

Review

Phospholipase D: a lipid centric review

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Abstract. Phospholipase D (PLD) hydrolyzes the phosphodiester bond of the glycerolipid phosphatidylcholine, resulting in the production of phosphatidic acid and free choline. Phosphatidic acid is widely considered to be the intracellular lipid mediator of many of the biological functions attributed to PLD. However, phosphatidic acid is a tightly regulated lipid in cells and can be converted to other potentially bioactive lipids, including diacylglycerol and lysophosphatidic acid. PLD activities have been described in multiple organisms, including plants, mam-

mals, bacteria and yeast. In mammalian systems, PLD activity regulates the actin cytoskeleton, vesicle trafficking for secretion and endocytosis, and receptor signaling. PLD is in turn regulated by phosphatidylinositol-4,5-bisphosphate, protein kinase C and ADP Ribosylation Factor and Rho family GTPases. This review focuses on the lipid precursors and products of mammalian PLD metabolism, especially phosphatidic acid and the roles this lipid performs in the mediation of the functions of PLD.

Key words. Phospholipase D; phosphatidic acid; diacylglycerol; phosphatidylcholine; signal transduction.

Introduction

Classical phospholipase D (PLD) enzymes hydrolyze phosphatidylcholine (PC) to yield phosphatidic acid (PA) and free choline (see fig. 2). More broadly, PLD performs a transphosphatidylation reaction using water or primary alcohols such as ethanol or 1-butanol as the nucleophile to generate PA, phosphatidylethanol or phosphatidylbutanol (PBut), respectively. Ethanol and 1-butanol are preferentially used over water as the nucleophile by 1000-fold or more [1, 2]. PLD superfamily members are found in organisms ranging from viruses to bacteria, yeast, plants and animals. In mammalian cells, PLD activity is found in most cell types with the exception of leukocytes and a few lymphocyte lines [3, 4, see also 1999 BBA issue 1439]. The following review briefly covers the history of the PLD field and structure, local-

ization, activation and regulation of mammalian PLD1 and PLD2 [reviewed in 2, 5-8], followed by an in-depth discussion of the lipid precursors and products of PLD enzymatic action and the functions of the lipid products, including their actions on downstream targets.

History

A PLD-type activity was first described by Hanahan and Chaikoff in carrot extracts in 1947 [9, 10]. PLD activity was not demonstrated in a mammalian system until 1975, when Saito and Kanfer described a release of choline and ethanolamine from rat brain preparations. Interestingly, the enzymatic activity was found to cleave both PC and phosphatidylethanolamine (PE) [11]. Classical biochemical preparation of the enzyme yielded several activities with varying responses to Ca^{2+} concentrations, detergents, pH, unsaturated fatty acids and phosphatidylinositol-4,5-bisphosphate ($\text{PI}(4,5)\text{P}_2$) [reviewed in 7]. The first

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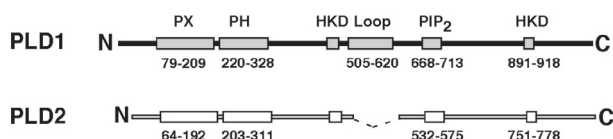


Figure 1. Basic structure of PLD1 and PLD2. Linearized cartoon of structure showing amino (N) and carboxy (C) terminals with conserved domains as boxes. Domains shown are the catalytic HKD motif (HKD), phox consensus sequence (PX), plekstrin homology (PH), phosphatidylinositol biphosphate (PIP₂) and PLD1 loop region.

purified PLD enzymes were independently isolated from cabbage [12] and castor bean [13]. The purification of the two plant PLD enzymes led to the cloning of PLD α from the castor bean [14], followed by rice, maize, tomato and others [15–17].

SPO14, a yeast sporulation mutant identified through a screen of mutated strains that were defective in meiosis, was found to have sequence similarity to plant PLD α and to exhibit PLD activity [18–20]. This protein was activated by PI4,5P₂ [18] similar to a reported mammalian activity [21], but unlike the mammalian activity was unresponsive to ADP Ribosylation Factor (ARF) [22]. Cloning of *SPO14* facilitated the subsequent cloning of a mammalian 120-kDa protein designated as PLD1 [23] that was stimulated by PI4,5P₂ and GTP γ S-loaded ARF [23]. A splice variant, still of unknown biological significance, was subsequently found, necessitating the designation of the original enzyme as PLD1a and the splice variant as PLD1b [24, 25]. Both enzymes were similarly activated by protein kinase C (PKC), Rho GTPases and ARF GTPases [24–26]. A second mammalian PLD enzyme was discovered and designated as PLD2 [26–28]. Initial characterization of PLD2 revealed that it exhibited a significantly higher basal activity and was not activated by ARF or Rho GTPases. However, PLD2 did require PI4,5P₂ [27]. PLD1 and PLD2 comprise the classical mammalian PLD enzyme family.

