

Chapter 6

Phospholipase A₂ as a Molecular Determinant of Store-Operated Calcium Entry

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Abstract Activation of phospholipases A₂ (PLA₂) leads to the generation of biologically active lipid products that can affect numerous cellular events. Ca²⁺-independent PLA₂ (iPLA₂), also called group VI phospholipase A₂, is one of the main types forming the superfamily of PLA₂. Beside of its role in phospholipid remodeling, iPLA₂ has been involved in intracellular Ca²⁺ homeostasis regulation. Several studies proposed iPLA₂ as an essential molecular player of store operated Ca²⁺ entry (SOCE) in a large number of excitable and non-excitable cells. iPLA₂ activation releases lysophosphatidyl products, which were suggested as agonists of store operated calcium channels (SOCC) and other TRP channels. Herein, we will review the important role of iPLA₂ on the intracellular Ca²⁺ handling focusing on its role in SOCE regulation and its implication in physiological and/or pathological processes.

Keywords Phospholipases A₂ • SOCE • TRP channels • Lysophospholipids • STIM1 • Orail

Abbreviations

AA	Arachidonic acid
AdPLA ₂	Adipose-specific PLA ₂
ARC	Arachidonic acid-regulated calcium channels
BEL	Bromo-enol lactone
CaM	Calmodulin
cPLA ₂	Cytosolic PLA ₂

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DAG	Diacylglycerol
ER	Endoplasmic reticulum
iPLA ₂	Calcium-independent PLA ₂
LA	Lysophosphatidyl acid
LyPLA ₂	Lysosomal PLA ₂
OAG	1-oleoyl-2-acetyl-sn-glycerol
PAF-AH	Platelet-activating factor acetylhydrolases
PC	Phosphatidylcholine
PE	Phosphatidylethanolamine
PG	Phosphatidylglycerol
PS	Phosphatidylserine
ROC	Receptor operated channels
SMC	Smooth muscle cell
sPLA ₂	Secretory PLA ₂
SOCC/SOCE	Store operated Ca ²⁺ channels/entry

6.1 Classification of Phospholipase A₂

The phospholipase A₂ superfamily enzymes are characterized by their ability to catalyze the hydrolysis of glycerophospholipids at the sn-2 position and generate several classes of bioactive lipids, fatty acids and lysophospholipids [1]. Six main families of phospholipases have defined physiological implications. They comprise secretory PLA₂ (sPLA₂), cytosolic PLA₂ (cPLA₂), lysosomal PLA₂, adipose-specific PLA₂ (AdPLA₂); and two major Ca²⁺-independent groups, calcium-independent PLA₂ (iPLA₂) and platelet-activating factor acetylhydrolases (PAF-AH). This subdivision was based on their structures, catalytic mechanisms, localizations and evolutionary relationships, and they are collectively identified as groups, using roman numerals (i.e. Group I to Group XVI), with capital letters to distinguish individual sub-families [2]. Many of PLA₂ have contrasted role in cell signaling that involve intracellular Ca²⁺ homeostasis regulation.

6.1.1 Secretory PLA₂ (sPLA₂)

The secretory PLA₂s (belonging to Groups I, II, III, V, IX, X and XII in mammals) were the first type of PLA₂ enzymes discovered. They were identified in organisms such as snakes and scorpions; in components of pancreatic juices; arthritic synovial fluid; and in many different mammalian tissues [3]. Most sPLA₂ isoforms are calcium-dependent, and require millimolar concentrations of the ion to function optimally [2, 4, 5]. Consequently, sPLA₂s typically function at the external side of the cell hydrolyzing a wide variety of phospholipids [2, 6]. sPLA₂ hydrolyzes the sn-2 ester bond in the glyceroyl phospholipids presents in lipoproteins and cell

membranes, inducing structural and functional changes and forming arachidonic acid (AA), lysopholipids and non-esterified fatty acids with direct proinflammatory effects [7, 8]. In general, sPLA₂ isoforms have solid preference for negatively charged phospholipid head groups, in particular phosphatidylserine (PS), phosphatidylglycerol (PG) and phosphatidylethanolamine (PE) [9]. Recent studies have suggested that some sPLA₂ isoforms can modify cell functions by binding to receptors and other proteins [5].

6.1.2 Cytosolic PLA₂ (cPLA₂)

The cPLA₂ family (also named Group IVA–F) is one of the major PLA₂ that contains six isoforms, ranging in size from 60 to 85 kDa, which are generally localized in the cytosol. They are active in the presence of mM levels of Ca²⁺ and, with the exception of cPLA₂γ (Group IVC), contains in their N-terminals a C2 domain for the binding of two Ca²⁺ ions as well as two conserved phosphorylation sites. cPLA₂ family members have a catalytic domain characterized by a three-layer architecture employing a conserved Ser/Asp catalytic dyad, instead of the classical catalytic triad, that is similar in structure to that of iPLA₂ [10, 11]. The first group IV cPLA₂ (Group IVA) was firstly identified in human platelets in 1986 [12] and was cloned and sequenced 5 years later [13, 14]. cPLA₂ is perhaps the far most widely studied cytosolic enzyme and, besides transacylase activity, is also known to have PLA₂ and lysophospholipase activities [15]. cPLA₂ is activated by several different mechanisms, and is recruited to the membrane by a Ca²⁺ dependent translocation of the C2 domain. A recent work has localized the lipid binding surface of the enzyme in the presence of Ca²⁺ [16].

