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## Patatin-like phospholipases in microbial infections with emerging roles in fatty acid metabolism and immune regulation by Apicomplexa

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### Summary

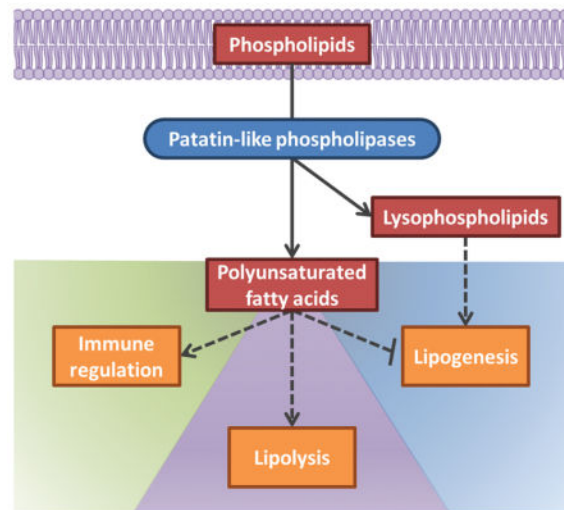
Emerging lipidomic technologies have enabled researchers to dissect the complex roles of phospholipases in lipid metabolism, cellular signaling, and immune regulation. Host phospholipase products are involved in stimulating and resolving the inflammatory response to pathogens. While many pathogen-derived phospholipases also manipulate the immune response, they have recently been shown to be involved in lipid remodeling and scavenging during replication. Animal and plant hosts as well as many pathogens contain a family of patatin-like phospholipases, which have been shown to have phospholipase A<sub>2</sub> activity. Proteins containing patatin-like phospholipase domains have been identified in protozoan parasites within the Apicomplexa phylum. These parasites are the causative agents of some of the most widespread human disease. Malaria, caused by *Plasmodium* spp., kills nearly half a million people worldwide each year. *Toxoplasma* and *Cryptosporidium* infect millions of people each year with lethal consequences in immunocompromised populations. Parasite-derived patatins are likely effective drug targets and progress in the tools available to the Apicomplexan field will allow for a closer look at the interplay of lipid metabolism and immune regulation during host infection.

### Abbreviated Summary

Animal and plant hosts as well as many pathogens contain a family of patatin-like phospholipases, which have been shown to have phospholipase A<sub>2</sub> activity. Proteins containing patatin-like phospholipase domains have been identified in protozoan parasites within the Apicomplexa phylum. Parasite-derived patatins are likely effective drug targets and progress in the tools available for Apicomplexa will allow for a closer look at the interplay of lipid metabolism and immune regulation during host infection.

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## Keywords

*Apicomplexa; Toxoplasma; Plasmodium; Cryptosporidium; Patatin-like phospholipases*

## Introduction

The phospholipase A<sub>2</sub> (PLA<sub>2</sub>) superfamily contains a wide range of enzymes that cleave the *sn*-2 ester bond of phospholipids to release free fatty acids and lysophospholipids (Burke & Dennis, 2009). However, there is great diversity among this family of enzymes (Six & Dennis, 2000). The most common groups of human PLA<sub>2</sub>s are secreted PLA<sub>2</sub> (sPLA<sub>2</sub>), calcium-independent PLA<sub>2</sub> (iPLA<sub>2</sub>), cytosolic PLA<sub>2</sub> (cPLA<sub>2</sub>), and patatin-like PLA<sub>2</sub> (PLP). The sPLA<sub>2</sub>s are the most extensive group of PLA<sub>2</sub>s and play a variety of roles in the inflammatory properties of venoms, digestion of dietary phospholipids, production of eicosanoids, and signal transduction in the inflammatory response (Lambeau & Gelb, 2008). iPLA<sub>2</sub> enzymes are important in phospholipid remodeling and homeostasis as well as signal transduction in many cell types (Winstead *et al.*, 2000). cPLA<sub>2</sub> enzymes have a high specificity for arachidonic acid (AA) at the *sn*-2 position of its substrate phospholipid (Kramer & Sharp, 1997). PLP enzymes were first described as lipid acyl hydrolases involved in potato tuber storage (Senda *et al.*, 1996; Shewry, 2003). In many plants, PLPs are induced by infection to help control the spread of disease, whereas in mammals, PLPs are mostly used in lipid metabolism and turnover.

