

Chapter 6

Phosphoinositide 3-Kinases in Health and Disease

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Abstract In the last decade, the availability of genetically modified animals has revealed interesting roles for phosphoinositide 3-kinases (PI3Ks) as signaling platforms orchestrating multiple cellular responses, both in health and pathology. By acting downstream distinct receptor types, PI3Ks nucleate complex signaling assemblies controlling several biological process, ranging from cell proliferation and survival to immunity, cancer, metabolism and cardiovascular control. While the involvement of these kinases in modulating immune reactions and neoplastic transformation has long been accepted, recent progress from our group and others has highlighted new and unforeseen roles of PI3Ks in controlling cardiovascular function. Hence, the view is emerging that pharmacological targeting of distinct PI3K isoforms could be successful in treating disorders such as myocardial infarction and heart failure, besides inflammatory diseases and cancer. Currently, PI3Ks represent attractive drug targets for companies interested in the development of novel and safe treatments for such diseases. Numerous hit and lead compounds are now becoming available and, for some of them, clinical trials can be envisaged in the near future. In the following sections, we will outline the impact of specific PI3K isoforms in regulating different cellular contexts, including immunity, metabolism, cancer and cardiovascular system, both in physiological and disease conditions.

Keywords Cancer · Immunity · Inflammation · Glucose metabolism · Heart failure

6.1 Class I PI3Ks in Cancer

The PI3K pathway participates in several processes of cancer biology including cell transformation, proliferation, survival, motility and angiogenesis. In cancer cells, hyperactivity of PI3K signaling results from (i) gain-of-function mutations of a class

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I PI3K, and/or (ii) abnormal activation upstream (e.g. tyrosine kinase receptors) or downstream PI3Ks (e.g. AKT and PTEN). In particular, the gene encoding for p110 α (PIK3CA) is one of the most frequently mutated oncogenes in human tumors (Gymnopoulos et al. 2007), as somatic mutations of the PIK3CA gene have been reported in several cancer types including colon, ovary, breast, brain, liver, stomach, endometrial and lung cancer (Samuels et al. 2004). Three hot-spot mutations (E542K, E545K and H1047R) represent 80% of all PIK3CA mutations found in tumors and map two distinct domains of the p110 α protein (Zhao and Vogt 2008). E542K and E545K mutations are situated within the helical domain, while H1047R lies in the kinase domain. Mutations in the helical domain seem to alter the binding of p110 α to the regulatory subunit p85 and possibly interfere with the inhibitory action of p85 on p110 α , thus mimicking an activation state by tyrosine kinase receptors. The H1047 is the most frequent mutation and occurs at the end of the activation loop of p110 α , where it appears to directly influence the interaction between p110 α and PIP₂ (Chaussade et al. 2009).

PIK3CA mutations either participate in the initiation of tumorigenesis or sustain cell growth in advanced tumors. When expressed in chicken embryo fibroblasts, E542K, E545K and H1047R p110 α mutants induce oncogenic transformation with high efficiency (Bader et al. 2006). Although the expression of p110 α mutants *in vitro* results in constitutive activation of Akt even in the absence of growth factors, the impact of p110 α mutation on Akt *in vivo* is variable (Morrow et al. 2005; Vasudevan et al. 2009). Importantly, gain-of-function mutations in PIK3CA genes often coexist with additional alterations in the PI3K pathway in several types of tumors. For instance, mutated p110 α has been associated with mutations of PTEN and K-Ras (Silvestris et al. 2009; Velasco et al. 2006) or with ERBB2 over-expression (Bachman et al. 2004; Saal et al. 2005). Co-occurrence of p110 α gain-of-function with other specific oncogenic alterations in the PI3K pathway suggests that the mutational status of p110 α and p85 α may have different consequences on tumor formation and progression depending on tissue specificity and cell type.

Somatic mutations have also been reported in the regulatory subunit p85 α (PIK3R1 gene), even though they are less frequent compared to mutations of p110 α . On the contrary, mutations in the genes encoding other PI3K regulatory subunits (p85 β —PIK3R2, and p55 γ —PIK3R3), are rare events, which suggests an isoform-specific role for p85 α in cancer. Most p85 α mutations (i.e. D560Y, N564D, QYL579 deletion, DS459delN and DKRMNS560del) cluster in the two SH2 domains and in the inter-SH2 domain (Berenjeno and Vanhaesebroeck 2009; Jaiswal et al. 2009). Analysis of this region has revealed that these mutants, while retaining the ability to bind the p110 catalytic subunit, lose their inhibitory activity on p110. In addition, p85 α mutations lead to unspecific activation of all class IA p110 isoforms. As p110 β and p110 δ have been found over-expressed in certain human cancers, the co-expression of mutated p85 α in these tumors may thus further enhance the tumorigenic activity of PI3Ks.

To date, no genetic alterations have been found in the genes encoding for p110 β , γ and δ . Conversely, increased expression of p110 β and p110 δ has been identified in glioblastomas (Knobbe and Reifemberger 2003), colon and bladder tumors (Benistant

et al. 2000). Indeed, over-expression of wild-type p110 β , δ and γ is sufficient to induce an oncogenic phenotype in cultured cells (Kang et al. 2006). Moreover, expression of myristoylated p110 β induces the development of prostate intraepithelial tumors in mice (Lee et al. 2010) and expression of myristoylated p110 γ induces a constitutive activation of Akt in Rat1 fibroblasts (Link et al. 2005). In line with this finding, p110 γ has been found over-expressed in pancreatic cancer, where it is required for cell proliferation, as shown by reduced cell growth in the lack of p110 γ lipid kinase activity (Edling et al. 2010). Taken together, these findings suggest that contrary to p110 α , p110 β , p110 γ and p110 δ explicate their oncogenic potential as wild-type proteins.

p110 β has emerged as an interesting target in tumors such as breast and prostate cancers (Carvalho et al. 2010; Hill et al. 2010). In a mouse model of breast cancer driven by hyperactivation of the HER-2 signaling pathway, the absence of p110 β lipid kinase activity strongly delays the appearance of the first tumor and reduces tumor growth *in vitro* even in a context of PTEN down-regulation (Ciraolo et al. 2008). Similarly, ablation of p110 β blocks PTEN loss-driven tumorigenesis in the prostate. In this model, PTEN-mediated transformation appears to strictly depend on p110 β , since prostate-specific knockout of p110 α fails to affect tumor formation (Jia et al. 2008). These observations demonstrate the existence of a link between PTEN loss and p110 β signaling. As a matter of fact, in the absence of p110 α mutations, cancer cells harboring PTEN-null alleles depend on p110 β lipid kinase activity, as treatment with p110 β -selective inhibitors can block cell growth (Wee et al. 2008).

The role of PI3Ks in cancer has been extensively described in the last decade. Since our group has mainly focused on the area of non-oncological diseases, for broader description of PI3Ks in cancer we refer to dedicated reviews of expert authors (Engelman et al. 2006; Wong et al. 2010).

6.2 PI3Ks in Immunity and Inflammation

Protection against pathogens is achieved through concerted and synergic actions of a variety of cell types, which constitute the innate and adaptive immune responses. Innate immunity has evolved to rapidly recognize and eliminate non-self molecules through specialized phagocytic/effector cells, neutrophils and macrophages, which cooperate by providing the first line of antimicrobial defense. Neutrophils are the first to infiltrate inflamed tissues, where they carry out their defensive strategy based on bulky production of reactive oxygen species. Macrophages participate in the later phases of the inflammatory response. These cells are characterized by a high phagocytic activity and represent the principal scavengers of the immune system. Moreover, they secrete pro-inflammatory cytokines, which in turn boost the host defense. Other cell types, including mast cells and eosinophils, participate in the response to parasites, by releasing important mediators. Adaptive immunity constitutes a more sophisticated mechanism of defense, whose key feature is represented by specific antigen recognition of the invaders by T and B lymphocytes, which clonally