From the different PLA₂s, cPLA₂ is the only one described to have a preference for AA in the sn-2 position of phospholipids [10, 14]. Upon activation and translocation to intracellular membranes, cPLA₂ generates and releases AA from membrane phospholipids leading to an active lipoyxygenase and cyclooxygenase metabolism [17]. AA, which acts as precursor for the generation of eicosanoids, is a key player in the prostanoid signaling cascades and therefore its activation is important for regulating various physiological and pathological processes including immune and inflammatory-related processes [2, 18, 19]. Furthermore, AA is also considered as an agonist that induces cytosolic Ca²⁺ entry through cationic channels called arachidonic acid-regulated calcium channels (ARC) [20, 21].

6.1.3 PAF Acetyl Hydrolase/Oxidized Lipid (PAF-AH/LpPLA₂)

Platelet activating factor (PAF) acetylhydrolases (AH) (PAF-AH, Group VIIA and B, and VIIIA and B) have low molecular weight (26–45 kDa) and represent a unique group of acyl hydrolases with a catalytic serine that is capable of releasing acetate

from the sn-2 position of PAF, a 1-*O*-alkyl-PC [22]. However, they can also catalyze the release of oxidized acyl groups from the sn-2 position of PC and PE, not just PAF [2, 4, 23]. Its active site is composed of a serine, histidine, and aspartic acid hydrolase triad, unlike all other PLA₂s, which have dyads [24]. There are four members of this family that specifically catalyze these reactions; one of them is a secreted protein (GVIIA PLA₂), known as plasma-type PAF-AH or “lipoprotein-associated PLA₂” (LpPLA₂), that has generated interest as a therapeutic target for atherosclerosis [22, 26–29]. On the other hand, LpPLA₂ is a potent phospholipid activator that is secreted by multiple inflammatory cells including monocytes/macrophages, T lymphocytes and mast cells [30, 31]. This enzyme was cloned from human plasma in 1995 and was shown to have anti-inflammatory activity in vivo [25]. The LpPLA₂ role in cytosolic Ca²⁺ regulation is still unknown.

6.1.4 Lysosomal PLA₂ (LyPLA₂)

Lysosomal PLA₂ was purified from bovine brain as an enzyme that esterifies an acyl group with the hydroxyl group in the C-1 position of ceramide using phospholipids as the acyl group donor, so the enzyme was first named 1-*O*-acylceramide synthase (ACS). The protein possesses Ca²⁺ independent PLA₂ and transacylase activities. Hiraoka et al. [32] proposed that the hydrolyzed acyl group is transferred through an enzyme-acyl intermediate to ceramide or water, resulting either in the production of either 1-*O*-acyl- ceramide (ACS activity) or the release of free fatty acids (PLA₂ activity). In terms of catalytic activity, Ly-PLA₂ specifically prefers PC and PE head groups at pH 4.5 in a Ca²⁺-independent manner. Ly-PLA₂ is ubiquitously expressed in diverse cell types, but highly expressed in alveolar macrophages. In fact, it plays a role in surfactant metabolism, and specifically in the phospholipid catabolism of pulmonary surfactant [33, 34].

6.1.5 Adipose Specific PLA₂ (AdPLA₂)

Duncan et al. [35] discovered recently a novel intracellular PLA₂, highly and differentially expressed only in adipocytes and induced during preadipocyte differentiation, that releases sn-2 fatty acid from phospholipids in a Ca²⁺-dependent manner. This recently discovered enzyme named adipose-specific PLA₂ (AdPLA₂, Group XVI), has a molecular weight of 18 KDa. It is found abundantly in white adipose tissue, 40–150 times higher than found in liver. The enzyme is not an acyltransferase, but it functions entirely as a phospholipase, producing lysophosphatidylcholine and AA from the phospholipids. In addition, Duncan and colleagues studied the properties of AdPLA and found its optimal pH was 8.0, requiring cysteine and histidine residues at the active site, with maximal enzymatic activity in the presence of 1.0 mM Ca²⁺ [35]. AdPLA₂ have been also implicated in energy regulation as it modulates the release of fatty acids, from stored triglycerides in white adipose

