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IRBIT: It Is Everywhere

Dongki Yang, Nikolay Shcheynikov, and Shmuel Muallem

Epithelial Signaling and Transport Section, Molecular Physiology and Therapeutics Branch, NIDCR, Building 10, Room 1N-113, NIH, Bethesda, MD 20892, USA

Abstract

IRBIT (IP₃Rs binding protein released with IP₃) is a protein originally identified by the Mikoshiba group as an inhibitor of IP₃ receptors function. Subsequently it was found to have multiple functions and regulate the activity of diverse proteins, including regulation of HCO₂⁻ transporters to coordinate epithelial HCO₃⁻ secretion and to determine localization of the Fip1 subunit of the CPSF complex to regulate mRNA processing. This review highlights the remarkably diverse functions of IRBIT that are likely only a fraction of all the potential functions of this protein.

Keywords

IRBIT; IP₃ receptors; NBCe1-B; CFTR; NHE3; Fip1

Introduction

IRBIT was discovered multiple times in different contexts but it was not until its re-discovery by the Mikoshiba group [4] that we began to understand its function and appreciate its potential in regulating a remarkably diverse physiological systems that do not have any component in common besides their regulation by IRBIT.

IRBIT was identified as a protein induced during antigen-presenting Dendritic cells (DCs) differentiation [16] and as a gene that is down-regulated in response to treatment with DNA damaging agents [54]. The first function of IRBIT found is interaction with the IP₃ receptors (IP₃Rs) that is regulated by IP₃ and was thus renamed IRBIT (for IP₃Rs binding protein released with IP₃) [4]. Interaction of IRBIT with IP₃Rs turned to play important role in Ca²⁺ signaling and through this interaction IRBIT regulates the function of the IP₃Rs [3,18]. The Mikoshiba group then discovered that IRBIT regulates the activity of the ubiquitous Na⁺-HCO₃⁻ co-transporter NBCe1-B [52], that has important roles in epithelial HCO₃⁻ secretion [9,41,53,59]. More recently, the Mikoshiba group reported an important role for IRBIT in mRNA polyadenylation to regulate gene expression [28]. These findings probably describe only a fraction of the functions regulated by IRBIT that are suggested by its known domains. Discovering these functions and the relationship between them will be a challenge for the future.

The IRBIT Domains

Two IRBIT isoforms have been identified; a short IRBIT and a long IRBIT with high homology to short IRBIT but with an N terminal extension [5]. In this review we refer to short IRBIT as IRBIT and specify when referring to long IRBIT. Fig. 1 depicts the IRBIT

and long IRBIT domains identified so far. The IRBITs form the AHCYL subfamily of the adenosyl homocysteinase (AHCY) superfamily by virtue of their C terminus AHCY domain. The AHCY members have S-adenosyl-L-homocystein hydrolase activity that catalyzes the reversible hydrolysis of S-adenosyl-L-homocystein to adenosine and L-homocysteine to maintain low cellular activity of S-adenosyl-L-homocystein [55]. Accumulation of S-adenosyl-L-homocystein is cytotoxic due to inhibition of DNA and RNA methylation [50]. However, the IRBITs AHCY domain does not have s-adenosyl-L-homocystein hydrolase activity, and thus its role in IRBIT function is not known at present.

The two important domains within the AHCY domain are a coiled-coil domain and a PDZ ligand [19]. At the N terminus the IRBITs have a PP1 anchoring site that is followed by a PEST domain [17,19]. The PEST domain has multiple phosphorylation sites [3] that have a permissive role in all known functions of IRBIT, regulation of IP₃ receptors function [3,18], activation of NBCe1-B [52,59] and of the Cystic Fibrosis Transmembrane conductance Regulator (CFTR) [59], and mRNA polyadenylation [28]. Long IRBIT has an N terminal extension rich in proline and alanine and was termed LISN, for Long IRBIT Specific N terminal domain [5], which plays a critical role in its function (see below).