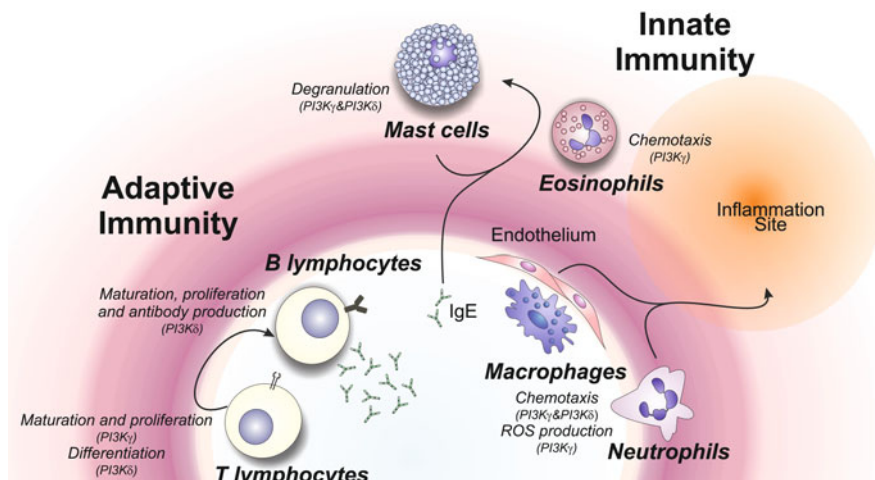


Fig. 6.1 PI3Ks control multiple aspects of innate and adaptive immunity. Class I PI3K δ and PI3K γ function as master regulators of distinct cell types, orchestrating innate and adaptive immune responses. In neutrophils and macrophages, both isoforms are required for correct directional movement, while ROS production is mainly controlled by PI3K γ . The functional interaction between PI3K δ and PI3K γ is also relevant for mast cell degranulation. On the other hand, only PI3K γ contributes to eosinophil migration. Within adaptive immunity, PI3K δ and PI3K γ cooperate in regulating distinct functions of T lymphocytes. While PI3K γ is essential for thymocyte maturation and T cell proliferation, PI3K δ mainly participates to T cell differentiation. Instead, B cell function is uniquely controlled by PI3K δ

express a large repertoire of antigen receptors. Upon antigenic recognition, lymphocytes maintain a memory of this event, thus mounting a more rapid and efficient response upon subsequent exposures to the same agent.

Several mechanisms have evolved to allow innate and adaptive immunity to recognize and eliminate foreign antigens, while maintaining tolerance to the self. Among these, the PI3K signaling pathway is a major example of a mechanism that requires fine tuning in order to ensure proper defense without developing excessive inflammation and autoimmunity. In this context, PI3Ks are activated by stimulation through a variety of receptor types, including antigen receptors, co-stimulatory receptors and certain cytokine receptors. Hence, PI3Ks profoundly impact on the pathophysiological regulation of innate and adaptive immunity. In the last decades, studies based on pharmacological and genetic inhibition of PI3Ks have highlighted the role of distinct PI3K isoforms in regulating specific aspects of immune responses (Fig. 6.1). Although immune cells express all class I PI3Ks, a prominent role is held by PI3K δ and PI3K γ . Indeed, PI3K δ and PI3K γ mutant mice show relevant phenotypes in their immune responses (Clayton et al. 2002; Hirsch et al. 2000; Jou et al. 2002; Li et al. 2000; Patrucco et al. 2004; Sasaki et al. 2000).

In the following sections, we will summarize the role of PI3Ks in innate and adaptive immunity, with a main focus on PI3K δ and PI3K γ , both in physiological and disease conditions.

6.2.1 PI3Ks in Neutrophils and Macrophages

Neutrophils and macrophages provide the first defensive barrier against the invasion by pathogens and microbial agents. Recruitment of these cells to the site of infection is initiated by sensing of specific inflammatory signals (chemokines and cytokines) released by the inflamed tissue. This directional cell migration is known as chemotaxis. The importance of PI3Ks in chemotaxis has been firstly uncovered by means of pan-PI3K inhibition with wortmannin (Okada et al. 1994). In the last 10 years, the availability of isoform-selective compounds and genetic modified animals has allowed for further dissection of the specific contribution of distinct PI3K isoforms. Amongst class I PI3Ks, PI3K δ and PI3K γ have clearly emerged as the main determinants of leukocyte migration, both *in vitro* and *in vivo*.

Neutrophils and macrophages from mice lacking PI3K γ (PI3K $\gamma^{-/-}$) show impaired *in vitro* migration in response to different G-protein coupled receptor (GPCR)-related stimuli such as fMLP, C5a, RANTES, IL-8 (Hirsch et al. 2000; Li et al. 2000; Patrucco et al. 2004; Sasaki et al. 2000). In agreement, PI3K $\gamma^{-/-}$ animals display reduced number of infiltrating cells in a peritonitis model (Hirsch et al. 2000; Li et al. 2000; Sasaki et al. 2000). This phenotype can be explained by the inability of PI3K $\gamma^{-/-}$ cells to correctly assemble and activate their molecular machinery controlling cell polarization, which represents an essential prerequisite for directional movement. Knock-in mice expressing a membrane-targeted PI3K γ enzyme (characterized by delocalized production of PIP₃) recapitulate the phenotype of PI3K $\gamma^{-/-}$ mice, demonstrating the importance of controlled spatial and temporal production of PIP₃ in leukocyte migration (Costa et al. 2007). Thus, PI3K γ catalytic function is crucial for proper PIP₃ generation, and, in turn, for the regulation of Rac activity and cytoskeleton rearrangement at the leading edge (Barberis et al. 2009; Costa et al. 2007; Ferguson et al. 2007). In addition to PI3K γ , PI3K δ contributes to the fine modulation of directional movement, as the PI3K δ -specific inhibitor IC87114 significantly dampens migration of neutrophils *in vitro* (Puri et al. 2004; Sadhu et al. 2003), as well as recruitment of inflammatory cells in a *in vivo* model of pulmonary inflammation (Puri et al. 2004).

The recruitment of inflammatory cells at the site of infection is a multistep process, including a first event of selectin-mediated “capture” of circulating leukocytes and subsequent “rolling” on the vascular endothelium, followed by integrin-mediated firm adhesion and extravasation. Both PI3K γ and PI3K δ are expressed in endothelial cells, where they regulate the complex interplay between leukocytes and the inflamed, sticky and leaky endothelium. Selective blockade of PI3K γ in endothelial cells has been shown to reduce selectin-mediated attachment of neutrophils and to increase their rolling velocity (Puri et al. 2005). Similarly, endothelial PI3K δ plays a central role in neutrophil adhesion and subsequent transendothelial migration in response to tumor necrosis factor α (TNF α) and leukotriene B4 (LTB4) (Puri et al. 2004). Consistent with an essential role for both isoforms in leukocyte migration, double knock-out PI3K $\gamma^{-/-}\delta^{-/-}$ mice display a more dramatic phenotype than single mutants (Puri et al. 2005). Nonetheless, PI3K γ and PI3K δ do not play overlapping roles,

as they regulate temporally distinct events. Neutrophil emigration toward CXCL2 or CXCL1 is severely impaired in PI3K $\gamma^{-/-}$ mice at an early time (first 90 min), but more prolonged responses are almost entirely PI3K γ -independent and largely dependent on PI3K δ (Liu et al. 2007).

After recruitment to the inflammation site, neutrophils and macrophages exert their antimicrobial function by producing and secreting reactive oxygen species (ROS), an event known as respiratory burst. In the absence of PI3K γ , ROS production evoked by cytokine-primed neutrophils in response to fMLP is significantly reduced (Hirsch et al. 2000; Li et al. 2000; Sasaki et al. 2000). Pharmacological inhibition of PI3K γ with selective inhibitors further demonstrates that in TNF α -primed human neutrophils PI3K γ is needed to initiate the first phase of a temporally biphasic pathway of ROS production induced by fMLP. Instead, PI3K δ and at least in part PI3K α and PI3K β , are necessary for the subsequent amplification phase (Puri et al. 2004; Sadhu et al. 2003). Although the second phase of ROS production is mediated by PI3K δ , both phases actually depend entirely on the first phase of ROS production, which is regulated exclusively by PI3K γ (Condliffe et al. 2005).