Table 6.1 Isoforms of calcium-independent (Group VI) PLA₂

PLA ₂ family	Group	Source	MW (kDa)	Alternate name
iPLA ₂	VIA-1	Human/murine	84–85	iPLA ₂ α
	VIA-2	Human/murine	88–90	iPLA ₂ β
	VIB	Human/murine	88–91	iPLA ₂ γ
	VIC	Human/murine	146	iPLA ₂ δ, neuropathy target esterase (NTE)
	VID	Human	53	iPLA ₂ ε, adiponutrin
	VIE	Human	57	iPLA ₂ ζ, TTS-2.2
	VIF	Human	28	iPLA ₂ η, GS2

tissue, which will be later used as energy source by other tissues. AdPLA₂ has been also proposed to play a major role in the supply of AA for prostaglandin E₂ (PGE₂) synthesis in white adipose tissue [36]. Thus, AdPLA is considered a major regulator of adipocyte lipolysis and is crucial for the development of obesity, although it seems possible that AdPLA could promote obesity through a mechanism distinct from PGE₂ signaling [37].

6.1.6 Calcium Independent PLA₂ (iPLA₂)

The Ca²⁺ independent PLA₂s are members of the GVI family of PLA₂ enzymes. Currently, six isoforms of iPLA₂ (Group VIA–F) have been identified as shown in Table 6.1. While their catalytic sites are similar to that of cPLA₂, they do not require Ca²⁺ for catalytic activity and they are generally larger in size, with molecular weights ranging from 55 to 146 kDa except for Group VIF PLA₂ (~28 kDa). iPLA₂s are localized either in the cytosol, the endoplasmic reticulum (ER) or in the mitochondrial membrane [38]. iPLA₂ are entirely involved in lipid remodeling, in the Land's Cycle, and also mediate cell growth signaling [2, 4]. Members of this family share a protein domain initially discovered in patatin, the most abundant protein of the potato tuber.

In the next part of this chapter, we will go through iPLA₂ classification, regulation, and its role in intracellular Ca²⁺ regulation.

6.2 Sub-classification of iPLA₂

6.2.1 GVIA PLA₂ (iPLA₂α and iPLA₂β)

Many new iPLA₂ (GVI PLA₂) members have been identified in the last years, but the first member and the best characterized of this family is the GVIA PLA₂, which was purified from macrophages in 1994 [39, 40]. GVIA PLA₂ is expressed in

multiple different splice variants [41] and, similar to cPLA₂ (GIV PLA₂), it catalyzes the cleavage of the sn-2 ester bond. However, it does not show specificity for AA in the sn-2 position and is fully active in the absence of Ca²⁺. The GVIA PLA₂ also possesses sn-1 lysophospholipase and transacylase activity [41]. The enzyme has a conserved glycine-rich nucleotide-binding motif (GXGXXG) proximal to the catalytic site and it is activated several-fold by ATP [42]. The N-terminal domain of GIVA PLA₂ is composed of seven to eight ankyrin repeats, which are responsible for protein-protein interaction between monomers [43]. It is thought that ankyrin repeats enable the oligomerization of Group VIA monomers required for catalytic activity [39]. In fact, the active form of Group VIA PLA₂ is a tetramer [39].

Several splice variants of GVIA PLA₂ have been identified [39, 44]. Group VIA-1 or iPLA₂α, and Group VIA-2 or iPLA₂β [44–48], for example, comprise two catalytically active forms of this enzyme [44–48]. Both isoforms are similar in size, 85 and 88 kDa respectively, and contain eight N-terminal ankyrin repeats and a consensus lipase motif (GXS⁴⁶⁵XG), whereas in GVIA-2 PLA₂ the 8 ankyrin repeats are interrupted by an insertion of 54 amino acids and they exhibit a glutamate residue at position 450, while the corresponding position in Group VIA-1 is glutamine.

Three additional splice variants of GVIA iPLA₂ have been identified: Group VIA-3 (also known as iPLA₂-2); Group VIA Ankyrin-1 (or Ankyrin-iPLA₂-1), and Group VIA Ankyrin-2 (or Ankyrin-iPLA₂-2). The Group VIA-3 splice variant encodes an iPLA₂ that is identical to Group VIA-2 PLA₂ (iPLA₂β) at the N-terminus, that retains the GTS⁵¹⁹TG active site and that has a truncated C-terminus. However, it is not known whether Group VIA-3 encodes a functional phospholipase A₂. Group VIA Ankyrin-1 is identical to Group VIA-2 at the N-terminus but it ends prior to the GTS⁵¹⁹TG active site with a three amino acid modification at the C-terminus; it does not encode a functional PLA₂ enzyme [46]. Similar to Group VIA Ankyrin-1, Group VIA Ankyrin-2 also lacks the GTS⁵¹⁹TG active site and additionally present with a 73 amino-acids shorter N-terminus and a 50-amino-acid variation at the C-terminus. Group VIA ankyrin-1 and Group VIA ankyrin-2 may act as negative regulators of Group VIA-1 and Group VIA-2 by precluding catalytically active tetramer aggregation [39, 46]. Processes in which GVIA PLA₂ has been implicated include phospholipids remodeling, AA release causing eicosanoid formation, protein expression, acetylcholine-mediated endothelium-dependent relaxation of the vasculature, secretion, and apoptosis. iPLA₂ plays also an important role in lymphocyte proliferation and in Ca²⁺ signaling regulated by calmodulin (CaM) and by a Ca²⁺ influx factor as detailed below [41, 49–52].