IRBITs Expression Pattern

IRBIT is ubiquitous with high levels in the cerebrum and the cerebellum [4], site of high expression levels of IP₃ receptors [42,44]. Relatively high IRBIT expression levels are also found in epithelial tissues such as testis, ovaries, lung, kidney, and spleen [4]. However, IRBIT expression levels appear dynamic and vary with the cellular physiological state. For example, freshly isolated Dendritic and Langerhans cells express low, while activated cells express high IRBIT mRNA levels. Furthermore, the high IRBIT mRNA level is mainly in dermal Dendritic cells [16]. IRBIT levels also change during development. IRBIT mRNA level increases during zebrafish embryogenesis and interference with IRBIT expression level changes the zebrafish morphogenesis [7].

Long IRBIT is expressed in most tissues and, as with IRBIT, the highest levels are found in the cerebrum and cerebellum with high levels in epithelia like the kidney, testis and ovary, and lower levels in the lung and liver [5]. However, long IRBIT is expressed at a much lower levels than IRBIT in all tissues in which they are co-expressed [5], suggesting that their roles are not complementary but rather unique. This is further emphasized in their cell-specific expression in the brain. Long IRBIT is expressed at high levels mainly in cerebellar molecular layer interneurons, while IRBIT is mainly expressed in glial cells [5].

Another level of differential expression is by localization of the IRBITs in cellular domains. When expressed in HeLa cells IRBIT is found in the cytosol and in the ER, most likely associated with IP₃ receptors [4,18]. IRBIT can undergo cleavage within the PEST domain at residue 72 [18]. N terminally cleaved IRBIT translocates to the nucleus [4], where it may regulate gene expression [19]. In addition, IRBIT phosphorylation appears to determine its cellular localization. IRBIT and long IRBIT have multiple phosphorylation sites located in the PEST domain [3,5]. Phosphorylation of long IRBIT increases during neuronal differentiation and, notably, IRBIT phosphorylation enhances its interaction with the plasma membrane [5]. This may account in part for the accumulation of IRBIT at the apical pole of the polarized pancreatic duct [59]. Like most epithelia [29], the ducts express high level of IP₃Rs at the apical pole [34]. The combination of high level of IP₃Rs at the apical pole, together with IRBIT phosphorylation may lead to the constitutive high level of IRBIT at the apical pole of the duct. The physiological significance of such localization is discussed below.

The IRBITs and the Function of the IP₃ Receptors

IRBIT importance was highlighted by the seminal discovery by the Mikoshiba group that IRBIT interacts with the IP₃ receptors and can thus regulate Ca²⁺ signaling [4]. The receptor-evoked Ca²⁺ signal is initiated by receptor-mediated activation of PLC, hydrolysis of PIP₂ and release of IP₃. IP₃ activates the ER-resident Ca²⁺ channels, IP₃Rs to rapidly release Ca²⁺ stored in the ER. This event initiates all forms of Ca²⁺ signaling, including Ca²⁺ oscillations and Ca²⁺ waves [29,44]. ER Ca²⁺ release by the IP₃Rs is followed by activation of Ca²⁺ influx channels at the plasma membrane that are mediated by the STIM1-regulated Orai and TRPC channels [32,56]. Ca²⁺ is then cleared from the cytosol partially by its extrusion through the PMCA type plasma membrane Ca²⁺ pumps and partially by its reuptake into the ER by the SERCA type ER Ca²⁺ pumps [29]. The Ca²⁺ signal is usually initiated at a defined microdomain and spreads to other parts of the cell in the form of propagated Ca²⁺ waves. Periodical repeat of the Ca²⁺ release and Ca²⁺ uptake cycle results in Ca²⁺ oscillations [10,29].

Since the discovery of the neuronal IP₃R by Mikoshiba et al. [23], this group has been exploring the regulation and physiological roles of the channels [43,45]. There are three IP₃ receptors that are expressed in a tissue specific manner, with IP₃R1 expressed at high levels in neuronal tissues and IP₃R2 and IP₃R3 expressed at high levels in epithelial tissues [44,61]. The IP₃Rs have several well defined domains, including the C terminus channel pore domain and the N terminus IP₃ binding domain (residues 224–604 in IP₃R1) [42,44,61], which consists of a β domain (residues 224–436) and an α domain (residues 437–604) [43]. Mutation analysis and resolving the structure of the IP₃ binding domain [12,60] identified 12 amino acids in the IP₃ binding domain of IP₃R1 that coordinate IP₃ binding.