6.2.2 PI3Ks in Mast Cells and Eosinophils

In their action against parasites and infections, neutrophils and macrophages are assisted by mast cells. On the other hand, aberrant activation of mast cells causes different allergic diseases. Mast cells are characterized by large intracytoplasmic granules, containing histamine and heparin, which are rapidly released following cell activation, a process known as degranulation. In allergic reactions, mast cells remain inactive until an allergen binds to a special set of immunoglobulins of the IgE type, which are tightly associated to the IgE high affinity receptor (FC ϵ RI) at the plasma membrane. At molecular level, allergen stimulation, through IgE binding, triggers the activation of the protein tyrosine kinase Lyn and recruitment of Syk, resulting in the phosphorylation of immunoreceptor tyrosine-based activation motifs (ITAMs). These phosphorylated motifs provide a docking sites for the SH2 domains of class IA PI3Ks adaptor subunits. The subsequent PIP $_3$ production is then essential to activate Bruton's tyrosine kinase (Btk) and subsequently phospholipase C- γ (PLC γ). These signaling pathways cause the opening of plasma membrane calcium channels and granules release (Rommel et al. 2007).

The first indication of the involvement of PI3Ks in mast cells came from the use of non-selective PI3K inhibitors. Indeed, pan-PI3K inhibitors like LY294002 and wortmannin impair mast cell degranulation (Tkaczyk et al. 2003). Class I PI3K δ and PI3K γ appear to be the main isoforms involved in this process. Treatment with the PI3K δ -selective inhibitor IC87114 or genetic inactivation of PI3K δ activity (PI3K δ^{D910A}) dampen mast cell activity (Ali et al. 2004, 2008). Accordingly, PI3K δ^{D910A} mice are protected from passive cutaneous anaphylaxis induced by IgE- and antigen-injection (Ali et al. 2004, 2008). Similarly, blockade of the GPCR-coupled PI3K γ activity reduces mast cell degranulation and PI3K $\gamma^{-/-}$ animals are

resistant to passive systemic anaphylaxis (Laffargue et al. 2002). Recent findings suggest that only a restricted pool of PI3K γ is committed to the modulation of this process. Indeed, the mast cell phenotype of PI3K $\gamma^{-/-}$ animals is completely rescued by the co-expression of p110 γ catalytic subunit together with the regulatory subunit p84/87, but not with p101 (Bohnacker et al. 2009). The current view of the complex interplay between PI3K γ and PI3K δ in regulating mast cell function proposes a complex epistatic interaction, with PI3K δ acting earlier in response to IgE and PI3K γ functioning later to maximize degranulation (Hirsch et al. 2006).

Eosinophils are recruited and activated in response to mast cell degranulation, thus functioning as effector cells in the allergic disease. They are typical infiltrating cells at sites of allergen-IgE reactions, where they produce a wide array of mediators such as cytokines and ROS. PI3Ks have been shown to regulate eosinophil chemotaxis in response to different chemoattractants. IL-5-induced release of eosinophils from the bone marrow is severely impaired upon treatment with the pan-PI3K inhibitor wortmannin (Palframan et al. 1998). In addition, wortmannin decreases the number of eosinophils in the bronchoalveolar lavage (BAL) of ovalbumin (OVA)-challenged animals (Tigani et al. 2001). Wortmannin and LY294002 have also been found to inhibit platelet-activating factor (PAF)-induced eosinophil chemotaxis and respiratory burst, but not eotaxin-induced migration (Mishra et al. 2005). Furthermore, intra-tracheal administration of PI3K inhibitors wortmannin or LY294002 could significantly attenuate inflammation symptoms and airway hyper-responsiveness, due to sensitization with OVA inhalation in a mouse model of asthma (Duan et al. 2005; Ezeamuzie et al. 2001).

The specific PI3K isoforms involved in regulating eosinophil chemotaxis are still unclear. OVA-sensitized PI3K $\gamma^{-/-}$ mice display reduced levels of allergen-induced eosinophilic airway inflammation and airway remodeling (Lim et al. 2009; Takeda et al. 2009), thus pointing to a crucial role of this class I isoform. However, other studies suggest that PI3K γ mainly regulates the maintenance of eosinophilic inflammation *in vivo*, rather than the recruitment process, which seems to be modulated by other PI3Ks (Pinho et al. 2005). Further complexity comes from the unexpected finding that double mutant mice PI3K $\gamma^{KO}/\delta^{D910A}$ display marked eosinophilic inflammation in multiple mucosal organs, as well as increased amount of serum IgE, IL-4 and IL-5 levels (Ji et al. 2007).

6.2.3 PI3Ks in T Lymphocytes

T and B lymphocytes orchestrate a sophisticated mechanism of protection, featured by recognition of specific antigens and pathogens. T lymphocytes are involved in cell-mediated immunity and contribute to the control of humoral immunity, by exerting a strict control on the activity of B lymphocytes. The first suggestion of a key role of PI3Ks in regulating T lymphocyte function has come from studies with pan-PI3K inhibitors. Wortmannin impairs antigen (Ag)-induced IL-2 production, as well as Ag-induced CD4⁺ T cells differentiation (Shi et al. 1997). In addition, wortmannin

and LY294002 inhibit CD3-induced IL-2 synthesis and proliferation of CD8⁺ T cells (Phu et al. 2001).

More recently, the development of isoform-selective inhibitors and genetically engineered animals has allowed to show that distinct PI3K isoforms control different processes of T lymphocyte function, including development, proliferation and migration. For instance, class I PI3K γ and PI3K δ are both required for proper T cell differentiation. Indeed, PI3K $\gamma^{-/-}$ mice show a reduced number of peripheral T lymphocyte due to impaired maturation of thymocytes. In particular, ablation of PI3K γ increases the ratio of double negative (CD4⁻ CD8⁻) on double positive (CD4⁺ CD8⁺) cells in thymus, blocking thymocyte development (Sasaki et al. 2000). This phenotype is worsened by the double ablation of PI3K γ and PI3K δ , leading to a dramatic increase in the number of double negative thymocytes. On the contrary, PI3K δ inactivation (PI3K δ^{D910A}) alone does not affect thymocyte development (Ji et al. 2007; Webb et al. 2005).

Both PI3K δ and PI3K γ are essential for the subsequent phase of proliferation. In naïve T cells, PI3Ks are engaged by the cross-linking of T-cell receptor (TCR), with or without co-stimulation by CD28, or by activation of the IL-2 receptor or chemokine receptors (Alcazar et al. 2007; Fruman and Cantley 2002). T cells lacking PI3K γ show abnormal TCR-mediated signaling and reduced immunological synapse organization, as well as reduced proliferation (Sasaki et al. 2000). Similarly, knock-in mice expressing a kinase-inactive PI3K δ display impaired antigen-specific T-cell responses and a reduction in T-cell activation and proliferation upon *in vitro* stimulation (Okkenhaug et al. 2002).

On the other hand, PI3K δ is central for maturation of CD4⁺ T cell and differentiation in distinct T cell subsets (Th1, Th2, Th17, Treg). PI3K δ^{D910A} mice display reduction of both Th1 and Th2, *in vitro* and *in vivo* (Okkenhaug et al. 2006). Furthermore, PI3K δ cooperates with SHIP to maintain the correct ratio of Th17 and Treg cells. SHIP1^{-/-} mice show preferential differentiation in Treg compared to Th17 (Locke et al. 2009). On the other hand, in PI3K δ^{D910A} mice peripheral Treg maturation is impaired (Ji et al. 2007; Liu et al. 2009; Oak et al. 2006; Patton et al. 2006). Reduction of Treg function, associated with increased B cell-mediated IgE production, renders PI3K δ^{D910A} mice prone to autoimmunity (Ji et al. 2007; Oak et al. 2006). By contrast, the impaired Treg immunosuppressive function of PI3K δ^{D910A} mice appears beneficial in the case of infection by the parasite *Leishmania major*. Indeed, the reduced Treg expansion of PI3K δ^{D910A} mice seems to be responsible for a weakened Th1 response, thus preventing disease development (Liu et al. 2009).

The role of PI3Ks in the regulation of T cell migration is more controversial. In some circumstances, PI3K γ signaling appears important for T cell chemotaxis in the mouse (Camps et al. 2005; Reif et al. 2004; Sasaki et al. 2000; Webb et al. 2005). In addition, treatment with the PI3K γ specific inhibitor AS605240 has indicated that PI3K γ plays a dominant role in the migratory response to CXCL12 (Smith et al. 2007) in primary human T lymphocytes. In contrast, migratory responses to a range of chemokines, including CXCL12, of T cells derived from mice expressing a catalytically-inactive form of PI3K δ are largely unaffected (Reif et al. 2004), indicating that PI3K γ is the predominant isoform involved in T cell migra-

tion. However, recent works have suggested that T cell migration principally depends on pathways involving the Rac guanine nucleotide exchange factor (GEF) DOCK2, rather than on PI3K δ - and PI3K γ -dependent signaling (Nombela-Arrieta et al. 2004). Instead, PI3K δ is crucial for T lymphocyte trafficking, by regulating shedding and transcriptional shut off of the lymph node-homing receptor CD62L (L-selectin) (Sinclair et al. 2008).