6.2.2 GVIB PLA₂ or iPLA₂γ

The iPLA₂γ called also GVIB PLA₂ have been less studied. It has been involved in the release of AA that leads to eicosanoid formation [53, 54]. iPLA₂γ contains the consensus lipase motif (GX SXG), a C-terminal peroxisome localization

signal (SKL), and a glycine-rich nucleotide binding loop motif (GXGXXG). Interestingly, the nucleotide-binding motif commences 34 amino acids upstream of the putative active Ser, which is closely identical to the location of the nucleotide binding loop motif of Group VIA (35 amino acids upstream) [53]. A recent study demonstrated that iPLA₂γ is responsible for the release of AA and prostaglandin E2 (PGE2) and inflammatory mediators in cardiac myocytes infected by Chagas' disease parasite [55]. Previously, iPLA₂γ was also suggested as a critical participant in the Ca²⁺-induced opening of the mitochondrial permeability transition pore (mPTP) in Liver [56].

6.2.3 *GVIC, GVID, GVIE, GIVF PLA₂s*

Different Ca²⁺-independent lipases have been identified newly, and classified according to the terminology of the Group system GVIC, GVID, GVIE and GIVF PLA₂s. The GVIC PLA₂ enzyme has some sequence similarity to GVIA PLA₂ and might play a role in membrane homeostasis. This enzyme was previously known as NEST, the recombinantly expressed esterase domain of NTE (neuropathy target esterase), a membrane protein expressed in neurons of human and mice with physiological function elusive [57, 58] that possesses PLA₂ and lysophospholipase activities [59]. NEST might slowly hydrolyze the fatty acid in the sn-2 position of PC and subsequently, in a fast reaction, release the fatty acid in the sn-1 position.

The genes for the three other enzymes have also been identified before. Although, there was no catalytic activity attributed to corresponding proteins. The enzymes were shown to hydrolyze both LA and AA at the sn-2 position in the absence of free Ca²⁺ [60], thus these three enzymes might play a role in the regulation of triacylglycerol homeostasis which implicates the control of energy metabolism in adipocytes. Besides, PLA₂ activity, these enzymes possess high triacylglycerol lipase and acylglycerol transacylase activities and all of them were inhibited by bromoenol lactone (BEL) at sub-micromolar levels [60].

6.3 Regulation of iPLA₂

6.3.1 *ATP and PKC*

The iPLA₂ protein contains a lipase consensus sequence and a putative ATP-binding motif. ATP has been reported to stimulate iPLA₂ activity in rat islets [61], murine P388D1 cells [45], but not to affect the iPLA₂ activity of Chinese Hamster Ovary cells [44]. In an early study, Ackerman et al. discovered that both Triton X-100 and ATP enhanced the activity of iPLA₂ in P388D1 cells [39]. The enzyme activity was 1.2–6 fold higher in mixed micelles when assayed in the presence of ATP and other

di- or triphosphate nucleotides [39]. In other study, ATP stimulation of an iPLA₂ isoform was demonstrated in human pancreatic islet [42]. Interestingly, this same group demonstrated that ATP does not directly activate but rather protects iPLA₂ from a loss of its activity [61]. On the other hand, there is no consensus regarding the role of PKC in iPLA₂ activation [62]. An early study showed that the activation of PKC α ultimately provoked AA release via iPLA₂. This AA release was markedly inhibited by BEL or iPLA₂ antisense oligonucleotide [63]. Interestingly, we demonstrated that both diacylglycerol analog 1-oleoyl-2-acetyl-sn-glycerol (OAG) and store depletion with thapsigargin produced a PKC ϵ -dependent activation of iPLA₂ β in proliferating but not in confluent aortic SMC [64].