In a proteomic approach the Mikoshiba group isolated IRBIT as a protein that directly interacts with the N terminus of the IP₃R1. The key finding of the initial study was that IP₃ dissociated IRBIT from the IP₃ binding domain of the IP₃Rs with an apparent affinity of about 0.5 μ M, thus the name IRBIT: IP₃R Binding protein released with inositol 1,4,5 Trisphosphate [4]. IRBIT binds to the full-length IP₃Rs and to the IP₃ binding domain of the receptor and the binding requires phosphorylation of IRBIT [4,18]. Further analysis revealed that expressed IRBIT is found in the cytosol and the ER in HeLa cells. Deletion of the first 104 residues resulted in the complete translocation of IRBIT to the nucleus [4]. This may have physiological significance since it was reported that native IRBIT can be cleaved in vivo at residue 72 located within the PEST domain to translocate the truncated IRBIT to the nucleus [18]. However, the functional significance of nuclear IRBIT has not been directly examined, a topic worth careful and extensive examination.

In a careful follow-up study the Mikoshiba group showed that IRBIT and IP₃ compete for binding to the same site on IP₃Rs, with IRBIT right shifting the dose response for: (a) binding of IP₃ to the IP₃Rs, (b) activation of the IP₃Rs channel activity by IP₃ and (c) in Ca²⁺ release from ER stores [3]. This was confirmed in independent study by Devogelaere et al., with measurement of IP₃ binding to purified IP₃R1 and IP₃-mediated Ca²⁺ release in permeabilized cells [18,19]. These effects required phosphorylation of IRBIT at multiple sites at the PEST domain. Thus, mutations of S68, S70, S71, S72, S74 and S77 to Alanine inhibited interaction of IRBIT with the IP₃Rs and its effect on IP₃-mediated Ca²⁺ release [3]. Among all the sites, phosphorylation of S68 appears to be a key phosphorylation site. Preventing phosphorylation of S68 is sufficient to prevent the effect of IRBIT on all its known targets [3,17,24,28,59]. Phosphorylation of S68 is necessary for phosphorylation of S71 and S74 and phosphorylation of S71 and S74 appears to be sufficient for interaction

and inhibition of IRBIT by the IP₃Rs [17,18]. S68 is the target of Protein Phosphatase 1 (PP1) [17].

To date the kinases that phosphorylate the native IRBIT *in vivo* are not known with certainty. IRBIT is predicted to be phosphorylated by the Ca²⁺-dependent kinases PKD, AMPK, CamK-II-IV and CK1 [19]. Analysis of synaptic phosphoproteins suggested that IRBIT is constitutively phosphorylated at T82, S84 and S85 [14], all of which are different from the major phosphorylation sites identified as the sites regulating interaction of IRBIT with the IP₃Rs [3], and thus their significance remain unknown. In addition to the need to determine the kinases that phosphorylate IRBIT *in vivo*, it is necessary to determine the physiological conditions leading to IRBIT phosphorylation and dephosphorylation.

The study of Devogelaere et al. revealed novel aspects of the regulation by IRBIT. First, they identified a PDZ ligand at the C terminus of IRBIT that was essential for its interaction with the IP₃Rs [18]. The PDZ ligand was found to be required for regulation of NBCe1-B and CFTR by IRBIT [59]. These findings indicate that IRBIT is present in complexes with its targets that are assembled by PDZ domains-containing scaffold proteins. Formation of the complexes likely facilitates the direct interaction of IRBIT with its targets to regulate their function. The identity of the scaffolding proteins and whether the same or different scaffolds mediate the various IRBIT complexes is not known at present. IP₃Rs interact directly or indirectly with several scaffold proteins that have PDZ domains, like protein 4.1 [22,62] and Shank [51] and CFTR interact with multiple PDZ domains-containing scaffolds [35]. Second, Devogelaere et al. identified the PP1 binding ligand KQIQF in IRBIT. Binding of PP1 to this site specifically dephosphorylates S68 [17].