Mammalian PLD structure

The defining feature of PLD enzymes is the catalytic motif designated HKD, denoting the HxxxxKxD sequence, where the amino acids are histidine (H), any amino acid (x), lysine (K) and aspartic acid (D). Mammalian PLD1 and PLD2 both contain two HKD motifs, which are critical for enzymatic catalysis both in vitro and in vivo, as evidenced by the observation that point mutations in the motif disrupt PLD activity [29]. The mechanism of PC catalysis will be discussed later in this review.

Other highly conserved regions of the PLD genes are the phox consensus sequence (PX), the plekstrin homology (PH) domain and the PI4,5P₂ binding site (fig. 1). The PH domain is thought to function in the localization of the protein, as either careful deletion or point mutation causes mislocalization of the proteins [30, 31]. More recently,

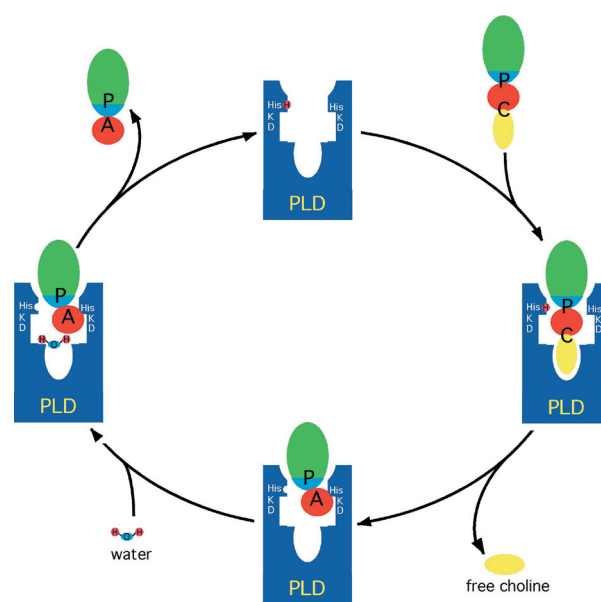


Figure 2. Cartoon of PLD hydrolysis of phosphatidylcholine (PC) to phosphatidic acid (PA) and choline. Shown in white are the essential amino acids of the two PLD catalytic domains: histidine (His), lysine (K) and aspartic acid (D). The steps of the process are summarized. Top center, open configuration with hydrogen (H) bound to amino-terminal histidine. Top right, PC enters PLD active pocket. Right center, PC in the active pocket. Bottom right, release of free choline. Bottom center, PA-PLD intermediate with PA bound to the carboxy-terminal histidine. Bottom left, water enters the active pocket. Left center, PA-PLD intermediate with water as the nucleophile in the active pocket. Left top, release of PA and regeneration of open state with bound hydrogen. Mechanism discussed in more detail in the text, and the lipids are color-coded to their structures in Figure 3.

the PH domain was demonstrated to mediate the PLD1 association with lipid rafts to facilitate an early step in the recovery of the enzyme to endosomes after stimulated translocation to the plasma membrane [32]. However, deletion of the PH domain demonstrated it is not required for enzymatic activity and furthermore did not alter the dependence on PI4,5P₂ for catalysis [33, 34]. This finding led to the discovery of the PI4,5P₂ binding motif [30, 32, 35]. The PX domain is thought to mediate protein-protein interactions or to bind phosphatidylinositol phosphates (PIP) [reviewed in 36]. Recently, the PLD PX domain was described to bind preferentially to phosphatidylinositol trisphosphate (PI3,4,5P₃), in comparison with other PIP species, including PI5P, as determined by a surface plasmon resonance assay [37]. In contrast, PX was determined to bind PI5P preferentially in a liposome binding assay, and the domain binding of PI5P, a lipid required for endocytosis, has been proposed to facilitate internalization of PLD1 from the plasma membrane [32]. Finally, PLD1 has a conserved loop region that is not found in PLD2. The loop region has been proposed to function as a possible negative regulatory element, as deletion of this region from PLD1 increased its basal activity threefold [33].

Overview of PLD localization

Study of the subcellular localization of PLD1 and PLD2 has yielded varying descriptions. Reports on PLD1 in numerous cell lines have described perinuclear localization suggestive of a Golgi, endoplasmic reticulum or late endosomal distribution [27, 33, 38, 39]. A contrasting report described PLD1 localizing to only the late endosomes and lysosomes [40]. Recently, PLD1 localized to the sorting/recycling endosomes and early endosomes with some PLD1 in the Golgi [32]. However, several groups have not found Golgi localization [40, 41]. PLD1 has also been localized to the plasma membrane in unstimulated cells [42]. Several papers now report that upon stimulation, PLD1 translocates to the plasma membrane [32, 43, 44]. With the emerging concept of dynamic cycling of PLD1 inside the cell, some of the varying reports of localization may be due to differential rates and number of vesicles cycling in the cell lines used and thus differential regulation of PLD1 localization.

