or transcriptional regulation by GRK5 (Figure 3-3) (140). Reciprocally, cardiac KO of GRK5 protected the heart during pressure overload, reducing hypertrophy and fetal gene induction (143). Together, these data demonstrate a non-canonical role for GRK5 through GPCR-mediated targeting of this GRK to the nucleus followed by kinase-dependent phosphorylation of the non-GPCR target HDAC5 (Figure 3-2a).

In addition to this non-canonical regulation of transcriptional activity, GRK5 has also been shown to directly bind to DNA, wherein activity of the hypertrophic transcription factor NFAT directly correlated with GRK5 expression levels, and deletion of NFATc3 protected mice from the rapid progression to HF seen in GRK5 overexpressing mice after pressure overload (Figure 3-2b) (144). Further, chromatin immunoprecipitation assays demonstrated direct binding of GRK5 to the Bcl-2 promoter and transcriptional repression in the brain, suggesting that GRK5 may also be involved in transcriptional regulation in other tissues through direct DNA binding at target promoter sequences (Figure 3-2c) (145). These data demonstrate a kinase-independent nuclear role for GRK5 in facilitating maladaptive cardiac hypertrophy and HF. Beyond the demonstrated role for GRK5 in transcriptional regulation, it has also been shown to be involved in the regulation of NFκB signaling, although without a consensus on the overall effect of this regulation on cardiac hypertrophy or inflammation (Figure 3-4). Studies using RNA interference in *Drosophila* cells report GRK5-mediated phosphorylation of IκB, leading to increased inflammation, as well as an evolutionarily conserved association of GRK5 with NFκB (Figure 3-4) (146). Conflicting reports also suggest both activation of NFκB through upregulation of the p50 and p65 subunits in neonatal rat ventricular cardiomyocytes, alterations in p105 subunit control in macrophages, and inhibition of NFκB signaling in bovine aorta endothelial cells (Figure 3-4) (147–150).

These studies indicate that the overall impact of GRK5 levels and activity on NF κ B signaling may significantly depend on the particular stimuli and cell type in consideration. Thus, the overall role of GRK5 in moderating NF κ B signaling, the mechanism by which it occurs, and the physiological outcome of this regulation for cardiovascular function remains poorly understood and may encompass additional, non-canonical protein interactions for GRK5 in the heart.

A growing area of research is the study of biased agonists that can bias receptor signaling through either G protein or β -arrestin signaling pathways. GRKs have been implicated in this signaling due to their selectivity for distinct GPCR phosphorylation sites that may serve as a molecular “barcode” to regulate the activation of downstream signaling pathways (151). For example, mechanical stretch in cardiomyocytes has been shown to alter the conformation of the angiotensin receptor (AT₁R) in a manner that selectively activates β -arrestin-mediated cell survival signaling, G protein signaling, and this signaling was lost in GRK5 KO hearts (152). GRK5 also plays a role in the transactivation of β_1 ARs and EGFR in a manner that confers cardioprotection (153). Tg mice with cardiac-specific overexpression of the wild-type murine β_1 AR or β_1 ARs lacking PKA phosphorylation sites exhibited no deleterious effect after 7 days of isoproterenol, while mice overexpressing β_1 ARs lacking GRK phosphorylation sites exhibited significant cardiac dysfunction and left ventricular dilation (Figure 3-1) (153). The mechanism for transactivation required GRK5-mediated phosphorylation of the β_1 AR and β -arrestin 1 and 2 recruitment in the mouse heart *in vivo*, with downstream Src, matrix metalloproteinase (MMP) activation and heparin-binding EGF-like growth factor (HB-EGF) stimulation of EGFR demonstrated in HEK293 cells *in vitro* (Figure 3-1) (152). These data imply that in contrast to the pathological signaling triggered by nuclear translocation of GRK5, phosphorylation of GPCRs at the membrane may be protective, highlighting a potential dichotomy for the canonical and non-canonical mechanisms of GRK5 signaling in cardiomyocytes (Figure 3). These data suggest that modulating the cellular localization of GRK5, perhaps by targeting the nuclear localization sequence (139), may be a more effective strategy to reduce the deleterious effects of GRK5 while allowing its known cardioprotective effects at the membrane.