The IP₃Rs-PDZ scaffold-IRBIT-PP1/kinase complex allows for multiple regulatory events and for flexibility in IRBIT action. In the resting state the majority of IRBIT is likely bound to the IP₃Rs to reduce the spontaneous activity of the receptor and Ca²⁺ leak. Recent studies pointed to the physiological importance of IP₃Rs-mediated Ca²⁺ leak in energy metabolism [13]. In this manner IP₃Rs serve to buffer the level of IRBIT available for regulation of other cellular processes and associate these processes with Ca²⁺ signaling. Cell stimulation that leads to generation of IP₃ can lead to shuttle of IRBIT between its targets, depending on the levels of IP₃ and the PDZ domain scaffold with which IRBIT and the target proteins interact. Future studies are likely to explore in more detail the role of the scaffolds and the IRBIT shuttle in determining the specificity of IRBIT action and the relationship between the activities of the various IRBIT targets.

IRBIT and Na⁺-HCO₃⁻ Co-Transport

Other transporters regulated by IRBIT with particular importance in epithelial electrolyte, fluid and HCO₃⁻ secretion are the Na⁺-HCO₃⁻ co-transporters (NBC) [52]. The NBCs are members of the superfamily of Na⁺-coupled HCO₃⁻ transporters (NCBT) [11]. The NCBT superfamily includes the electrogenic NBCe1-A-C and NBCe2a,c and electroneutral NBCn1-A-H and NBCn2-A-D Na⁺-HCO₃³⁻ co-transporters and the electroneutral Na⁺-dependent Cl⁻/HCO₃⁻ exchangers NDCBE-A-D. The domain structure, homology, conservation and specific function of the NCBTs were extensively discussed in [11,49] and will not be discussed here. The importance for our discussion is the most N terminal domain of the NCBTs comprising between 45–62 residues. This variable domain is found in several, but not all, members of the superfamily and also varies among isoforms of the same subfamily, including the NBCe1 subfamily [11]. The N terminal extension forms an inhibitory domain and when deleted results in marked activation of the relevant NCBTs [39].

As their name indicates, the NCBTs use the energy in the Na^+ gradient to transport HCO_3^- . Notable members are the three NBCe1 co-transporters. NBCe1-A is expressed almost exclusively in the kidney (also known as kNBC1) and functions as an electrogenic $1\text{Na}^+/3\text{HCO}_3^-$ co-transporter at the basolateral membrane to mediate $\text{Na}^+\text{-HCO}_3^-$ efflux [11,49]. NBCe1-B is nearly ubiquitous and is found at high levels at the basolateral membrane of all epithelia [49]. It was discovered as the $\text{Na}^+\text{-HCO}_3^-$ co-transporter in the pancreas (also known as pNBC1) [1]. $\text{Na}^+\text{-HCO}_3^-$ co-transport was described as the major HCO_3^- transport mechanism at the basolateral membrane of the pancreatic duct [63] and was later shown to mediate the majority of basolateral HCO_3^- influx during stimulated ductal HCO_3^- secretion [26,53]. $\text{Na}^+\text{-HCO}_3^-$ co-transport is also important in other epithelial HCO_3^- secretion, such as salivary glands [36,64], intestine [8,9] and the airway [31]. There is little information on the function of NBCe1-C except that it functions as a $1\text{Na}^+/2\text{HCO}_3^-$ co-transporter [39], and it is brain specific [11] (also known as bNBC1). The NBCe1-C stoichiometry was determined in *Xenopus* oocytes and it is not clear whether this stoichiometry is maintained in native cells, although a $\text{Na}^+\text{-HCO}_3^-$ co-transport activity with 1:2 stoichiometry was reported in glia [15] and astrocytes [46].