PLD2 is most often reported to localize to the plasma membrane [27, 45, 46], but has also been localized to the cytosol [45], submembraneous vesicular compartments [47] and co-localized with β -actin [48]. PLD2 has been described as translocating to membrane ruffles in response to serum [27] and epidermal growth factor (EGF) [45].

Intracellular regulators of PLD

Mammalian PLD activity is regulated by many factors, including phosphoinositides, PKC, ARF and Rho GTPases and non-PKC protein phosphorylation. Each of these regulators will be briefly discussed [reviewed in 2, 7, 49, 50].

Phosphoinositides are lipids related by the base molecule of phosphatidylinositol (PI). PI can be phosphorylated to form PIPs, PIP₂s and PIP₃. As mentioned above, mammalian PLDs have a PI₄,5P₂ binding domain. PLD activities from HL60 cellular extracts are stimulated by PI₄,5P₂ [21, 51], and both PLD1 and PLD2 enzymatic activities are dependent upon PI₄,5P₂ [23, 25, 27, 28, 52]. PIP₃ activates PLD with similar potency to PI₄,5P₂, but with lessened efficacy [25]. Clearly, the phosphoinositides are important mediators of PLD activation and regulation.

PLD activation has long been observed in response to PKC activating factors such as calcium ionophores and phorbol esters such as phorbol 12-myristate-13-acetate (PMA), which is a stable analogue of diacylglycerol (DAG). The PKC regulation of PLD activation is very intertwined and complex due to the large variety of PKC enzymes that may regulate PLD [reviewed in 7]. A few basic points on the interactions between PKC and PLD are presented. Much of the regulation of PLD by the classical PKCs was thought to involve the direct phosphorylation of PLD [reviewed in 53]. In support of this

model, studies employing downregulation of PKC by chronic PMA treatment rendered PLD unresponsive to activation [5, 54]. However, the classical PKCs also effect PLD activation independent of their kinase activity [25, 55, 56], and the activation may be mediated by the N-terminal portion of PLD [57]. PKC inhibitors, such as staurosporine and calphostin C, block PLD activation [58 61]. Care must be taken though, as more recent studies have shown that calphostin C has a direct inhibitory effect on PLD independent of its inhibition of PKC [62]. Some studies suggested the inhibition of PLD via PKC δ , thus antagonizing activation by PKC α [63]. Overall, the regulation of PLD by PKC appears most likely to involve direct interaction, phosphorylation and possibly other indirect mechanisms.

ARF was initially identified as an activator of a PLD activity extracted from HL60 cells [21, 51]. ARF directly activates PLD1 [23] and can activate PLD2 [28, 34]. However, in vitro assays have identified accessory factors, including guanine nucleotide exchange factors [reviewed in 64] and have indicated indirect regulatory pathways [65, 66]. Use of the ARF inhibitor Brefeldin A and expression of dominant negative ARF1 or ARF6 blocked stimulation of PLD by various means [67 69]. Evidence for the role of ARF in PLD activation is most strong in vesicular transport [reviewed in 70].

Rho GTPases such as RhoA, Cdc42Hs and Rac1 activate PLD in many cell types and tissues [71 74]. In the presence of GTP γ S, these Rho proteins interact directly with purified PLD1 [25, 75, 76]. Pretreatment of *Clostridium botulinum* C3 toxin or *Clostridium difficile* toxins, all of which inactivate Rho proteins, blocks PLD activation [77 81]. Mutation of the Rho binding site on PLD1 [82, 83] demonstrated direct binding of RhoA and PLD1, and defined possible in vivo roles for the interaction [84]. However, the myriad possibilities of indirect Rho activation of PLD complicates the study of PLD as a downstream effector of Rho proteins.

PLD is likely to be regulated by protein phosphorylation beyond that mentioned for PKC kinase activity. Several studies using protein kinase inhibitors have implicated both receptor and non receptor tyrosine kinases in this regulation, along with serine/threonine kinases, calcium calmodulin dependent protein kinase and cyclic AMP (cAMP) kinases [85 88]. The role for phosphorylation of PLD by the above kinases remains poorly defined, but is likely to be involved either directly or indirectly in PLD function.