Overall, these findings suggest that class I PI3K δ and PI3K γ cooperate in regulating T cell signaling, with PI3K δ impacting more profoundly than PI3K γ on regulation of cell-based immunity.

6.2.4 PI3Ks in B Lymphocytes

B lymphocytes represent the other major cellular component of the adaptive immune response. In contrast to what found in T cells, PI3K γ does not play a significant role in B cells. Conversely, PI3K δ has been shown to control different aspects of B lymphocyte function, including their maturation process and proliferation.

B cell development occurs through several stages. Immature B cells are produced in bone marrow, through Ig chain rearrangement of B cell progenitors (at pro-B and pre-B stages), followed by repertoire selection. These immature B cells then migrate to the spleen where, upon a further selection process, they differentiate into mature B lymphocytes by forming follicular (FO) and marginal zone (MZ) niches. Lack of PI3K δ has been shown to affect the early steps of B cell maturation, as suggested by the increased pro B/pre B ratio. In agreement, the few immature B cells of PI3K δ^{D910A} mice are unable to sustain FO and MZ pools (Clayton et al. 2002; Jou et al. 2002; Okkenhaug et al. 2002). Interestingly, B cell development is not further impaired when both PI3K δ and PI3K γ are eliminated and PI3K $\gamma^{-/-}$ mice do not show any clear defect in B cell maturation, thus demonstrating that PI3K γ does not contribute to regulation of B cell development (Webb et al. 2005).

Also B cell proliferation is strictly dependent on PI3K δ signaling. B-cell proliferation in response to IgM stimulation and BAFF is decreased in cells expressing a catalytically-inactive form of PI3K δ , whereas proliferation induced by IL-4, CD40 or LPS is only partially affected (Henley et al. 2008; Okkenhaug et al. 2002). In addition, PI3K δ activity is indispensable for B-cell-receptor-induced DNA synthesis and proliferation, as well as IL-4-induced survival (Bilancio et al. 2006; Sujobert et al. 2005). PI3K $\delta^{-/-}$ and PI3K δ^{D910A} B lymphocytes also display reduced antibody production upon T cell-dependent and independent stimulation (Clayton et al. 2002; Jou et al. 2002; Okkenhaug et al. 2002). More specifically, PI3K δ^{D910A} mice show reduced IgM and IgG antibody responses (Okkenhaug et al. 2002). By contrast, IgE production is paradoxically increased by genetic or pharmacological inactivation of PI3K δ , despite reduced Th2 responses (Zhang et al. 2008) due to the ability of PI3K δ to modulate IgE switch (Omori et al. 2006; Zhang et al. 2008).

Similar to the case of T cells, migration of B cells is not regulated by PI3Ks. Rather, this process is mediated by DOCK2 and PI3K-independent Btk signaling

(de Gorter et al. 2007; Nombela-Arrieta et al. 2004). Nonetheless, the complete response to CXCL13 is reduced in PI3K δ^{D910A} , but not in PI3K $\gamma^{-/-}$ B lymphocytes, revealing a surprising and not well clarified role of PI3K δ downstream G-protein coupled chemokine receptors (Nombela-Arrieta et al. 2004; Reif et al. 2004).

6.2.5 PI3Ks in Inflammatory and Autoimmune Diseases

Given the central role of class I PI3K δ and PI3K γ in the homeostasis of both innate and adaptive responses, these enzymes can also participate to the onset and/or progression of diseases characterized by deregulated activation of innate and/or adaptive immunity. Indeed, genetic inactivation of PI3K γ or PI3K δ modulates the susceptibility to specific diseases.

6.2.5.1 Rheumatoid Arthritis

Rheumatoid arthritis (RA) is an autoimmune disorder that affects the joints and is characterized by the progressive destruction of articular structures (Harris 1990). The pathogenesis of RA is not completely understood. Chemokines and other chemoattractants have been detected in the inflamed joints and are responsible for the local recruitment of leukocytes. Amongst these, neutrophils constitute the most abundant population and actively induce inflammatory response and tissue damage (Brennan and Feldmann 1996; Edwards and Hallett 1997; Szekanecz et al. 2003). As PI3K γ is key in neutrophil chemotaxis, PI3K γ deficiency is protective in different mouse models of RA. Camps et al. first showed that PI3K $\gamma^{-/-}$ animals are largely resistant to α CII-induced arthritis, where type II collagen-specific monoclonal antibodies are injected to initiate RA. Moreover, blockade of PI3K γ by oral delivery of the isoform-selective compound AS605240 reproduces the protective effect of PI3K $\gamma^{-/-}$ mice in a model of collagen-induced arthritis, where typical features of the disease are triggered by intra-dermally injection of collagen II (Camps et al. 2005). In both cases, the protection correlates with defective neutrophil migration and thus to reduced accumulation of neutrophils in the joints. PI3K γ inactivation is associated to a milder inflammatory arthritis also in an alternative mouse model of RA based on the transgenic overexpression of the human TNF α (Hayer et al. 2009). Interestingly, the genetic disruption of PI3K γ reduces the severity of arthritis through both reduced invasion of leukocytes and reduced proliferation of synovial mesenchymal-derived fibroblasts. These findings challenge the concept of a leukocyte-restricted role of PI3K γ in the pathogenesis of RA and suggest that the therapeutic potential of specific PI3K γ inhibitors might be expanded to a broader spectrum of cell targets, thus yielding superior results in the potential treatment of RA.

In line with a cooperative role of PI3K γ and PI3K δ in regulating neutrophil function, also PI3K $\delta^{-/-}$ mice are protected from RA. Randis et al. [2008] have shown that administration of arthritogenic serum to PI3K $\delta^{-/-}$ mice results in a significant

reduction of paw edema, similar to what observed in $PI3K\gamma^{-/-}$ animals. A more pronounced protection is also observed in double $PI3K\delta^{-/-}\gamma^{-/-}$ mice, indicating the existence of a functional interaction between $PI3K\gamma$ and $PI3K\delta$ in inflammatory arthritis. Accordingly, combined inhibition of $PI3K\delta$ and $PI3K\gamma$ might represent an intriguing innovative treatment for RA.

6.2.5.2 Systemic Lupus Erythematosus

Systemic lupus erythematosus (SLE) is a chronic autoimmune disease characterized by deregulation of T-cell mediated B-cell activation, resulting in generalized B-cell expansion and hypergammaglobulinemia (Liu and Wakeland 2001). The involvement of PI3Ks in the pathogenesis of SLE was first uncovered by two works showing that increased PI3K activity, due to either PTEN ablation ($PTEN^{+/-}$) or overexpression of an activating form of the p85 regulatory subunit ($p65^{PI3K}$) in T lymphocytes, leads to a SLE-like phenotype (Borlado et al. 2000; Di Cristofano et al. 1999). Interestingly, the severity of the disease is attenuated in $p65^{PI3K}Tg/PI3K\gamma^{-/-}$ animals, thus suggesting that $PI3K\gamma$ plays a crucial role in SLE (Barber et al. 2006). Blockade of $PI3K\gamma$ by the selective inhibitor AS605240 has also found effective in another mouse model of SLE, the MRL-lpr SLE-prone model (Barber et al. 2006). Taken together, these data encourage further study of selective PI3K inhibitors in the treatment of SLE.

6.2.5.3 Asthma

Asthma is a pulmonary disease characterized by bronchial hypersensitivity and involving a Th2 immune response mounted by $CD4^+$ T cells. Other inflammatory cells such as mast cells and eosinophils also play important roles. In particular, neutrophils contribute to the chronic evolution of the disease (Baraldo et al. 2007). The availability of pan-PI3K inhibitors first allowed to uncover the correlation between PI3K hyperactivity and the development of allergic conditions. Indeed, intratracheal administration of wortmannin or LY294002 significantly attenuates inflammation symptoms and airway hyperresponsiveness in a mouse model of asthma (Duan et al. 2005; Ezeamuzie et al. 2001).