While searching for IRBIT-interacting proteins by identifying proteins that co-immunoprecipitate with IRBIT in a membranous brain extract, the Mikoshiba group isolated NBCe1-B as an IRBIT-interacting protein [52]. Structure-function analysis revealed that the unique N terminal domain of NBCe1-B (residues 1-62) interacts with IRBIT. The interaction required phosphorylation of the PEST domain at S68, S71, S74 and S77 [52]. Indeed, deletion of the PEST domain eliminated interaction of NBCe1-B with IRBIT, while deletion of the coiled-coil domain and the PDZ ligand weakened the interaction [59]. Most importantly, when expressed in *Xenopus* oocytes NBCe1-B had low basal activity and IRBIT markedly increased its activity [52]. Moreover, NBCe1-A, which lacks the N terminal extension of NBCe1-B, had high basal activity and was not further activated by IRBIT [52].

Activation of NBCe1-B by IRBIT when expressed in *Xenopus* oocytes is illustrated in Fig. 2a, c. NBCe1-C has the same N terminal extension as NBCe1-B with only a single residue not conserved. Interestingly, deletion of the NBCe1-B [52] and NBCe1-C [39] N terminal domain results in activation of both transporters, suggesting that both are regulated by IRBIT. Fig. 2 shows that this is indeed the case. Fig. 2b, c shows that the activity of NBCe1-C in *Xenopus* oocytes is low and it is markedly activated by IRBIT. Finally, Fig. 2d shows that knockdown of IRBIT in the pancreatic duct inhibits the native NBCe1-B activity, indicating that IRBIT regulates the native NBCe1-B. Ductal NBCe1-B activity was evaluated by measuring the Na^+ -mediated recovery from intracellular acidification due to incubation in HCO_3^- -buffered medium in the absence of external Na^+ . The contribution of the Na^+/H^+ exchangers was inhibited with EIPA and the sensitivity of the alkalization to H_2DIDS indicated that it is mediated by NBCe1-B. We note that other members of the Na^+ -driver HCO_3^- transporters have an N terminal domain similar to that of NBCe1-B [11], which predicts that their activity should also be regulated by IRBIT. This was suggested for NBCn1 and NDCBE [11], although it is not clear which isoform is activated by IRBIT. The N terminal extension of NBCn1-A-H and NDCBE-A-D differ substantially.

Structure-function analysis indicates that the N terminal domain of several Na^+ -coupled HCO_3^- transporters (NCBTs), including NBCe1-B and NBCe1-C, serves as an inhibitory domain to reduce the activity of the transporters [39]. Binding of IRBIT phosphorylated in positions S68, S71, S74 and S77 to this domain relieve the inhibition, resulting in activation of the transporters. How might IRBIT interact with the NCBTs to activate them? This is not known at present, although a clue is provided by the effect of Mg^{2+} and polycations [58] and of PIP2 [57] on NBCe1-B activity. The N terminus of NBCe1-B is highly charged with a

cluster of negatively charged residues at region 2-24 and a cluster of positively charged residues at region 37-59 [19]. Interaction of IRBIT with NBCe1-B is mediated by the negatively charged IRBIT PEST domain [3,59]. Thus, it is possible that the PEST domain interacts with NBCe1-B residues 37-59 by an electrostatic interaction.

Regulation by electrostatic interaction is supported by the effect of Mg^{2+} , neomycin and PIP2 on NBCe1-B activity. Mg^{2+} strongly inhibits NBCe1-B with a K_i of 0.01 mM. Deletion of the IRBIT-binding N terminal domain of NBCe1-B increased the K_i for Mg^{2+} inhibition by 30 folds [58]. Thus, Mg^{2+} has two inhibitory effects on NBCe1-B, a high affinity inhibitory effect that requires the IRBIT binding domain and a low affinity inhibitory effect that is independent of the IRBIT-binding domain. The two inhibitory effects were not specific for Mg^{2+} , but they are mimicked by the polycation neomycin [58]. It is possible that at low concentrations Mg^{2+} and neomycin interact with the negative charges at residues 2–24 of NBCe1-B to shield it and prevent interaction of IRBIT with the NBCe1-B N terminus. PIP2 also has dual effect on NBCe1-B [57]. In excised patches PIP2 activates NBCe1-A and prevents its rundown. However, in intact oocytes PIP2 does not activate NBCe1-A but it does activate NBCe1-B and NBCe1-C [57]. The combined findings suggest that PIP2 is required for the activity of the NBCe1. In addition, PIP2 interacts with the N terminal domain of NBCe1-B and NBCe1-C to prevent their auto-inhibition. PIP2 may do so by interacting with the positive charges at residues 37–59 of NBCe1-B auto-inhibitory domain.