PLD as a lipid-modifying enzyme

Mammalian phospholipase D enzymatic action produces PA (fig. 2), which is a bioactive lipid. In contrast, free choline is not thought to fulfill any intracellular signal-

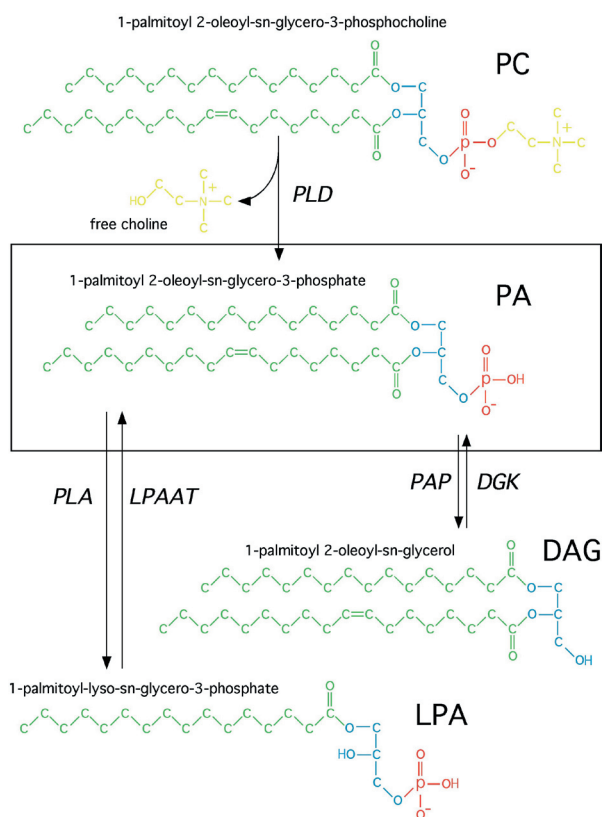


Figure 3. Generation of (16:0/18:1) phosphatidic acid (PA) from (16:0/18:1) phosphatidylcholine (PC) and interconversion of PA to (16:0/18:1) diacylglycerol (DAG) and (16:0) lyso-phosphatidic acid (LPA). Enzymes abbreviated are phospholipase D (PLD), phosphatidic acid phosphohydrolase (PAP), diacylglycerol kinase (DGK), phospholipase A (PLA) and lyso-phosphatidic acid acyltransferase (LPAAT). Fatty acid acyl chains are in green, glycerol backbone in blue, phosphate in red and choline in yellow.

ing roles [89]. The *in vivo* nucleophile is water, which attacks the diester phosphate group of PC. Both HKD motifs of PLD are needed for the enzymatic action of hydrolysis [29]. The current model of PC catalysis is a two-step mechanism based upon the crystallization of a bacterial endonuclease, which has a divergent HKD motif [90–92]. Initially, the amino-terminal HKD motif is proposed to be protonated on the histidine. Subsequently, PC enters the active pocket of PLD containing both HKD motifs. Next, free choline is released by liberation of the amino-terminal proton, and a PLD-PA intermediate is thought to be formed with the histidine of the carboxy-terminal HKD domain. Finally, the amino histidine re-acquires a proton from a water molecule, leaving the hydroxyl group to attack the PLD-PA intermediate and release PA [29, 90]. The use of ethanol or 1-butanol allows for a cumulative measurement of PLD activity, as the non-endogenous PBut or phosphatidylethanol thus formed are relatively stable lipids [93].

Structure of PA

PA is composed of three distinct parts (fig. 3). The basis of the molecule is the three-carbon glycerol backbone. The hydroxy groups of carbons 1 and 2 are ester-linked to fatty acids forming the non-polar acyl chains of the lipid. The fatty acids can vary in length (14–22 carbons long endogenously) [94] and the number of double bonds present in the carbon chain (saturation). The terminal carbon 3 is ester-linked to a phosphate group forming the small, negatively charged polar headgroup of PA. PC has the addition of an ester-linked choline to the phosphate headgroup of PA, thus forming the large polar headgroup of this lipid.

Further conversion of PA

The PLD-produced PA can be converted into DAG by the family of enzymes known as phosphatidic acid phosphohydrolases (PAPs) [95–97], which are highly active *in vivo*. As discussed in more detail below, activation of PLD results in the increase of both PA and DAG. The DAG produced can be reconverted to PA via phosphorylation by diacylglycerol kinases (DGKs). The regulation of PA and DAG levels appears to be tightly controlled via the activities of PAP and DGK. Furthermore, PA can be deacylated by a phospholipase A (PLA) activity to form lysoPA (LPA), a monoacylated form of PA [97], and subsequently reconverted to PA by lysophosphatidic acid acyltransferases (LPAAT). Figure 3 summarizes the above lipid conversion pathways and details the lipid structures of PC, PA, DAG and LPA.