6.3.2 *Ca²⁺/Calmodulin Regulation of iPLA₂*

The first evidence of iPLA₂ modulation by CaM came from the observation that Ca²⁺ addition to the cytosol of cardiac myocytes inhibited iPLA₂ activity induced by ischemia. This inhibition was demonstrated to be due to CaM [65]. In fact, molecular and structural studies showed that in the absence of CaM, the active site of iPLA₂ interacts with the CaM-binding domain, resulting in a catalytically competent enzyme, whereas reversible disruption of this interaction through the binding of CaM abrogates this interaction, resulting in a loss of iPLA₂ activity [65–67]. iPLA₂ was shown to form a catalytically inactive ternary complex with CaM-Ca²⁺ that could be reversibly dissociated by chelation of Ca²⁺ ion with EGTA to regain full catalytic activity. Although iPLA₂ activity is independent of Ca²⁺, it is able to inhibit the iPLA₂ activity by Ca²⁺-activated CaM and this inhibition is apparently due to the binding to the IQ motif. In fact, the dissociation of CaM from iPLA₂ is the main mechanism that changes the Ca²⁺-independent enzyme into an enzyme that is sensitive to modification in intracellular Ca²⁺ ion homeostasis. Moreover, conformational changes provoked in CaM using agents that inhibited the interaction of CaM with its target proteins resulted in iPLA₂ activation. Wolf et al. in 1997 have shown that W7, CaM antagonist, activated iPLA₂ in A-10 smooth muscle cells (SMC) [68]. Smani and colleagues also demonstrated that CaM inhibition with calmidazolium and a membrane-impermeable CaM inhibitory peptide, promoted iPLA₂ activation in SMC and RBL cell line [69]. Later on, compelling evidences have shown that store depletion with thapsigargin or cyclopiazonic acid stimulated iPLA₂ activation through displacement of inhibitory CaM [68–70].

6.3.3 *Chemical Inhibition of iPLA₂*

The most important inhibitor for iPLA₂ is BEL, which has specificity 1,000 times higher for iPLA₂ over other PLA₂ isoforms [41]. BEL is a suicidal substrate for iPLA₂ that is widely used as an irreversible mechanism-based, time- and temperature-dependent, inhibitor. For cell-based studies, it has been described previously that

high concentrations of BEL (25 μ M) partially inhibit the magnesium-dependent phosphatidate phosphohydrolase (PAP-1), which converts phosphatidic acid to diacylglycerol (DAG) [71, 72]. To some extent it is possible to identify promiscuous effects of BEL on iPLA₂ and PAP-1 by performing experiments with BEL and propranolol in parallel [71, 73]. The latter compound inhibits PAP-1 and not iPLA₂. Others and we confirmed that iPLA₂ activation induced by Ca²⁺ release from the store is inhibited by BEL [68, 70, 73, 74]. Importantly, Jenkins et al. [75] demonstrated that the commonly used BEL is composed of two enantiomers with different specificity for iPLA₂ isoforms. S-BEL has higher specificity to iPLA₂ β , and R-BEL is more specific to iPLA₂ γ , which allowed identifying the type of iPLA₂ involved in several different cellular processes. Indeed, we confirmed that S-BEL, but not R-BEL, selectively inhibited iPLA₂ β activity stimulated by intracellular store depletion in SMC and RBL, indicating that S-BEL is a valuable tool to determine the role of iPLA₂ β in intracellular signaling processes [64, 76].

6.4 iPLA₂ Role in the Ca²⁺ Signaling Network

As described above, for long time iPLA₂'s main role was especially related to cellular phospholipids remodeling [41]. However, different reports have demonstrated that the specific beta isoform of iPLA₂ (iPLA₂ β) is involved in several agonist-stimulated signaling cascades. iPLA₂ has several unique features which confused researchers for many years. One of them relies on its activation independently of the presence or absence of Ca²⁺. iPLA₂ is able to function in the presence of strong Ca²⁺ chelators as BAPTA. At the same time iPLA₂ is able to bind the Ca²⁺-CaM complex. Interestingly, conditions for iPLA₂ activation are similar to those described for store operated calcium entry (SOCE). In fact, iPLA₂ can be activated by depletion of intracellular Ca²⁺ stores caused by vasopressin or by thapsigargin, an inhibitor of Sarco/Endoplasmic reticulum Ca²⁺-ATPase pump [68, 77, 78].

6.4.1 Overview of the Store Operated Ca²⁺ Channels Signaling Pathway

To increase cytoplasmic Ca²⁺ concentration, Ca²⁺ is either released from intracellular stores or enters into the cell by crossing the plasma membrane through ion channels. Store operated Ca²⁺ channels (SOCC) and receptor operated channels (ROC) are considered the main route for Ca²⁺ entry in non-excitabile cells, but they also exist in excitable cells such as skeletal muscle, neurons or smooth muscle [79]. In excitable cells, Ca²⁺ entry is achieved largely through opening of voltage and/or voltage independent channels ROC or SOCC that are responsible of SOCE [80]. The concept of SOCE activation seems to be simple: basically upon depletion of ER

stores, a signal is produced that activates specific Ca^{2+} -conducting channels SOCC, in plasma membrane that allows Ca^{2+} entry into the cell. SOCC role was originally linked only to refilling the intracellular store. However, now it's widely agreed that these channels provide a sustained Ca^{2+} influx for a variety of important functions in eukaryotic cells. Among those functions are exocytosis, vascular contraction and relaxation, Ca^{2+} oscillations, gene transcription, regulation of enzymatic activity, cell proliferation and apoptosis [80, 81].