IRBIT and Epithelial HCO_3^- Secretion

The critical finding of activation of NBCe1-B by IRBIT opened the way in understanding the mechanism and regulation of epithelial HCO_3^- secretion. Epithelial HCO_3^- secretion involves NBCe1-B-mediated HCO_3^- entry across the basolateral membrane. HCO_3^- is then secreted to the luminal side by the CFTR-SLC26 transporters complex in which the solute carrier family 26 (SLC26) Cl^-/HCO_3^- exchangers secrete HCO_3^- in exchange for Cl^- , while CFTR mainly re-circulates the Cl^- to maintain the HCO_3^- secretory process [21,30]. In some tissues, like the airway [20] and the distal pancreatic duct [47] CFTR can also secrete some of the HCO_3^- . It was then not unexpected that IRBIT has a prominent role in epithelial HCO_3^- secretion. Knockdown of IRBIT markedly inhibited pancreatic duct fluid and HCO_3^- secretion [59].

Inhibition of ductal fluid and HCO_3^- secretion by knockdown of IRBIT can be due to inhibition of NBCe1-B (see Fig. 2d) and also due to inhibition of luminal HCO_3^- transporters. To examine whether IRBIT regulates both basolateral HCO_3^- entry and luminal HCO_3^- exit we tested the effect of IRBIT on the luminal transporters. IRBIT activates native CFTR in the pancreatic duct and the recombinant CFTR by increasing CFTR open probability due to a reduction in CFTR interburst duration [59]. Interestingly, although activation of CFTR by IRBIT required phosphorylation of S68 [59], the mode of interaction of IRBIT with CFTR is different from that of NBCe1-B. Thus, deletion of any single IRBIT domain, the PEST, coiled-coil or the PDZ ligand, did not prevent interaction with CFTR. Preventing the interaction required deletion of the combined PDZ ligand and the PEST or PDZ ligand and the coiled-coil domains. However, deletion of any of the IRBIT domains prevented activation of CFTR by IRBIT [59], suggesting that another unknown protein is required for activation of CFTR by IRBIT. The findings in the pancreatic duct and with expressed NBCe1-B and CFTR lead to the model in Fig. 3 for coordination of epithelial fluid and HCO_3^- secretion by IRBIT.

Another effect of IRBIT on ion transport reported recently is modest activation of the Na^+/H^+ exchanger isoform 3 (NHE3) [24]. The activation appears to be Ca^{2+} dependent [25],

requires phosphorylation of S68, S71 and S74 and may mediate activation of NHE3 by Angiotensin II [24]. NHE3 is prominently expressed in the proximal tubule luminal membrane, where it mediates the bulk of renal Na^+ absorption and H^+ secretion [6]. NHE3 is also expressed in the luminal membrane of the pancreatic [33] and salivary glands duct [36], in which it was suggested to mediate HCO_3^- salvage at the resting state. Another Na^+ -dependent HCO_3^- salvage mechanism in the duct is NBCn1 (also known as NBC3) [48], which can also be activated by IRBIT (see above). NHE3 can salvage HCO_3^- by secretion of H^+ to the duct lumen that then interacts with luminal HCO_3^- to generate CO_2 that diffuses into the duct to be converted to HCO_3^- . HCO_3^- salvage by NBCn1 is by direct absorption of the leaked HCO_3^- from the duct lumen. Interestingly, NHE3 [2] and NBCn1 [48] are inhibited by CFTR. Hence, it is possible that IRBIT coordinates HCO_3^- salvage at the resting state and HCO_3^- secretion at the stimulated state by shifting between NHE3/NBCn1 and CFTR as a result of duct stimulation. This is modeled in Fig. 3.