PLD substrate specificity

The initial mammalian PLD activity described was reported to use both PC and PE as *in vitro* substrates [11]. In the first report on the cloned and purified recombinant isoforms, reactivity against PC but not PE was observed [23]. More recently, PLD-enriched lysates were reported to exhibit robust activity on PC, marginal activity on PE and no activity on phosphatidylinositol, although since the PLD was not purified, it is not clear whether the minor PE-hydrolyzing activity was directly mediated by the classical PLD isoforms [94]. However, several early papers, especially Pai et al., clearly demonstrated PLD enzymatic activity on PC *in vivo*, solidifying PC as the natural substrate [98–102], and subsequent work using the recombinant PLD1 and PLD2 proteins has confirmed this [94].

These early papers also partially defined the species of PC acted upon by PLD *in vivo* in terms of their fatty acid composition, mostly through the study of the PA and DAG produced. Cockcroft and Allan [103] described a rapid increase in PA, followed by an increase in DAG in response to cytochalasin and formylmethionyl-leucyl-

phenylalanine (now thought to activate PLD) treatment of neutrophils. Analysis of the fatty acid composition of the PA and DAG revealed a composition mainly of palmitate (16 carbons long with no double bonds, 16:0), stearate (18:0) and oleate (18:1). In contrast, the PI fatty acid composition of stearate (18:0) and arachidonate (20 carbons long with four double bonds 20:4) indicates that the PA and DAG produced were not likely to be from cleavage of PI [103]. In response to phorbol diesters, Besterman et al. [101] showed a rapid production of DAG and PA (15–80 s) that had fatty acid compositions resembling that of endogenous PC. Although not mentioned, the responsible enzyme activated by the phorbol diester, perhaps through PKC, is presumed to be PLD [101]. Subsequently, vasopressin was found to rapidly (2–5 min.) produce PA and DAG in a PLD-dependent manner. Analysis of the PA and DAG produced indicated that the fatty acid composition of these lipids was stearate, (18:0) and arachidonate (20:4) [100].

The most recent and comprehensive studies on PLD hydrolyzed and produced lipids, including PBut, which is exclusively formed by PLD, have clearly defined the fatty acid composition of these lipids [94, 104]. Stimulation of Swiss 3T3 cells by bombesin or LPA resulted in PA and PBut with acyl chains that are predominantly saturated or monounsaturated. In this case, the acyl chains that were derived from PLD activation were palmitate (16:0), stearate (18:0) and oleate (18:1) [104]. In addition, the DAG produced by PAP dephosphorylation of PA is different from polyunsaturated DAG produced via phospholipase C cleavage of PI4,5P₂ [104]. PLD was shown to hydrolyze all forms of PC in both in vitro and in vivo assays [94]. The in vitro specificity of PLD hydrolysis of egg PC was preferential to species of 16:0/18:2, 16:0/18:1 and 18:0/18:2 or 18:1/18:1. However, the in vivo specificity for PC was limited to mainly monounsaturated or saturated acyl chains (16:0/18:1, 18:0/18:1 and 18:1/18:1 or 18:0/18:2) and was determined by analysis of the PBut formed. The diacyl profile of PBut formed was comparable to that of endogenous PC [94]. Interestingly, endogenous PA levels were not significantly altered with incubation of 1-butanol, indicating that a majority of cellular PA is not derived from PLD action; however, the speciation of this PA was similar to that of PA produced via PLD [94]. Overall, PLD seems to hydrolyze PC with either monounsaturated and/or saturated acyl chains, forming PA of the same diacyl composition.

PA as mediator of PLD function

The PA generated via PLD activity can play multiple roles in cellular function. PA can function in signal transduction events, such as activation of a phosphoinositide kinase, or as a lipid-binding partner to several proteins,

thus effecting protein recruitment. PA can also be an intermediate for the production of bioactive DAG or LPA via the mechanisms previously discussed. Finally, PA production has been shown to be important in vesicle trafficking, endocytosis and secretion. The role for PA in these processes is likely to be a combination of such activities as second messenger, lipid anchor and possibly fusogenic lipid. The following sections will focus upon these cellular functions.

PA in signal transduction

PA has been linked to many events of intracellular signal transduction through the wide use of 1-butanol as an inhibitor of PA accumulation via PLD. These pathways of activation include signaling through PI4P 5-kinase, activation of mammalian target of rapamycin (mTOR), and direct binding with Raf kinase, among other proteins.