6.4.1.1 Mechanism of SOCE Activation: Emerging Role of STIM1 and Orai1

One of the most intriguing mysteries of the store-operated pathway is the mechanism of its activation. Questions of how do the stores communicate with the plasma membrane channels and which is the signal produced by the stores upon their depletion, have been a matter of intense investigation for long time. Hypotheses presented can be mainly grouped into two main categories: those that propose the generation of a diffusible molecule with ability to induce SOCC opening, and those that assume a physical interaction between channel subunit and an element of the ER (for review see [80, 82]). Soon after the identification of SOCE Robin Irvine proposed a physical or conformational coupling between elements in the ER and SOCC in the plasma membrane [83], as a mechanism that resembles the classical excitation-contraction coupling between ryanodine receptors and dihydropyridine receptors in the skeletal muscle [84]. Consequently, most of the early studies focused on the association between inositol-triphosphate receptors (IP_3R) and the subunit channel suggested to form SOCC. This hypothesis received support from studies demonstrating that, under resting conditions; TRPC1, TRPC3 and TRPC6 can be co-immunoprecipitated with IP_3R [85, 86]. However, the major challenge for this model came from the studies in triple IP_3R knockout DT40 cells, in which SOCE seemed completely normal [87–89]. Importantly, in 2005 and 2006 the Ca^{2+} sensor of the ER was identified as the STIM1 (Stromal Interaction Molecule-1) protein, and Orai1 was identified as the structural subunit of the channel conducting the Ca^{2+} selective CRAC [90–92]. Several reports have showed that upon Ca^{2+} depletion, STIM1 lose Ca^{2+} from its EF hand, oligomerize and accumulate into punctate structures in the ER membrane located in close proximity (10–25 nm) to the plasma membrane. Furthermore, STIM1 and Orai1 have been reported to accumulate and colocalize in punctate structures along the plasma membrane and to associate by a reversible and physical coupling mechanism upon depletion of the intracellular Ca^{2+} stores which support the conformational coupling model (for review see [93]). While direct coupling of ER-resident STIM1 to PM-resident Orai1 is considered as the most straightforward mechanism for signal transduction, there is a growing body of evidence for the presence of additional structural and/or functional linker(s) between STIM1 and Orai1. Indeed, Balla's group suggested the presence of additional molecular components within the STIM1-Orai1 complex [94]; meanwhile Rosado and colleagues nicely showed that both STIM1 and Orai1

also co-immunoprecipitate with other TRPC channels when stores are depleted [95–97]. Recently, we have demonstrated that store depletion stimulated STIM1 and iPLA₂β colocalization required for SOCE in coronary artery [98].

6.4.1.2 Calcium Influx Factor and SOCE Activation

The other hypothesis focuses on diffusible messengers generated upon intracellular stores depletion. Different signaling molecules have been reported to play an essential role in the activation of SOCE in different cell types, including cGMP [99], tyrosine kinases [100], and small GTP-binding proteins [101], among others. However, special efforts were dedicated to the still uncharacterized molecule known as Ca²⁺ influx factor (CIF) by Victoria Bolotina's group. Refined CIF extract was obtained from different cell lines, including human platelets, which stimulated an extracellular Ca²⁺ influx and I_{CRAC} (CRAC current) sensitive to the well-known SOCC inhibitors [76]. Interestingly, soon after STIM1 discovery, Bolotina and co-workers presented compelling evidences demonstrating that CIF production is tightly linked with STIM1 expression and requires the functional integrity of glycosylation sites in its intraluminal SAM domain [102]. In this study, authors demonstrated that upon store depletion, CIF is produced before STIM1 accumulation in puncta and activation of SOCE. Authors showed that lack of STIM1 in the rare neuronal cell line (NG115-401L), which features virtually no SOCE responses [103], or STIM1 downregulation in cells transfected with siRNAs, dramatically impaired active CIF production confirming CIF and STIM1 relationship [102]. Unfortunately, the molecular identity of CIF is still unknown, although its presence and its biological activity were detected by numerous groups in a wide variety of cell types ranging from yeast to human (for review see [51, 79]). Previously, we have characterized in our earliest studies that iPLA₂β is the physiological target of CIF and the mechanism of CIF-induced activation of SOCE was depicted as illustrated in Fig. 6.1 [69, 76, 104].