$PI3K\delta$ and $PI3K\gamma$ act as master regulators of mast cells and eosinophils, which constitute the principal mediators of allergy. Accordingly, $PI3K\gamma^{-/-}$ animals are completely protected against systemic anaphylaxis (Laffargue et al. 2002). Similarly, $PI3K\delta$ knock-in mice are partially resistant to passive cutaneous anaphylaxis induced by IgE- and antigen-injection (Ali et al. 2004, 2008). Furthermore, intratracheal administration of the $PI3K\delta$ -selective inhibitor IC87114 significantly attenuates allergic airway inflammation and suppresses OVA-induced airway hyper-responsiveness to inhaled methacholine (Lee et al. 2006). Farghaly et al. have shown that the Th2 cytokine IL-13 fails to induce hyper-responsiveness in isolated tracheal rings from $PI3K\delta^{D910A}$ mice. In this context, the reduced hyper-responsiveness may be attributed

to a direct effect on airway structural cells rather than on infiltrating immune cells (Farghaly et al. 2008).

Overall, these studies have unveiled a key role for PI3K δ , in addition to PI3K γ , in the pathogenesis of allergic asthma. However, whether selective inhibition of PI3K δ might be protective in allergy is still controversial. In OVA-immunized mice, blockade of PI3K δ leads to a paradoxical increase of both total and OVA-specific IgE levels, despite diminished Th2 responses (Omori et al. 2006; Zhang et al. 2008). Hence, additional studies are needed to clarify the role of PI3K δ in regulating allergen-mediated IgE production, as well as the resulting clinical implications in the treatment of allergic disease. As PI3K γ and PI3K δ cooperate in the onset and progression of allergic conditions, a combined inhibition of these isoforms appears as a reasonable therapeutic strategy (Doukas et al. 2009).

6.2.5.4 Chronic Obstructive Pulmonary Disease

PI3K δ and PI3K γ cooperate in the pathogenesis of chronic obstructive pulmonary disease (COPD). COPD is a common respiratory disease which, unlike allergic asthma, involves CD8⁺ T cells releasing Th1-type cytokines, with the additional contribution of macrophages and neutrophils. In COPD, airflow limitation is progressive and may be steroid-resistant (Baraldo et al. 2007; Doherty 2004). The double selective inhibitor TG100-115, targeting both PI3K δ and PI3K γ , has been shown effective in controlling COPD in different mouse models. TG100-115 significantly reduces neutrophil accumulation as well as production of the classical Th1 cytokine TNF α in a LPS-induced model of COPD. Interestingly, TG100-115 is successful even in a steroid-resistant form of COPD induced in mice by cigarette smoke exposure (Doukas et al. 2009). Recent reports suggest that this beneficial effect is achieved through a selective involvement of PI3K δ , as genetic inactivation of this isoform, and not of PI3K γ , restores glucocorticoid responsiveness in smoke-induced airway inflammation (Marwick et al. 2009, 2010). Therefore, the complex interplay between PI3K γ and PI3K δ in the development of COPD needs further study. Currently, double selective compounds might represent the most promising response to the urgent need of new treatments for steroid-unresponsive inflammatory diseases.

6.3 PI3Ks in the Regulation of Glucose Metabolism and Insulin Sensitivity

The tight control of glucose metabolism represents a fundamental physiological mechanism regulated by a series of key metabolic hormones. The main player in this process is insulin, a peptide hormone secreted from pancreatic β -cells in response to elevated glucose concentrations. Insulin mainly acts by (i) inhibiting liver gluconeogenesis and glycogenolysis and (ii) stimulating glucose uptake in insulin-sensitive peripheral tissues, mainly skeletal muscle and adipocytes. In addition, insulin affects

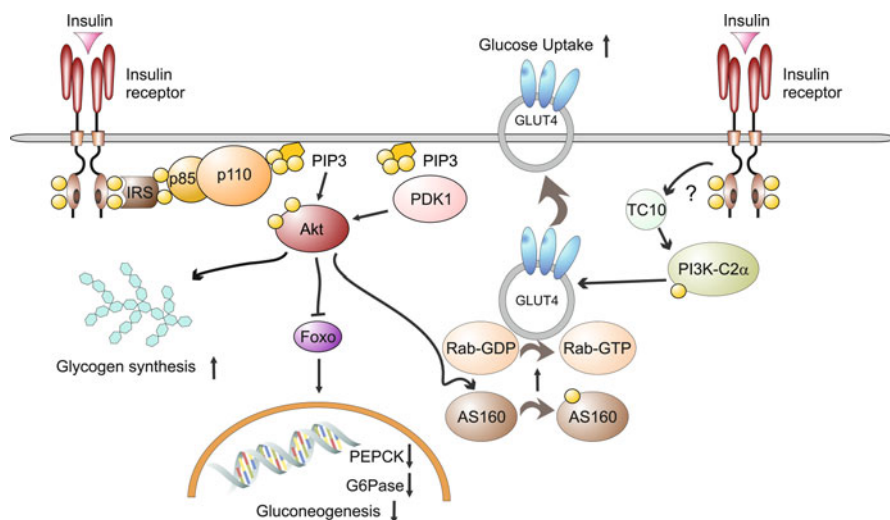


Fig. 6.2 PI3K function in glucose metabolism. Upon binding of insulin to its receptor (IR), the IRS adaptor proteins recruit class I PI3Ks, thus triggering PIP₃ production and PKB/Akt activation. PKB, in turn, mediates the translocation of the glucose transporter GLUT4 to the plasma membrane, which leads to glucose uptake from the extracellular space. Furthermore, Akt mediates the inhibition of FOXO transcription, thereby negatively regulating the expression of gluconeogenic enzymes such as PEPCK and G6Pase. Insulin also modulates glycogen synthesis through PKB-mediated inhibition of GSK3 and the consequent activation of glycogen synthase. On the other hand, class II PI3K-C2 α , following its TC10-dependent activation, contributes to GLUT4 translocation. However, the exact mechanisms linking IR activation to PI3K-C2 α are yet to be defined

lipid metabolism and stimulates the uptake of aminoacids, thus enhancing protein synthesis. Defects in insulin production and signaling underlie important pathological conditions such as diabetes mellitus and the metabolic syndrome. Type 2 diabetes represents a common disease and is characterized by impaired insulin-stimulated glucose uptake, increased hepatic glucose production and inadequate compensation by the pancreatic β -cells, ultimately leading to hyperglycemia (Kahn 1994).

The action of insulin is initiated by its binding to the insulin receptor (IR), a transmembrane glycoprotein with intrinsic protein tyrosine kinase activity. The adaptors IRS (insulin receptor substrate) are the first IR substrates that undergo tyrosine phosphorylation upon insulin stimulation (Myers and White 1993). Six IRS isoforms are expressed in mammals and play the role of linkers between the upstream tyrosine kinase and the downstream regulatory enzymes and adaptor molecules. PI3K was the first enzyme found to be associated with the IR/IRS signaling. Within this context, upon receptor activation, IRS serves as a docking site for the SH2 domains of the regulatory subunit of PI3K, which in turn recruit the p110 enzyme to the plasma membrane (Myers et al. 1992; Sun et al. 1993) (Fig. 6.2). Upon activation, the p110 catalytic subunit of PI3Ks produces the lipid second messenger PIP₃, which in turn activates downstream PH domain-containing effectors that control various metabolic

processes such as glucose uptake, lipolysis inhibition, triglyceride formation, and glycogen synthesis. Within these processes, a key molecule activated following PIP₃ generation is PKB/Akt (Taniguchi et al. 2006). However, other phosphoinositide-activated kinases, such as atypical PKC, have also been implicated in insulin action (Farese et al. 2005).

Amongst the downstream effectors of IR-PI3Ks, Akt represents the central node in the insulin signaling network, stimulating blood glucose disposal and glycogen synthesis, and inhibiting gluconeogenesis. Three different isoforms of Akt, encoded by different genes, are found in mammals. The study of knock-out mice have identified the specific functions of each Akt isoform. Of the three isoforms, Akt2 is in particular the main regulator of glucose homeostasis *in vivo* (Cho et al. 2001). Indeed, the disruption of Akt2 in mice results in impaired glucose uptake and in a complete failure of insulin to suppress hepatic glucose output (Cho et al. 2001). Akt2 plays an important role also in humans in the regulation of glucose homeostasis, since a germline mutation in Akt2 correlates with development of type 2 diabetes (George et al. 2004).