Lipoxygenases (LOX) are a family of iron-binding enzymes that catalyze the dioxygenation of polyunsaturated fatty acids (PUFA), primarily AA, released from lipids by PLA<sub>2</sub>s. Cyclooxygenases (COX) catalyze the *bis*-dioxygenation and subsequent reduction of PUFAs (Rouzer & Marnett, 2008). In mammals, the products of LOX and COX are eicosanoids, which can help regulate immune responses via both pro-inflammatory and anti-inflammatory activities (Tam, 2013). Eicosanoids are transported from the cell via the multidrug resistance-associated protein family of ATP-dependent efflux transporters, which export compounds conjugated to anionic molecules (Gao *et al.*, 1998). Once these

eicosanoids are transported out of the cell, they can bind their specific lipoxin or leukotriene receptors to activate various signaling cascades resulting in a range of downstream effects on both the inflammatory response and cell proliferation (Wang & DuBois, 2010).

The enzyme cascades that produce eicosanoids have been increasingly studied in the context of infection. Both host and pathogens produce the enzymes involved in these pathways to regulate metabolism and the inflammatory response. Most studies of PLA<sub>2</sub>s focus on either their role in lipid metabolism or on the downstream production of eicosanoids. In this review, we will show the connection between the two pathways (Fig. 1), with a focus on pathogen-derived enzymes during host infection. We will also discuss a family of apicomplexan-derived PLPs, which have been largely uncharacterized at the time of this review.

### Patatin-like phospholipases in lipid hydrolysis

Humans have 9 PLPs, annotated in mammals as PNPLA, within the broader lipase family. All of the PNPLAs have a catalytic serine lipase motif G-X-S-X-G, a serine-aspartate dyad, and a glycine-rich oxyanion hole. While all studied members have shown acyl-hydrolase activity, several have lacked significant phospholipase activity under the conditions tested *in vitro*. The mammalian PNPLAs have diverse and often specialized functions, but most are involved in lipid metabolism and turnover (diagram in Fig. 2). PNPLA2, or adipose triglyceride lipase (ATGL), is the rate-determining enzyme in triglyceride lipolysis (Kienesberger *et al.*, 2008; Qiao *et al.*, 2011). ATGL expression is upregulated by fasting glucocorticoids and downregulated by feeding and insulin (Villena *et al.*, 2004; Lake *et al.*, 2005; Kershaw *et al.*, 2006). However, PNPLA3 and PNPLA5 show the opposite pattern, reminiscent of genes involved in lipogenesis, such as FAS (Baulande *et al.*, 2001; Liu *et al.*, 2017). The insulin-dependent activation of PNPLA3 is mediated by the sterol regulatory element-binding protein (SREBP) transcription factors to promote triglyceride synthesis (Kim *et al.*, 2016). ATGL, PNPLA3, and PNPLA5 contain two distinct C-terminal lipid droplet targeting motifs responsible for their recruitment to lipid droplets (Murugesan *et al.*, 2013). PNPLA8 is also regulated by the SREBP family, but PNPLA8 associates with mitochondria and peroxisomes and has both PLA<sub>1</sub> and PLA<sub>2</sub> activity. PNPLA8 activation induces lipid droplet mobilization through autophagy to provide the cell with new lipids faster and with less energy consumption than uptake or *de novo* synthesis (Kim *et al.*, 2016). The fatty acids released by lipid hydrolysis can provide twice as much ATP as carbohydrates relative to their mass and are important in energy storage, especially in adipose tissue. Fatty acids are catabolized by the fatty acid oxidation, or  $\beta$ -oxidation, pathway (Carracedo *et al.*, 2013). The diverse cellular localizations and tissue expression patterns of the PNPLA family suggest non-redundant roles in lipid metabolism.

### Patatin-like phospholipases in host cellular signaling pathways

The polyunsaturated fatty acids (PUFA) and lysophospholipids released by PLA<sub>2</sub> activity can act as secondary messengers for downstream cellular responses; however, in mammalian hosts these secondary messengers come from sPLA<sub>2</sub>, iPLA<sub>2</sub> and cPLA<sub>2</sub> but not the PLPs. In contrast, plant PLPs play an active role in defense signaling. Arabidopsis encodes 10 PLPs and the PUFAs produced can inhibit the protein phosphatase MP2C, which is involved in the