IRBIT and Other Cellular Functions

Other, less understood functions of IRBIT are the control of dendritic cells (DCs) maturation [16] and mRNA processing [28]. DCs are major cells in the immune system with central role in the inflammatory response. In response to foreign pathogens or to inflammation DCs undergo maturation to secrete cytokines, migrate to lymph nodes and present the major histocompatibility complexes to T cells [40]. IRBIT mRNA is markedly increased during DCs maturation [16]. However, the role of IRBIT in DCs maturation is not understood at any level.

Recently, the Mikoshiba group reported that IRBIT regulates pre-mRNA processing and thus gene regulation [28]. Processing of pre-mRNA at the 3' end is mediated by cleavage and polyadenylation [37]. Cleavage is mediated by the cleavage and polyadenylation specific factor (CPSF) complex [38]. The CPSF complex contains the Fip1 (factor interacting with PAP1) subunit [27] that interacts with IRBIT [28]. Polyadenylation is catalyzed by poly(A) polymerase (PAP) [37]. IRBIT interaction with Fip1 requires phosphorylation of the serines in the PEST domain, including S68, and resulted in translocation of Fip1 from the nucleus to the cytoplasm [28]. Through the interaction with Fip1, IRBIT is recruited to PAP to reduce its activity and thus pre-mRNA polyadenylation. Regulation of pre-mRNA polyadenylation by IRBIT may be part of the cellular stress response since cell stress increases IRBIT phosphorylation and its interaction with CPSF [28].

Conclusions

The many diverse roles of IRBIT discussed here highlight this remarkable protein as a multifaceted cellular regulator. Undoubtedly, this is due to the multiple and versatile interactions mediated by its PEST domain that is required or mediate all the functions of IRBIT known to date. The PEST domain mediates interaction of IRBIT with IP_3 receptors, the NDBTs, CFTR, NHE3 and Fip1 which do not have any domain in common. This would suggest that the PEST domain interacts with conformation that may have a similar fold in all the targets. Nevertheless, these diverse interactions highlight the versatility of the IRBIT PEST domain. The three additional IRBIT domains uncovered so far, the PP1 and PDZ binding ligands and the coiled-coil domain, most probably recruit additional regulators and factors to the IRBIT targets. There are likely additional functional/interacting domains within the IRBIT AHCY domain that increase the spectrum of IRBIT interactions and the physiological processes it regulates. It is quite clear that so far only a small fraction of the cellular functions mediated by IRBIT have been discovered and that we are only at the

beginning of our understanding how IRBIT regulates all of these cellular functions and how the function of IRBIT is regulated in resting and stimulated states.

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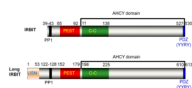


Fig. 1. The IRBIT domains. The figure shows the boundaries of the domain identified so far in short (*upper*) and long (*lower*) IRBITs

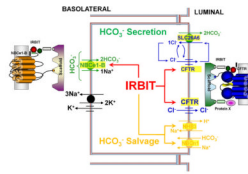


Fig. 3. IRBIT coordinates pancreatic duct fluid and HCO_3^- secretion. The model shows the key transporters involved in pancreatic duct fluid and HCO_3^- salvage and secretion. In the resting state, IRBIT forms complexes with the luminal NHE3 and NBCn1 to salvage leaked fluid and HCO_3^- . Cell stimulation results in formation of complexes between IRBIT and the basolateral NBCe1-B and the luminal CFTR that are assembled by PDZ domains-containing scaffolding proteins. The interaction is mediated by the IRBIT PEST domain (*red circles*) and requires the IRBIT coiled-coil domain (*green circles*). In the case of CFTR, an additional unknown protein (marked as protein X) is needed for activation of CFTR by IRBIT. Activation of NBCe1-B and CFTR by IRBIT coordinates HCO_3^- entry at the basolateral membrane and HCO_3^- exit at the luminal membrane to ensure the fidelity of epithelial fluid and HCO_3^- secretion