This potential dichotomy is particularly important given the ongoing development of selective GRK inhibitors. While seeking to develop more specific small molecular inhibitors of GRK2, the Tesmer lab generated the rationally designed inhibitor CCG215022, and found through *in vitro* phosphorylation and cardiomyocyte contractility assays that it exhibited nanomolar potency at both GRK2 and GRK5 (154). This compound significantly stabilized GRK5 during a heat denaturation assay; therefore, it was utilized to optimize crystallization conditions for bovine GRK5, producing a 2.4 Å structure with the inhibitor bound within the hydrophobic region of the kinase domain (154). This solved crystal structure of GRK5 will facilitate investigation not only into the design of kinase inhibitors, but also a more thorough investigation of other protein interactions and a potential means for their allosteric modulation, that may prove useful in targeting the nuclear translocation of this enzyme.

Summary

It has become clear from all of these studies that GRK2, GRK3, and GRK5 play distinct and important roles in regulating cardiovascular physiology and in the development of pathophysiology during cardiac disease. Furthermore, one can appreciate that this GRK-mediated regulation does not occur strictly through the classic activity of GPCR phosphorylation, but through phosphorylation of non-GPCR targets and kinase-independent protein-protein and protein-DNA interactions. The diverse expression patterns of these kinases, as well as their unique functions within each cell type, underlie their diverse biological functions. While some of these have been elucidated as seen above, in general little is still known regarding several key aspects of GRK function. For example, work outlined in this article hints at G β γ subunit selectivity as a mechanism for GPCR selectivity of GRK2 and GRK3; however, it is also known that GRKs contain GPCR recognition sequences within their N-termini and these may also play a role in receptor targeting. Nonetheless, these studies support the idea of a dynamic “GRK interactome” in which novel interacting partners may associate with functionally distinct domains of GRKs and thereby participate in GRK-mediated regulation of cell signaling and function (43, 59). GRKs are known to regulate diverse cellular processes including cell migration (155), metabolism (156–158), and apoptosis (89), often through translocation to distinct intracellular compartments such as the mitochondria for GRK2 and the nucleus for GRK5. Therefore, elucidating the identity and any GRK selectivity for these intermolecular interactions and how they modulate various cellular processes may provide novel insight into the canonical and non-canonical mechanisms of action of GRKs in cardiac physiology and pathophysiology. In general, much remains to be elucidated regarding the mechanisms that regulate GRK expression, intermolecular interactions, localization and activity and how these mechanisms translate to alterations in cardiovascular signaling and function.

As mentioned above, cardiac expression levels of both GRK2 and GRK5 are elevated during human HF. Thus, an important element of GRK activity that remains to be elucidated is the mechanism governing GRK transcriptome regulation. Circulating catecholamines and β AR activity correlate with increased GRK2 mRNA (159), and pharmacological stimulation of mitogenic T cells enhances GRK2 mRNA levels, while neither effects GRK5 or GRK6 mRNA expression (160). Further, analysis of the human GRK2 gene promoter in aortic smooth muscle cells uncovered increased GRK2 promoter activity in response to vasoconstriction and hypertrophy, while inflammatory cytokine exposure led to transcriptional repression (161). One potential mechanism for these alterations in GRK transcript levels may be microRNA regulation, as these approximately 22 nucleotide transcripts bind to the 3' untranslated region (3'UTR) of mRNA transcripts repress protein translation by decapping and deadenylation (162). Importantly, changes in microRNA expression are dynamic, and the expression of several microRNAs has recently been shown to be altered in both murine and human HF (162–165). Analysis of the 3' UTR of both GRKs has revealed potential microRNA binding sites that may regulate the expression of GRK2 and GRK5, and Kaposi's sarcoma-associated herpes virus microRNA has recently been shown to directly target GRK2, altering migration and infiltration of endothelial cells (166). This raises an interesting question of whether downregulation of GRK-targeting

microRNAs during HF may relieve translational regulation and allow for their increased levels during disease. This would open new avenues of therapeutic intervention wherein microRNA mimics could be delivered to restrict the elevation in GRK levels and thereby prevent the pathologic activity of these enzymes in cardiac remodeling. This would require an elucidation of the microRNA species that target GRKs and whether they demonstrate specificity in their targeting.