6.4.2 Essential Role of iPLA₂ in Store Operated Calcium Entry

In the last 1990s, several works established an interesting scenario for iPLA₂ activation, showing that it could be activated by depletion of Ca²⁺ stores caused by vasopressin or by thapsigargin in A10 SMC line [68, 77]. A10 cells stimulation with thapsigargin induced release of AA that was directly correlated to thapsigargin-induced depletion of intracellular Ca²⁺ stores [68]. Next, iPLA₂β, and not iPLA₂γ, was identified as the mediator of vasopressin-induced AA release in SMC [75]. Therefore, the role of iPLA₂β in SOCE activation was explored and the first evidence of iPLA₂ requirement for SOCE activation was obtained by studying SOCE in primary culture of SMC as a model for excitable cells, and RBL cells as a model for non-excitable cells. The functional inhibition of iPLA₂ with BEL prevented the

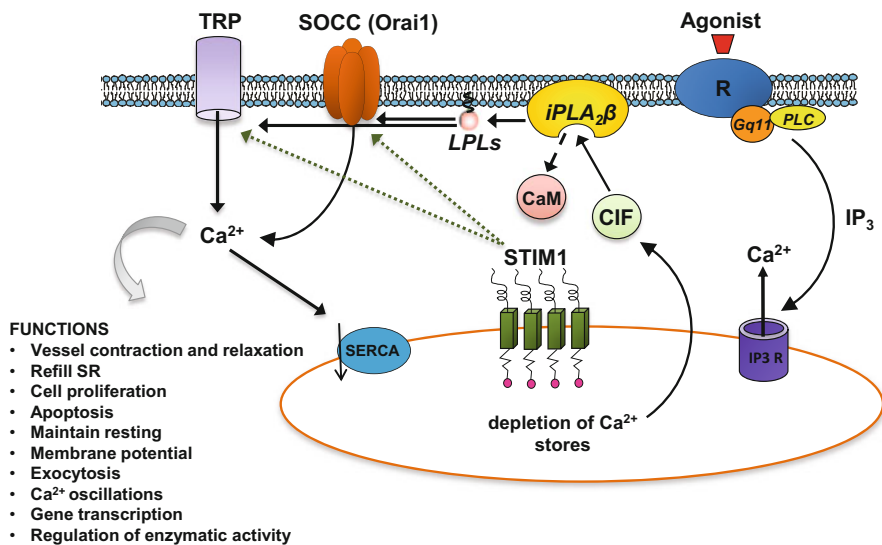


Fig. 6.1 Mechanism suggested for store operated Ca²⁺ entry (SOCE), involving Ca²⁺ independent phospholipase A₂β (*iPLA*₂) pathway. We propose that agonist binding to R, promotes IP₃-induced Ca²⁺ release, activation/translocation of STIM1, Calcium Influx Factor (*CIF*) release, displacement of calmodulin (*CaM*), activation of *iPLA*₂, lysophospholipids (*LPLs*) production, and activation of store-operated Ca²⁺ channels (*SOCC*) (*Orai1*) and other transient receptor potential channels (*TRP*). The subsequent Ca²⁺ entry is responsible for a large number of functions as indicated

activation of single SOCC in SMC, and whole cell CRAC currents in RBL induced by TG and/or BAPTA-induced depletion of intracellular stores. In addition, molecular inhibition using antisense against *iPLA*₂, or its functional blocking with BEL impaired dramatically SOCE, while Ca²⁺ release from the stores was not affected, which confirmed the novel role of *iPLA*₂ in SOCE pathway [78]. Furthermore, the use of S-BEL enantiomer confirmed that *iPLA*₂β is the isoform responsible of SOCE in RBL [76] and SMC [64]. Interestingly, cell dialysis with recombinant *iPLA*₂β could substitute the endogenous *iPLA*₂β and rescue activation of *I*_{CRAC} in the cells in which endogenous *iPLA*₂β was knocked down [76]. One of the most important features of *iPLA*₂ is that it exists in a complex with CaM, which keeps it in a catalytically inactive state; and removal of CaM results in *iPLA*₂ activation [66]. Therefore, the inhibition of CaM was found to mimic the effects of thapsigargin-induced SOCE as it activated *iPLA*₂; it evoked a 2APB and BEL-sensitive Ca²⁺ influx; and finally it stimulated single SOCC in SMC [69]. Similar effect of CaM inhibition was also observed in astrocytes [70] and in rat cerebellar granule [105].

The role of *iPLA*₂β in SOCE was further confirmed by us and by many other investigators in a growing number of cell types, including platelets, Jurkat T lymphocytes [69, 78], RBL-2H3 [104], neuroblastoma/glioma [70], keratinocytes [106], skeletal muscle [107], fibroblasts [108], prostate cancer cells [109] and others. In all these studies molecular knock-down and/or functional inhibition of *iPLA*₂β caused full impairment of SOCE. Strikingly, genetic screening of *Drosophila*

melanogaster performed by Vig et al. indicated that not only STIM1 and Orai1, but also an orthologue of iPLA₂β encoded by the CG6718 gene, are gene products with a great impact on SOCE activation [110]. Recently, we have demonstrated that agonist-induced coronary artery contraction involved the activation of SOCE by STIM1, Orai1 and iPLA₂ [98]. We have shown that on cells stimulation, STIM1 colocalized with iPLA₂β in submembrane compartments suggesting their functional communication and we confirmed that lysophospholipids, product of iPLA₂, stimulated an Orai1- but not STIM1- dependent SOCE, suggesting that the functional role of iPLA₂β is downstream of STIM1 and upstream of Orai1 in coronary SMC. The complex relationships between the components of the CRAC channel, namely Orai1, STIM1, and iPLA₂β in the SOCE pathway have been detailed in a previous review [79].