The stimulation of type I PI4P 5-kinase, to produce PI4,5P₂ from PI4P, has emerged as a key downstream effect of PA generation via PLD. PA, but no other phospholipid tested including LPA, was initially found to activate PI4P 5-kinase in an in vitro assay of enzyme purified from bovine brain [105]. Further purification and in vitro assays revealed that PA stimulated only type I, but not type II PI4P 5-kinase [106]. Subsequent cloning of a third isoform of a type I PI4P 5-kinase confirmed the aforementioned activation of the enzyme by PA and linked the function to actin polymerization in vivo [107], in which PLD has been suggested to play a role [108]. The activation of PI4P 5-kinase in membrane ruffling mediated by EGF was described to proceed via activation and translocation of PLD2 to the ruffles resulting in PA production in the ruffles, where the PI4P 5-kinase α is also localized [45]. LPA treatment of porcine aortic endothelial cells caused activation of type I PI4P 5-kinase α that was determined to be dependent upon PLD production of PA [109]. In this paper, the authors showed that PA with mixed diacyl chain speciation from egg yolk extracts stimulated kinase activity. Furthermore, a dioctanoyl (8:0) PA had similar efficacy in stimulating PI4P 5-kinase [109]. The specificity of what type of PA can or cannot activate PI4P 5-kinase is still to be determined. The early findings probably used mixed acyl chain PA extracted from various sources. However, the comparable efficacy of the dioctanoyl PA does indicate that the length of the acyl chains need not be in the endogenous range of 14–22 carbons long [94].

PLD has been implicated in survival pathways that prevent apoptosis [110–113 among others]. As an effector of cell cycle progression and cell proliferation, mTOR represents an attractive downstream effector of PLD's potential anti-apoptotic function. HEK293 cells transiently increased PA in response to serum stimulation, resulting in activation of mTOR and its downstream acti-

vation of S6 kinase1 (S6K1), whose blockage by 1-butanol implicates PLD involvement [114]. Furthermore, PA was found to directly interact with mTOR at the FK506 binding protein 12-rapamycin-binding domain of mTOR via in vitro binding assays [114, 115]. The binding was specific for PA among several phospholipids (PC, PS, PE, PI and PIPs) tested. Pretreatment with rapamycin, an inhibitor of mTOR, blocked PA interaction with mTOR, thus demonstrating competitive binding [114]. Overexpression of PLD2 was found to confer resistance to rapamycin blockage of cell proliferation, further involving PLD in mTOR regulation [116]. Lipopolysaccharide (LPS) stimulation caused an increase in PA, and this increase was determined to play a role in cytokine release through activation of mTOR. The cytokine release was potentiated by addition of propranolol (inhibitor of PAP) and blocked by 1-butanol, implicating PLD. The authors proposed PLD2 as the relevant enzyme, due to its high expression level as determined by Western blotting [117]. However, Fang et al. (2003) demonstrated in HEK293 cells that PLD1 was the enzyme responsible for mTOR signaling and suggested that Cdc42 is upstream of PLD1. Overexpression of the wild-type PLD1 increased S6K1 activity in response to serum stimulation, while overexpression of the catalytically inactive PLD1 decreased activity compared with control cells. In addition, the use of small interfering RNA (siRNA) against PLD1 in two different cell lines almost completely inhibited S6K1 activity in response to serum stimulation [118]. More recent work has agreed with PLD1 being the enzyme responsible for mTOR activation [119, 120]. Overall, mTOR is emerging as a well-defined target of PA produced by PLD1, and this effect has been determined to be parallel to the phosphoinositide 3-kinase survival pathway [114, 118–121].

In spite of the importance of PA in the mediation of various signaling events, the direct targets of PA remain elusive. A few proteins, including mTOR, which bind PA directly have been described. PA bound to agarose beads was found to pull down ARF, N-ethylmaleimide-sensitive factor and kinesin [122]. One of the first proteins to emerge as a well-defined PA binding protein was Raf-1 kinase [123, 124], and this protein was shown to translocate to PA-enriched membranes [125, 126]. Dioleoyl PA (18:1/18:1) was determined to interact directly with the protein via an in vitro assay using both phospholipids and sphingolipids such as PC, PS, PI, sphingosine and ceramide; however, cardiolipin also bound the protein. The carboxyl terminus of Raf-1 kinase was determined to contain a 35-amino acid segment that bound PA [125], and mutation of a conserved basic amino acid, arginine 398 to alanine, in this region reduced the PA binding. Also, fusion of the binding region to green fluorescent protein (GFP) was sufficient to translocate the recombinant protein to membranes [124]. Finally, a specific

tetrapeptide motif was defined for the binding of PA to Raf-1 kinase [123]. Protein phosphatase-1 γ (PP1 γ) has emerged as a direct target for inhibition by PA [127]. Phosphatase activity of this protein was inhibited by PA, but no effect was found for DAG, PBut, LPA and phosphatidylethanol. Binding of the catalytic subunit of PP1 γ was specific for PA since PS, PI, PC, PE and LPA, among other phospholipids, did not bind. The diacyl composition of PA needed for inhibition was not dependent upon the saturation of the fatty acyl chains [127]. A microdomain in the N-terminal region of PDE4A1 cAMP-specific phosphodiesterase bound PA, but not PC, PS, PIP or PIP₂ in an in vitro assay. TAPAS-1 (tryptophan anchoring phosphatidic acid selective binding domain 1) was defined in this amino-terminal microdomain and shown to provide the membrane association through PA for this phosphodiesterase [128]. Sphingosine kinase1 (SK1) also binds PA, and this direct interaction is needed for its translocation. SK1 is also proposed as an intracellular effector of PA [129].