Over the last 20+ years GRKs have been a focus of research investigations into the mechanism by which they coordinate both the activity of diverse GPCRs in numerous cells types throughout the body, and how they regulate additional, non GPCR activities from cell motility to metabolism. This research has uncovered mechanisms for receptor selectivity, identified non-receptor targets, and uncovered regulatory post-translational modifications and trafficking that all contribute to the complex function of GRKs. Throughout these studies GRK2 and GRK5, in particular, have arisen as major contributors not only in the regulation of cardiovascular signaling and function in a normal heart, but as driving forces in the molecular alterations occurring during cardiac disease (167). The role of GRK2 in downregulating β AR density and facilitating sympathetic overdrive during systolic HF and the role of GRK5 in mediating the increase in hypertrophic gene transcription during pressure overload have now been well characterized. The role of both GRK2 and GRK5 in metabolism and cell survival signaling are not completely understood, but an appreciation that their upregulation may be detrimental has emerged. Overall, GRK2 and GRK5 have become viable targets for the development of human HF therapies, and research has begun to achieve selectivity and potency for small molecule inhibition of these enzymes. As research continues to define the regulation of GRK2 and GRK5 and their mechanism of action during canonical and non-canonical interactions, more informed decisions may be made regarding the targeting of their kinase domain or other allosteric sites for the inhibition of these kinases in the treatment of human disease.

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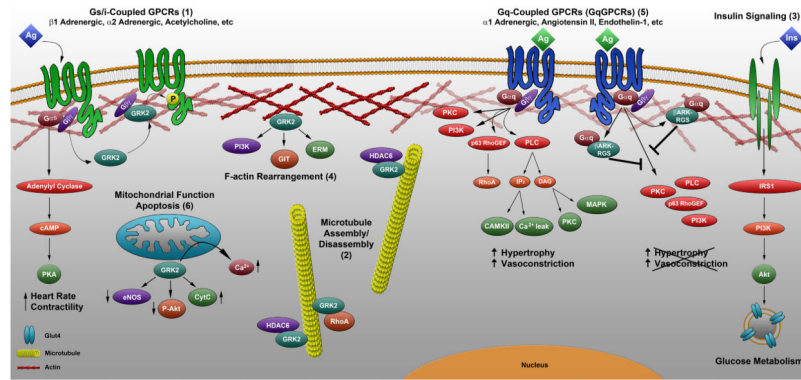


Figure 1. Summary diagram of the predominant canonical and non-canonical activities of GRK2 that alter cardiac physiology and disease progression. (1) The historically classical function of GRK2 in regulating GPCR activity wherein phosphorylation of β_1 ARs triggers desensitization to attenuate downstream effector signaling. (2) Phosphorylation of non-GPCR targets HDAC6, tubulin, synucleins, and ezrin for GRK2-mediated regulation of cytoskeletal rearrangements and cell migration. (3) GRK2 as a negative regulator of insulin-dependent glucose uptake and insulin signaling by an unknown mechanism. (4) GRK2-mediated recruitment of PI3K to the membrane for enhanced internalization of agonist bound β ARs and less well understood interactions for regulating endocytosis. (5) Selective interaction of the GRK2 N-terminal peptide β ARKrgs, but not full-length GRK2, with $G_{\alpha q}$ in the heart, thereby inhibiting activation of $G_{\alpha q}$ -coupled GPCR effectors to reduce hypertrophic signaling. (6) GRK2 localization to the mitochondrial outer membrane, where phosphorylation of non-GPCR targets reduces the induction of vital cell survival pathways such as Akt and nitric oxide, thereby altering mitochondrial biogenesis and cell survival.