wound-induced MAP kinase pathway (Scherer *et al.*, 2010). Arabidopsis PLP2 and PLP7 are pathogen-induced patatin-like phospholipases. PLP2 promotes a hypersensitive reaction, or programmed cell death, in infected cells that are critical in the resistance of Arabidopsis to cucumber mosaic virus but detrimental during infection with the fungus *Botrytis cinerea* and the bacteria *Pseudomonas syringae*. Higher induction of the downstream oxylipins in response to *B. cinerea* and *P. syringae* compared to the virus led to increased host damage from the induced hypersensitive reaction (Camera *et al.*, 2005; Camera *et al.*, 2009). Similarly, infection of tobacco leaves with tobacco mosaic virus strongly induced transcription and activity of three tobacco PLPs. Fatty acid conversion to 12-oxophytodienoic and jasmonic acid defense-signaling eicosanoids induced the onset of necrotic lesions to inhibit viral spread (Dhondt *et al.*, 2000, Ryu, 2004). There are also complex feedback loops involving other phospholipases. For example, phospholipase D (PLD)-derived PA can stimulate PLA<sub>2</sub> activity in animals, whereas PLD is inhibited by the LPE generated by PLA<sub>2</sub> in both plants and animals. PLD can also be activated by the PUFAs generated by PLA<sub>2</sub> (Ryu, 2004).

### Patatin-like phospholipases in microbes

In addition to their mammalian and plant hosts, PLPs are also found in many microorganisms. In a screen of 123 bacterial genomes, 55 strains contained at least one gene with a PLP domain including *Bacillus* sp., *Brucella* sp., *Rickettsia* sp., *Staphylococcus aureus*, and *Yersinia pestis*. Genomes of pathogens and symbionts had significantly higher numbers of PLP-containing genes than the genomes of free-living bacteria, suggesting a role in host-pathogen interaction for these PLPs (Banerji & Flieger, 2004). One of the best characterized PLP is ExoU in *Pseudomonas aeruginosa* (Phillips *et al.*, 2003; Sato & Frank, 2004). ExoU is a cytotoxic effector protein secreted through the type III secretion system upon cellular contact (Sawa *et al.*, 2016). Host ubiquitination is required to activate the PLA<sub>2</sub> activity of ExoU leading to destruction of infected cell membranes (Anderson *et al.*, 2011; Anderson *et al.*, 2015). *Rickettsia typhi* encodes two PLPs, one of which has similar cytotoxic activity to ExoU and also requires a eukaryotic host cofactor for activation (Rahman *et al.*, 2010). The intracellular pathogen *Legionella pneumophila* encodes four PLPs, three of which are secreted into the host cell through the type IVB secretion system (Banerji *et al.*, 2008). The best characterized of these PLPs, VipD, hydrolyzes phosphatidylcholine (PC) and phosphatidylethanolamine (PE) specifically on the mitochondrial membrane and not the plasma membrane. The release of fatty acids and lysophospholipids destabilizes the membrane and allows for the release of cytochrome c from the mitochondria. Cytochrome C activates caspase 3, a major regulator of apoptotic cell death (Zhu *et al.*, 2013). VipD also interferes with endosomal trafficking and subsequent lysosomal degradation that contributes to bacterial survival within the host cell (Banerji *et al.*, 2008; Ku *et al.*, 2012).

PLPs released by fungi during infection in a mammalian host have been implicated in nutrient acquisition, tissue invasion, and modulation of the host immune response (Köhler *et al.*, 2006). The triacylglycerol (TAG) lipases in *Saccharomyces cerevisiae* contain patatin-like domains and release TAG from lipid storage particles (Athenstaedt & Daum, 2003; Athenstaedt & Daum, 2005). *S. cerevisiae* also encodes a human PNPLA6 homolog

involved in phosphatidylcholine turnover. Pathogenic fungi like *Candida albicans* produce PLPs, but their role in pathogenesis and virulence is still unclear.

### Eicosanoid production and regulation

Eicosanoids are lipid mediators made by the oxidation of PUFAs and are involved in the regulation of inflammation (diagram in Fig. 3). Eicosanoids were first discovered in fungi and are involved in sexual maturation and life cycle regulation as well as pathogenesis in virulent strains (Kock *et al.*, 1991). Eicosanoids are largely produced by cells of the innate immune system, using arachidonic acid (AA as the PUFA substrate (Harizi *et al.*, 2008). The three major enzymes involved in eicosanoid production are cytochrome P450, LOX, and COX. AA metabolized by cytochrome P450 forms epoxides and hydroxyeicosatetraenoic acids (HETE), which likely contributes to tumor initiation and progression (Nebert & Dalton, 2006). COX-mediated AA oxidation forms prostaglandins (PG) and thromboxanes (TX). COX-1 and COX-2 are the two isoforms that have been identified in humans. COX-1 is constitutively expressed in most tissues, while COX-2 is induced in response to inflammation (Botting, 2007). PGs are produced by most human cells, are associated with both pro- and anti-inflammatory activity, and are responsible for many physiological symptoms of an inflammatory response. Aspirin and other nonsteroidal anti-inflammatory drugs function by blocking the active site of COX to reduce the general malaise caused by PG and TX activity (Harizi *et al.*, 2008).