PA as a lipid precursor

The conversion of PA by PAP produces DAG, which has long been studied as a lipid second messenger. PAP2b, a PAP isoform, co-localizes to PLD2-enriched membrane domains, thus possibly contributing to a rapid turnover of PLD-produced PA to DAG [95]. DAG has been repeatedly shown to activate the classical and most novel PKC families [reviewed in 130, 131]. The conversion of PA by PAP results in DAG species whose diacyl composition is primarily of the monounsaturated and/or saturated species as discussed in detail above [94, 104]. Significantly, the more saturated forms of DAG have been suggested to not activate PKC in vivo [104, 132]. Therefore, the possible role for these saturated DAGs produced from PA remains to be determined. Conversely, the production of DAG from PLD-derived PA may ultimately be a way to attenuate the PA signal.

PA can also be converted to mono-acylated LPA by phospholipase A activity [97]. LPA is a potent mitogen that performs key roles in cell proliferation, migration and survival [reviewed in 133]. The production of LPA from PLD-produced PA has not yet been fully demonstrated or intensively studied. The specific function of a monounsaturated or saturated acyl species of LPA produced from PLD PA is potentially an interesting question.

PA in vesicle trafficking, secretion and endocytosis

PLD and its enzymatic product PA have been linked to vesicular traffic, secretion and endocytosis [reviewed in 6]. PLD is associated with Golgi vesicle formation through its activation by ARF. The use of primary alcohols including ethanol blocked protein transport from the

endoplasmic reticulum to Golgi, and the block was alleviated by exogenous liposomes containing PA [6, 134, 135]. PA recruitment of proteins has been suggested in the formation of secretory vesicles from the trans-Golgi network [136]. However, the role for PLD in vesicle formation is unclear to date, and the localization of PLD to the Golgi remains debated, as mentioned in the cellular localization section.

In contrast, the role of PLD in secretion and secretory vesicle formation is much more established. PLD plays a role in exocytosis [137–140] in an ARF-dependent manner [141, 142]. The role for PLD in secretion has been studied mainly in neuroendocrine cells [66, 136, 143, 144], but has also been studied in adipocytes [44, 145], pancreatic β cells [146] and mast cells [43, 147, 148]. In neuroendocrine cells ARF6 has been specifically demonstrated to act through PLD1 in a $PI4,5P_2$ -dependent manner in the exocytic process [143, 149]. Recently, the PH domain of PLD1 was shown to be required for regulated exocytosis of neuroendocrine cells [46]. The inhibition of PLD has also been implicated in the sphingosine 1-phosphate-induced secretion of interleukin-8 from human bronchial epithelial cells [150].

PLD2 has recently emerged as an enzymatic mediator of receptor internalization via endocytosis. Initially, epidermal growth factor receptor (EGFR) internalization was found to be blocked by treatment with 1-butanol, and EGF binding to the receptor was determined to increase PA. These findings implicated PLD in this process. The internalization increased with overexpression of either PLD1 or PLD2 and decreased by overexpression of their catalytically inactive forms [151]. Examination of the μ -opioid receptor MOR1 uncovered a functional association between this receptor and PLD2. The authors showed that one receptor agonist that causes internalization activated PLD2, while one that does not cause internalization did not activate PLD2. Furthermore, the internalization was ARF-dependent [152]. Internalization of MOR1 was inhibited by either 1-butanol or overexpression of the catalytically inactive PLD2, thus defining the role of PLD2 in receptor internalization [152, 153]. In addition, both 1-butanol and siRNA against PLD2 blocked metabotropic glutamate receptor endocytosis [154]. Overexpression of the catalytically inactive PLD2 and siRNA against PLD2 individually blocked angiotensin II receptor internalization [46]. Overall, receptor endocytosis appears to be a function for PLD2 in cells.