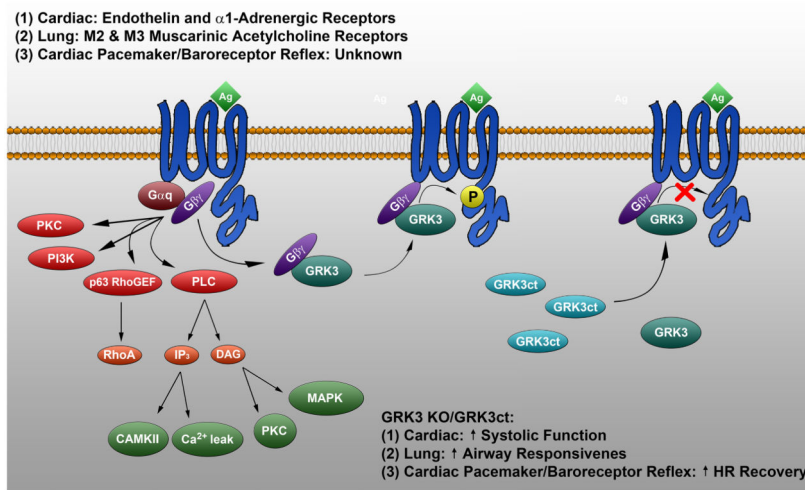


Figure 2. Summary diagram depicting the current understanding of GRK3 regulation and function in the cardiovascular and respiratory systems. 1) GRK3 may regulate cardiac growth and hypertrophy, since cardiac overexpression potently inhibits endothelin and α_1 AR signaling, whereas GRK3ct expression enhances these signaling pathways and cardiac systolic function. (2) GRK3 does not contribute to the regulation of cardiac M2 receptors; however, GRK3 homozygous KO mice exhibit an increase in cholinergic airway responsiveness by an undetermined mechanism. (3) GRK3 KO enhances HR recovery from muscarinic acetylcholine-induced bradycardia independent of GPCR signaling, thus GRK3 may play a role in desensitization of the baroreceptor reflex response downstream of MAPK signaling or regulate the chronotropic component by altering activation of adrenergic neurons in this reflex pathway.

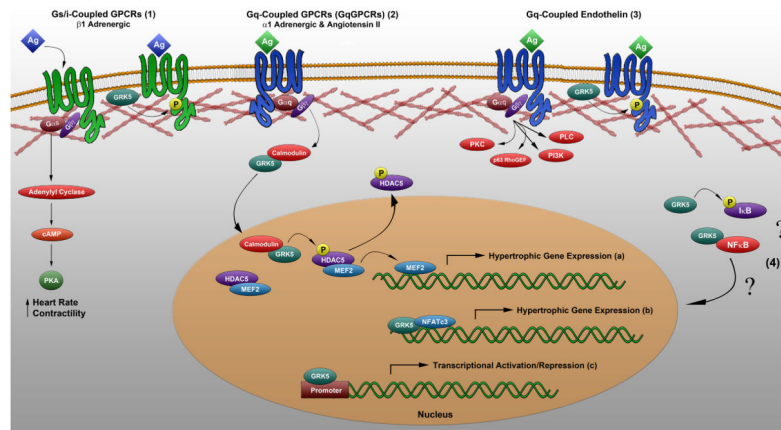


Figure 3.

Summary diagram of the predominant canonical and non-canonical activities of GRK5 in modulating GPCR signaling and gene transcription during cardiac hypertrophy and HF. (1) GRK5 expression is elevated in patients with various cardiovascular diseases and participates in desensitization of multiple GPCRs including β_1 ARs. (2a) GRK5 enhances hypertrophy through a unique, non-canonical activity in the nucleus. Following $G\alpha_q$ -coupled α_1 AR or angiotensin receptor signaling, calmodulin binds the N-terminus of GRK5 to facilitate nuclear translocation. There, GRK5 acts as an HDAC kinase, phosphorylating HDAC5 and leading to de-repression of the hypertrophic gene transcription factor MEF2. (2b) GRK5 directly binds to DNA and activates the hypertrophic transcription factor NFATc3, further exaggerating the response to pressure overload. (2c) GRK5 may also be involved in transcriptional regulation in cardiac and other tissues through direct DNA binding at target promoter sequences. (3) The $G\alpha_q$ -coupled endothelin receptor is desensitized by GRK5, and does not cause nuclear translocation or transcriptional regulation by GRK5. (4) GRK5 regulates NF κ B signaling through phosphorylation of I κ B and alterations NF κ B subunit expression in various cell models, with no overall consensus on the mechanism or impact on cardiac hypertrophy or inflammation.