In adipocytes and muscle cells, PI3K-dependent activation of Akt2 (and to a lesser extent of Akt1) controls insulin-mediated glucose uptake by stimulating GLUT4 translocation from an intracellular compartment to the plasma membrane (Bai et al. 2007; Stenkula et al. 2010). GLUT4 exocytosis is highly regulated by PIP₃ production, although the exact mechanism is still unclear. A number of Akt substrates, including the Rab-GAP AS160 (Akt substrate of 160 kDa) (Chen et al. 2011; Sano et al. 2003) and PI5-kinase (PIKfyve) (Berwick et al. 2004), are involved in this process. Other PI3K-dependent mediators of glucose uptake are atypical PKC (aPKC) isoforms that regulate the kinesin and Rab4-dependent GLUT4 exocytosis (Imamura et al. 2003). Further support for this model is given by the muscle-specific knock-out of the aPKC PKC- λ , which results in systemic insulin resistance and glucose intolerance (Farese et al. 2007).

The class IA PI3K pathway is also involved in insulin-mediated inhibition of hepatic gluconeogenesis (Agati et al. 1998; Kotani et al. 1999), a process indispensable in a starved condition and switched-off when external resources are available. In the latter condition, insulin negatively regulates gluconeogenesis by suppressing the expression of key gluconeogenic enzymes through the Akt-mediated phosphorylation of the transcription factor FoxO1. Phosphorylated FoxO1 is excluded from the nucleus and consequently fails to activate the transcription of genes required for the gluconeogenesis, such as phosphoenolpyruvate carboxykinase and glucose-6-phosphatase (Nakae et al. 2001).

Together with class IA PI3Ks, PI3Ks of other classes might be involved in insulin-mediated glucose disposal. Indeed, insulin stimulation triggers the production of PI3P, thus possibly involving either class II or III PI3K. PI3P binds the PX and FYVE domains of proteins involved in the control of vesicular trafficking. It is thus possible that PI3K other than class IA are involved in processes needed for plasma membrane fusion of cytoplasmic vesicles containing GLUT4 (Shepherd 2005). Interestingly, insulin-mediated PI3P production appears insensitive to the action of wortmannin, thus excluding a role for class III enzymes, while suggesting a role

for the wortmannin-insensitive class II PI3K-C2 isoenzymes. In line with this view, PI3K-C2 α is activated in response to insulin-dependent activation of the small GTPase TC10, thus triggering PI3P elevation necessary for full-scale GLUT4 plasma membrane translocation (Maffucci et al. 2003).

6.3.1 Class I PI3K Regulatory Subunits in Glucose Metabolism

The crucial role of PI3Ks in insulin signaling suggests that a dysfunction of the PI3K pathway may deeply affect insulin sensitivity. Indeed, several lines of evidence have indicated that PI3K signaling is compromised in the obese diabetic ob/ob mouse model (Folli et al. 1993; Kerouz et al. 1997), as well as in diabetic patients (Bjornholm et al. 1997; Goodyear et al. 1995).

Despite the key role of PI3K in the insulin signaling, gene deletion studies of adaptors of the p85 family have reported unexpected paradoxical effects. Indeed, mice lacking p85 α develop hypoglycemia and increased insulin sensitivity (Fruman et al. 2000). This phenotype probably correlates with the up-regulation of the other *Pik3r1* splicing variants, p50 α and p55 α , in fat and muscle, leading to an elevation of PIP₃ levels and to facilitated GLUT4 translocation to the plasma membrane (Terauchi et al. 1999). A slight enhancement of insulin signaling is also present in mice lacking either p50 α /p55 α or p85 β (Chen et al. 2004; Ueki et al. 2002). On the other hand, deletion of all *Pik3r1* gene products (p85, p55, and p50), results in perinatal lethality, associated with a substantial decrease in the expression and activity of class IA PI3K catalytic subunits. Nonetheless, *Pik3r1*-deficient mice are hypoglycemic and more insulin sensitive because of a more active glucose transport in insulin-responsive tissues (Fruman et al. 2000). Similar findings have been obtained with a hepatic deletion of *Pik3r1*, which causes improved insulin sensitivity in liver, muscle, and fat, but leads to a 60% decrease in total hepatic PI3K activity (Taniguchi et al. 2006). The phosphorylation of Akt downstream PI3K is enhanced as a consequence of reduced activity of the phosphatase PTEN, suggesting a role of p85 in PTEN regulation (Taniguchi et al. 2006). Indeed, PTEN is a potent negative regulator of the insulin signaling and loss of PTEN in adipose tissue results in increased insulin sensitivity and GLUT4 recruitment (Kurlawalla-Martinez et al. 2005). A recent study has shown that p85 directly binds and activates PTEN, which explains the paradox of increased insulin sensitivity in p85-deficient animals (Chagpar et al. 2010).

These studies indicate that a critical molecular balance between regulatory and catalytic subunits determines the optimal response of the PI3K pathway to insulin signaling (Ueki et al. 2002). In physiological conditions, the p85 regulatory subunit is more abundant than the catalytic p110 subunit. p85 monomers can thus inhibit PIP₃ production either by binding to phosphorylated IRS proteins (Ueki et al. 2002) or by altering subcellular localization of p110/p85 dimers (Inoue et al. 1998). Unbalanced p85 levels can compromise this regulatory mechanisms and lead to a paradoxical increase in PI3K activity. Finding of increased p85/55/50 protein expression, in mouse models of obesity as well as in type 2 diabetic patients further confirms this

view (Bandyopadhyay et al. 2005) and suggests that p85 family members play a complex role in the regulation of PI3K-mediated insulin signaling.

6.3.2 Class I PI3K Catalytic Subunits in Glucose Metabolism

The specific role of single p110 isoforms in insulin signaling has recently begun to emerge, thanks to the development of selective pharmacological inhibitors and of mouse genetic models. Although the lethal phenotype of mice lacking either p110 α or p110 β hampers the study of their specific roles in insulin signaling, analysis of insulin-mediated responses in heterozygous animals suggests that both proteins might be involved. Heterozygous mice lacking either p110 α or p110 β show normal responses to insulin. However, mice heterozygous for both isoforms have decreased insulin sensitivity (Brachmann et al. 2005), suggesting that p110 α and p110 β play complementary roles in insulin signaling. Nonetheless, heterozygous mice expressing a catalytically inactive p110 α become insulin resistant with aging, and develop glucose intolerance, hyperlipidemia, adiposity, as well as hyperglycemia and deregulate hepatic gluconeogenesis (Foukas et al. 2006). The use of isoform-selective p110 inhibitors has shown that p110 α constitutes the major effector downstream of the IR, while p110 β plays only a marginal role, by in providing a basal threshold of PIP₃ production that potentiates p110 α activity (Knight et al. 2006). Indeed, mice expressing a kinase-dead p110 β or carrying a liver-specific ablation of this enzyme develop only mild impaired insulin sensitivity and glucose homeostasis (Ciraolo et al. 2008; Jia et al. 2008). On the contrary, the disruption of p110 α in liver results in impaired insulin action and glucose homeostasis which cannot be rescued by p110 β (Sopasakis et al. 2010). These findings demonstrate that p110 α is the primary PI3K isoform required for the metabolic actions of insulin in the liver. Instead, p110 β plays a minor but not negligible role.