6.4.3 iPLA₂ and Lysophospholipids Activation of Store Operated Calcium Entry

Afterwards, numerous studies focused on the molecular mechanism of iPLA₂-dependent signal transduction. Several works from Bolotina's lab in the first decade of this century, provided compelling evidences demonstrating that SOCC can be activated by CIF produced upon depletion of Ca²⁺ stores in the ER, and it in turn, can displace the inhibitory CaM from iPLA₂β. The early studies have shown that CIF activated single SOCC in inside-out membrane patches [111], and the channels remained active even after the membrane patches were excised and CIF was washed away [112], indicating the presence of an additional cascade of plasma membrane-delimited reactions that might be involved in CIF-induced activation of SOCC. In 2004, a major finding has been described by Smani et al. demonstrating that CIF extract can displace inhibitory CaM from iPLA₂β leading to lysophospholipids production and the activation of SOCC in membrane-delimited manner in SMC [69]. By contrast, CIF dialysis of RBL cells transfected with antisense to iPLA₂β failed to activate I_{CRAC}, confirming the need of functional iPLA₂β to stimulate SOCE [76]. Furthermore, the exogenous application of lysophospholipids but not AA, products of iPLA₂β activation, were able to stimulate SOCE in intact cells and single SOCC in inside-out membrane patches in SMC [69, 74, 98]. Further studies have confirmed that lysophospholipids evoked SOCE in different cell lines such as astrocyte [70], rat cerebellar granule neurons [105], skeletal muscle [113], and keratinocytes [114], among others cells. Thus, several independent works established the need of active iPLA₂β, and lysophospholipids to stimulate SOCE in a wide range of cells.

However and independently of its role in SOCE signaling, few reports have shown that iPLA₂ might activate some TRP channels. Works from Prevarskaya's lab demonstrated that iPLA₂β activated both SOCC and TRPM8 channels [109, 115], and AL-Shawaf and colleagues showed recently that lysophosphatidylcholine and AA generated by iPLA₂ are involved in TRPC5 activation by sphingosine-1-phosphate [116].

6.5 Significant Potential as Targets for Novel Therapeutics Strategy

The role of $iPLA_2\beta$, and the consequent activation of SOCE in several physio- and pathological processes have been largely studied. For example, $iPLA_2\beta$ -dependent activation of vascular reactivity was demonstrated in aorta, cerebral, mesenteric, carotid and coronary arteries [98, 117, 118]. Furthermore, $iPLA_2\beta$ -induced SOCE seems involved in SMC proliferation [119] and in HEK cells migration [120]. Molecular knockdown of Orai1, STIM1 or $iPLA_2\beta$ caused a similar reduction in velocity and distance in migrating HEK cells. Previously, Vanden Abeele et al. demonstrated that $iPLA_2\beta$ activated SOCE in LNCaP prostate cancer proliferative cells [109], and they further showed that $iPLA_2\beta$ is also implicated in the lysophospholipid-dependent gating of TRPM8, a cold sensor [115]. On the other hand, Boittin and Reugg published several interesting studies highlighting the involvement of $iPLA_2$ -dependent activation of SOCC in dystrophic muscle fibers [109]. They found that $iPLA_2$ is mainly localized in the vicinity of the sarcolemma, suggesting a close proximity with SOCC, which may be located on the sarcolemma and/or in the T-tubular membranes. These authors have also demonstrated that lysophosphatidylcholine acts downstream of $iPLA_2$ and directly activates SOCC in dystrophic fibers [107, 113]. Interestingly, recent studies have determined that $iPLA_2$ can be targeted by secondary signaling pathway to potentiate or inhibit SOCE such as PKC ϵ [64], and Urocortin through cyclic AMP in SMC [98], in skeletal muscle [121], and in hepatoma carcinoma cell lines [122]. These few examples confirm the important role of $iPLA_2$ and SOCE in several physiological and pathological processes and confirm it as a valuable therapeutic target.

Acknowledgments This work was supported by Spanish Ministry of Economy and Competitiveness [BFU2013-45564-C2-1-P and BFU2013-45564-C2-2-P]; Institute of Carlos III and Cardiovascular Network “RIC” [RD12/0042/0041;PI12/00941]; and from the Andalusia Government [PI-0108-2012; P10-CVI-6095]. A.D.R. is supported by ITRIBIS FP-7-REGPOT.

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