PA derived from PLD hydrolysis of PC has many functions which probably contribute to vesicle trafficking in cells. PA can act as a lipid anchor and recruiter for proteins, activate $PI4P$ 5-kinase to form $PI4,5P_2$ and possibly undertake a biophysical role as a fusogenic lipid (fig. 4). $PI4,5P_2$, generated via PA activation of $PI4P$ 5-kinase, recruits CAPS, thus enabling exocytosis of dense core vesicles [155, 156]. Furthermore, the role for PLD in fu-

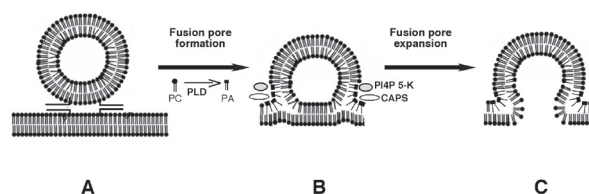


Figure 4. Vesicle fusion to a membrane. (A) Vesicle attached to the membrane. During fusion pore formation PLD is proposed to convert PC to PA. (B) Formation of a pore between the vesicle and membrane. At this point, PA is proposed to lower the energy of activation for the curvature of the inner membrane. In turn, PA may activate $PI4P$ 5-Kinase ($PI4P$ 5-K), increasing the membrane levels of $PI4,5P_2$ and thus recruiting CAPS. (C) Fully formed pore between vesicle and membrane.

sion is compelling since it cleaves a non-fusogenic lipid, PC, to form a fusogenic lipid, PA. Due to its small head-group and two fatty acyl chains, PA is thought to lower the activation energy required for negative curvature at the inward membrane curve [157]. PA can be further converted into two other fusogenic lipids, DAG [158] and LPA. LPA is thought to promote the opposite membrane curvature of PA [159]. The LPAAT enzyme, endophilin, has been reported to convert LPA to PA and is known to promote endocytosis [reviewed in 160]. In vitro reconstitution studies showed that the addition of PA to vesicles increases their rate of fusion [161]. Inhibition of PLD1 resulted in a lessening of the exposure of a glucose transporter on the external leaflet of the plasma membrane, but did not block the vesicle trafficking to the membrane. These findings indicate a possible block in fusion due to lack of PA generation [44]. Clearly, PLD-generated PA and its further metabolites such as LPA may function in both fusion with membranes and fission of vesicles from membranes.

Discussion

The study of mammalian PLD was significantly moved forward with the cloning of PLD1 and PLD2. This key event has led to the determination of many functional motifs and domains for PLD1 and PLD2. A great deal has been learned about the regulation of PLD enzymes from studies of these domains and has led to a further understanding of PLD enzymes and their possible *in vivo* roles. The ability of PLD to perform a transphosphatidylation reaction *in vivo* has caused the finding of a plethora of cellular stimuli which activate PLD. Unfortunately, this method does not determine which PLD isoform is activated, or whether the activation is sufficient or necessary for the given response to the various stimuli tested. However, the use of other experimental techniques has demonstrated a requirement for PLD activation in many cellular responses, such as signal transduction including

activation of PI4P 5-kinase, activation of mTOR for survival and a role in extracellular calcium entry into cells [162, 163]. PLD also has roles in vesicle formation and fusion in both endocytosis and secretion, cellular differentiation and proliferation. The study of PLD will be furthered with future development of specific inhibitors and a knockout mouse model. With several PLDs identified in mammalian cells and some unidentified PLD activities, discernment of the exact enzyme involved in a particular function has proven to be tricky. This problem is being overcome by the overexpression of catalytically active and inactive forms of the specific PLD enzymes *in vivo*. Furthermore, the rapid development of siRNA is leading to finer differentiation between the functions of PLD1 and PLD2, and may eventually lead to techniques to discern the relevance of PLD splice variants in a given cellular response. More careful study of PLD1 and PLD2 location and translocation is defining the subcellular compartments where these enzymes perform their functions and thus is contributing to a better understanding of their roles. Overall, the study of PLD is becoming much more focused on the specific PLD enzyme involved and subcellular location of action.

In contrast to the number of systems in which PLD is activated are the limited number of direct targets and direct functions for PA. Research is currently focusing on proteins that directly interact with PA, and this interaction can serve at least two functions: (i) regulation of enzymatic activities, and (ii) recruitment of proteins to specialized membranes. Also, theoretical models suggest that PA may play a biophysical role in mediating PLD functions such as fusion. The current and future development of PA sensors such as TAPAS1 and the yeast Opi1p [164] will help define where PA levels are changing in cells. These data will be compared to localization of PLD to better understand the coordination between enzyme, product and target. Additionally, the use of improved lipid measurements, such as tandem mass spectrometry, will allow for the discernment of increases in the molecular species of PA in a given situation, which will provide clues as to whether the PA is generated from diacylglycerol kinase activity on polyunsaturated PA or PLD cleavage of monounsaturated or saturated PC. Also, with the improved sensitivity of mass spectrometry analysis, one can potentially isolate defined subcellular compartments and measure PA levels and species therein. The further study of PA will lead to a more complete understanding of PLD.

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