6.4 Class I PI3Ks in Cardiac Physiology and Disease

Three different class I PI3Ks are expressed in the myocardial tissue (p110 α , p110 β and p110 γ). However, a growing amount of evidence indicates that different PI3K isoforms participate in distinct physiological and pathological processes within cardiomyocytes. In particular, class IA p110 α mostly functions as a critical regulator of cardiomyocyte viability and growth downstream tyrosine kinase receptors such as IGF-I and insulin. Based on available studies, p110 α activity can be generally considered as beneficial and protective for heart function. In contrast, class IB p110 β is uniquely controlled by GPCRs such as β -adrenergic receptors. Of note, robust activation of p110 γ is essentially detected in the context of maladaptive remodeling and during the natural history of heart failure, where p110 γ contributes to myocardial dysfunction and impaired contractility. Hence, pharmacological inhibition of p110 γ

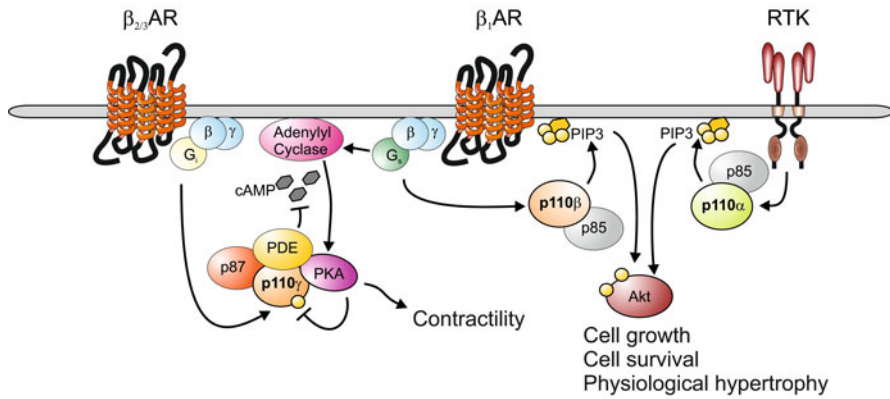
has emerged as a novel potential therapeutic strategy in cardiac disease. Finally, our understanding of p110 β function in the myocardium is still very initial and is awaiting for further and detailed study.

6.4.1 *PI3K α Regulates Cardiomyocyte Growth*

Studies performed on gain and loss-of function models have consistently shown that PI3K α activity represents a master switch leading to cardiomyocyte growth and survival (Fig. 6.3, upper panel). Systemic knockout of p110 α is embryonic lethal without obvious cardiac abnormalities, but a general impairment in cell growth is observed (Bi et al. 1999). In line with this finding, over-expression of a myocardial-selective dominant-negative p110 α results in smaller cardiomyocytes and reduced heart mass, without affecting tissue architecture and contractility (Crackower et al. 2002; McMullen et al. 2003; Shioi et al. 2000). On the other hand, over-expression of a cardiac-specific and constitutively active p110 α leads to myocardial hypertrophy and increased heart/body weight, but without progression to hypertrophic cardiomyopathy or cardiac dysfunction (Shioi et al. 2000). These findings phenocopy the genetic loss of myocardial PTEN, which leads to PIP₃ accumulation (Crackower et al. 2002). In both over-expression and dominant negative models, the changes in p110 α activity are paralleled by corresponding changes in Akt, Gsk3 β and p70S6K activity, indicating that p110 α boosts myocardial growth through the activation of canonical PIP₃-dependent anabolic pathways. Indeed, genetic manipulations of Akt lead to similar cardiac phenotypes: Akt1 knockout mice show reduced heart size, while different models of constitutively active Akt1 result in different degrees of cardiac hypertrophy (Condorelli et al. 2002; DeBosch et al. 2006; Matsui et al. 2002; McMullen et al. 2003).

Beyond cardiac development, the activity of p110 α appears to control essentially physiological hypertrophy, as mice expressing a dominant-negative p110 α are resistant to left ventricular hypertrophy induced by exercise training. Nonetheless, loss of p110 α leaves the animals prone to compensatory hypertrophy following pressure overload by aortic constriction, indicating that p110 α represents a master switch of physiological but not of pathological hypertrophy (McMullen et al. 2003). Importantly, cardiac p110 α is functionally relevant in conditions of myocardial damage, where p110 α protects cardiomyocytes from cell death and dysfunction caused by various pathological noxae (Fig. 6.3, lower panel). Indeed, it has been shown that in several heart disease models such as dilative cardiomyopathy, myocardial infarction, chronic adrenergic stimulation and pressure overload, the loss of p110 α is highly detrimental and accelerates adverse ventricular remodeling, while on the other hand constitutive p110 α activity exerts cardioprotective effects (Lin et al. 2010; McMullen et al. 2007). Taken together, our understanding of myocardial PI3K α suggests that any treatment targeting myocardial PI3Ks should leave p110 α activity unchanged to circumvent a negative impact on cardiac function, especially in the context of cardiotoxicity (e.g. tumor chemotherapy) and heart failure.

Normal myocardium



Failing myocardium



Fig. 6.3 PI3K signaling in normal and failing myocardium. *Upper panel.* In the myocardium, PI3K α is activated by tyrosine kinase receptors (RTKs) such as IGF-I, EGF and insulin receptor. Downstream p110 α , Akt and other classical PIP₃-dependent anabolic pathways promote normal myocardial development and growth. Moreover, PI3K α is required for physiological hypertrophy. On the other hand, p110 β represents the master PI3K isoform producing PIP₃ and activating Akt upon β -adrenergic stimulation. In physiological conditions, p110 γ is expressed at low levels and contributes residually to PIP₃ production upon β -adrenergic stimulation. p110 γ , along with the p87 regulatory subunit, is part of a macromolecular complex mediating the cAMP-dependent activation of PDEs, while the lipid kinase activity of p110 γ is blunted by PKA phosphorylation. *Lower panel.* The natural history of heart failure is characterized by the progressive increase in p110 γ lipid kinase activity, due to p110 γ upregulation, regulatory isoform switch (from p87 to p101) and loss of inhibition by PKA. By interacting with GRK2, in this context p110 γ leads to AP2 and β -arrestin mediated downregulation and desensitization of β -adrenergic receptors. In the presence of active myocardial damage, p110 α contributes to cardiomyocyte survival and provides protection for adverse remodeling and failure

6.4.2 *PI3K γ Regulates Cardiac Contractility and Remodeling*

PI3K γ is expressed at high levels in hematopoietic cells, especially in leukocytes. However, p110 γ is also present in the myocardium, including cardiomyocytes, endothelial cells and possibly myofibroblasts. Although p110 γ levels are relatively low in cardiomyocytes, this class IB PI3K isoform has important functions both in heart physiology and disease. In particular, p110 γ is a key player in the regulation of cardiac contractility, through combined kinase-dependent and kinase-independent molecular mechanisms interlacing cyclic AMP (cAMP) and PIP₃ signaling.

Hearts derived from p110 γ knock-out mice are hyper-contractile compared to wild-type controls both in basal and stimulated conditions, due to functional activation of their contractile machinery (Crackower et al. 2002; Patrucco et al. 2004). This phenotype is caused by increased cellular levels of cAMP, a key second messenger controlling myocardial contractility in response to β -adrenergic stimulation. β -adrenergic receptors (β -ARs, which include β_1 , β_2 and β_3 subtypes) are GPCRs physiologically activated by circulating or sympathetic nerve catecholamines (mostly epinephrine). All β -AR isoforms are coupled to G_s subunits, while β_2 and β_3 receptors also associate to G_i subunits (Brodde et al. 2006; Skeberdis et al. 2008). Catecholamine engagement of β -ARs leads to G_s-triggered stimulation of adenylyl cyclase, which in turn generates the second messenger cAMP. The main signaling effector of cAMP is protein kinase A (PKA), which is constituted by regulatory and catalytic subunits and whose function is compartmentalized and controlled by different proteins known as A-kinase anchor proteins (AKAPs) (Scott and Pawson 2009). In cardiomyocytes, PKA phosphorylates key players orchestrating myocardial contractility, such as phospholamban, the ryanodine receptor and troponin I (Chu et al. 2000; Marx et al. 2000; Stelzer et al. 2007).

Our group and others have shown that p110 γ plays a key role in the regulation of cAMP signaling, as p110 γ is required for the activation of cellular phosphodiesterases (PDEs) which hydrolyse cAMP to 5'-AMP and terminate signaling, such as PDE3s and PDE4s (Conti and Beavo 2007; Ghigo and Hirsch 2011; Kerfant et al. 2007; Patrucco et al. 2004; Perino et al. 2011). The regulation of PDE3B by p110 γ is operated within a macromolecular complex which includes p110 γ , the PI3K adaptor subunit p84/87 and PKA (Patrucco et al. 2004; Perino et al. 2011; Voigt et al. 2006). In this complex, p110 γ functions as an AKAP, as it directly binds the RII α subunit of PKA and thus allows the activation of PDE3B by PKA (Fig. 6.3, upper panel). Of note, this functional interaction does not require the kinase activity of p110 γ , which instead operates as a scaffold (Hirsch et al. 2009; Perino et al. 2011). In mice lacking p110 γ (and not in mice expressing a kinase-inactive p110 γ), disassembly of this critical signaling complex leads to a major reduction in the phosphodiesterase activity, thus resulting in abnormal levels of myocardial cAMP. When p110 γ -null mice are subjected to cardiac pressure overload, cAMP further raises uncontrolled and causes myocardial damage rapidly progressing towards overt cardiomyopathy and heart failure (Crackower et al. 2002; Patrucco et al. 2004). Similar to PDE3B, also PDE4 activity is controlled by p110 γ , thus modulating cAMP signaling within cardiomyocyte sub-cellular compartments containing SR Ca²⁺ ATPase

(Kerfant et al. 2007). Taken together, these findings picture a scenario where PI3K γ orchestrates a complex modulation of multiple phosphodiesterases, deeply affecting the intracellular compartmentalization of cAMP signaling in cardiomyocytes. Furthermore, we have recently shown that p110 γ -associated PKA not only influences phosphodiesterase activity, but also modulates the lipid kinase activity of p110 γ itself, as the proximity of PKA and p110 γ within the same macromolecular complex allows active PKA to phosphorylate also p110 γ on T1024. As a result of PKA phosphorylation, p110 γ lipid kinase activity is reduced (Perino et al. 2011) (Fig. 6.3, upper panel).

A strict interplay exists between β -ARs and PI3Ks, as the stimulation of myocardial β -ARs not only mobilizes adenylyl cyclase and cAMP, but also PI3K β , PI3K γ and thus PIP₃ (Rockman et al. 2002). By using mice expressing a kinase inactive p110 γ or p110 β , our group has recently shown *in vivo* that in physiological conditions, β -adrenergic stimulation of the myocardium essentially activates p110 β , which is required to activate Akt. Instead, p110 γ activation only produces a minor fraction of β -adrenergic engaged PIP₃, as in the normal myocardium p110 γ is expressed at low levels and is strictly controlled by PKA-mediated inhibition (Perino et al. 2011). During the natural history of heart failure, the signaling scenario changes deeply, as p110 γ levels and activity increase due to (i) up-regulation of p110 γ , (ii) regulatory subunit switch (from p84/87 to p101) of p110 γ and (iii) reduction of PKA-dependent inhibition of p110 γ . As a result, β -adrenergic stimulation of the failing myocardium engages unbalanced p110 γ activity, which contributes to adverse remodeling and left ventricular failure (Patrucco et al. 2004; Perino et al. 2011).

A key pathophysiological feature of heart failure is represented by uncontrolled catecholamine release, which produces a situation of chronic and abnormal stimulation of β -adrenergic receptors. Amongst the maladaptive effects of chronic β -adrenergic engagement is the progressive loss of the ability of β -ARs to transduce signals, a process called desensitization. Furthermore, continuous adrenergic stimulation culminates in β -AR endocytosis and cell surface downregulation. Due to desensitization and downregulation, adrenergic signaling is therefore progressively impaired in the failing myocardium, which loses tonic and phasic contractile responses to catecholamine stimulation (Bristow et al. 1982; Rockman et al. 2002). Both β -adrenergic desensitization and internalization processes depend on the phosphorylation of β -ARs, which permits the interaction between β -ARs and β -arrestins, cytoplasmic proteins that block coupling to G-proteins and start the internalization process. Once in early endosomes, phosphorylated β -ARs can be either dephosphorylated and recycled to the cell surface or subjected to degradation in late endosomes (Rockman et al. 2002). Nonetheless, β -ARs can induce maladaptive signaling pathways at the level of the early endosomes, before being degraded (Lefkowitz and Whalen 2004). Several studies have shown that p110 γ and PIP₃ are key players in these detrimental processes. In particular, p110 γ preferentially cooperates with G protein-coupled receptor kinase-2 (GRK-2, also known as β -adrenergic receptor kinase-1, β -ARK-1) via its PIK domain (Naga Prasad et al. 2001; Nienaber et al. 2003). GRK-2 constitutes a cytoplasmic complex with p110 γ and, upon β -AR stimulation, translocates to the activated receptor, where p110 γ is activated by G-proteins (Naga Prasad et al. 2000). Herein, PIP₃ produced by p110 γ is then

required for AP-2 adaptor recruitment at the plasma membrane, which leads to the consequent organization of clathrin-coated pits orchestrating the internalization of the activated receptor (Naga Prasad et al. 2002). *In vivo* studies have confirmed these mechanistic insights. In mice, over-expression of the PIK domain of PI3K reduces GRK-2-associated PI3K activity and consequently β -AR internalization, without affecting Akt or MAPK pathways (Naga Prasad et al. 2002; Nienaber et al. 2003). In pigs subjected to ventricular pacing-induced heart failure, overexpression of the PIK domain derived from failing hearts rapidly reverts contractility to normal levels (Perrino et al. 2005b). Furthermore, in a model of murine cardiomyopathy (calsequestrin over-expression), over-expression of a catalytically inactive p110 γ is protective from β -adrenergic perturbation in heart failure, leading to reduced mortality (Perrino et al. 2005a). Our group has further shown that β -AR density remains unchanged after pressure overload in mice expressing a kinase-inactive p110 γ and that in wild type mice suffering from pressure overload-induced heart failure, administration of a p110 γ -specific pharmacological inhibitor can significantly improve both β -AR density and left ventricular contractility (Perino et al. 2011). Taken together, these findings picture a scenario where p110 γ deregulation leads to maladaptive β -adrenergic perturbation during heart failure, by coupling to GRK-2 and AP-2 (Fig. 6.3, lower panel).

Our group has further shown that mice expressing a kinase-inactive p110 γ are protected from adverse remodeling following pressure overload by transverse aortic constriction. By using bone marrow chimeras, Damilano et al. have provided evidence that interestingly, the detrimental effects of p110 γ on the myocardium are multifactorial. In particular, cardiomyocyte p110 γ plays a role in the long term deterioration of left ventricular contractility and diameter, as mice expressing a kinase-inactive p110 γ in cardiomyocytes are protected from left ventricular dilation and failure at later time points (Damilano et al. 2011). Nonetheless, leukocyte p110 γ is also key to myocardial infiltration by inflammatory cells, orchestrating local cytokine release and ultimately leading to cardiac fibrosis and diastolic dysfunction (Damilano et al. 2011). Indeed, the loss or inhibition of p110 γ activity strongly reduces tissue inflammation in the context of cardiovascular diseases such as myocardial infarction and aortic atherosclerosis (Fougerat et al. 2008; Siragusa et al. 2010). These findings are in line with our broader understanding of PI3K γ as a cornerstone signaling enzyme in the context of inflammatory and immune diseases.

In conclusion, these data indicate that p110 γ signaling occupies a central spot in the molecular pathophysiology of heart failure, which is dominated by abnormal β -adrenergic stimulation and p110 γ deregulation. In this context, p110 γ escapes physiological feedback control mechanisms and orchestrates key aspects of myocardial damage and remodeling, such as β -adrenergic desensitization and downregulation, myocardial inflammation and fibrosis. As several proof-of-concept studies have suggested, p110 γ inhibition by pharmacological inhibitors appears therefore as a promising strategy for the treatment of heart disease and calls for further translational and pharmacological studies.

6.5 Concluding Remarks

In the last decade, efforts from basic science have uncovered PI3K signaling as a fundamental biological process of eukaryotes. The high number of different isoforms grouped in the PI3K family might envisage a complex regulation of this signal transduction pathway, based on intricate interplays between distinct isoenzymes. Instead, there is growing evidence that specific cellular functions are peculiar to distinct PI3K isoforms. While the ubiquitous PI3K α and PI3K β are mainly involved in glucose metabolism and cancer, the hematopoietic-restricted PI3K δ and PI3K γ play a major role in immunity, with specific functions of the two isoforms in selected subpopulations of immune cells. Furthermore, PI3K α and PI3K γ have emerged as master regulators of cardiac function, although further efforts are needed to clarify the role of other isoforms in this context. Overall, selective targeting of specific PI3K isoforms can be predicted to guarantee maximum of efficacy in the treatment of specific diseases, with minimal side effects. In some circumstances, however, different PI3K isoforms function in a synergistic manner in regulating specific biological process. Thus, some pathologic conditions might be more effectively treated with combined therapies targeting more than one selected PI3K. New isoforms-selective compounds are becoming now available, although their potency and isoform selectivity need further improvement before entering clinical trials. Only joint efforts of basic research on genetically engineered animals, pharmaceutical investigation and clinical trial will finally pave our way towards the clinical use of a PI3K inhibitor.

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