The LOX superfamily is found widely in plants, animals, fungi and bacteria. The main human LOXs are 5-, 12- and 15-LOX and the names reflect the specific carbon target for oxidation on the PUFA substrate. Soybean LOX was one of the first characterized and while it displays 15-LOX activity, it only shares 25% identity with any mammalian 15-LOX. The human 15-LOXs themselves only share 35% identity with each other, highlighting the sequence diversity of this enzymatic family (Lagocki *et al.*, 1976; Steczko *et al.*, 1992; Shureiqi & Lippman, 2001). LOX-mediated AA dioxygenation forms hydroperoxyeicosatetraenoic acids (HpETE), which are rapidly reduced to HETEs. In plants, these intermediates are converted to jasmonic acid and aldehydes, which are both involved in plant defense responses (Chehab *et al.*, 2008). In other organisms, LOX-derived HETEs can be further converted to hepoxilins (HX), leukotrienes (LT), and lipoxins (LX). HXs are associated with stimulated intracellular calcium release, including stimulation of AA, diacylglycerol and insulin secretion (Nigam *et al.*, 1990; Mrsny *et al.*, 2004). LTs are mainly produced by inflammatory cells and exhibit strong pro-inflammatory properties including T cell proliferation, chemotaxis induction and secretion of cytokines involved in the Th1 response (Samuelsson *et al.*, 1987; Wang & DuBois, 2010; Norris *et al.*, 2014). Conversely, LXs are involved in inflammation resolution through downregulation of pro-inflammatory chemokines and cytokines, reduced PMN infiltration, and increased IL-10 production (Serhan, 2014; Petri *et al.*, 2015).

Mediators like PGs and LTs are produced in response to infection, but failure to resolve inflammation can be as damaging as the initial infection, so pro-resolving eicosanoids like LXs, resolvins, protectins, and maresins are produced to protect the host tissues (Tam, 2013). Signaling networks between the eicosanoids that help mediate this balance between

pro- and anti-inflammatory responses. In fungi, inhibition of PGs leads to an increase in LOX products to compensate for the loss of eicosanoids (Noverr *et al.*, 2003). PGE<sub>2</sub> enhances IL-10 production in dendritic cells, which inhibits activation of the 5-LOX activating protein and results in lower LTB<sub>4</sub> production (Harizi *et al.*, 2003). Both PGE<sub>2</sub> and PGD<sub>2</sub> can upregulate 15-LOX, leading to increased synthesis of pro-resolving LXs (Tam, 2013). Differences in eicosanoid production by immune cells contribute to their downstream effects on the immune response. PMNs are the first leukocyte responders to an inflammatory insult. At the onset of inflammation, LTB<sub>4</sub>, PGE<sub>2</sub> and PGD<sub>2</sub> are the most abundant eicosanoids produced by PMNs and these eicosanoids enhance further leukocyte recruitment and vascular permeability. The PGs then stimulate lipid mediator class switching and upregulation of resolving eicosanoids at the sites of inflammation (Dalli & Serhan, 2012). Secreted products produced in one cell type can also be metabolized in a subsequent cell to generate the final lipid mediator. 15-HpETE or 15-HETE produced by 15-LOX in epithelial cells or monocytes can serve as substrates for neutrophil 5-LOX to produce LXA<sub>4</sub> and LXB<sub>4</sub>. Myeloid 5-LOX produces pro-inflammatory LTA<sub>4</sub>, which is then converted by platelet 12-LOX to anti-inflammatory lipoxins (Fierro & Serhan, 2001). Although there has not yet been a direct link between microbial PLPs and eicosanoid production, a mammalian PLP has been implicated in human mast cell eicosanoid production (described below under lipid scavenging). The balance of cytokines and lipid mediators is critical for an effective host response to infection, but pathogens can take advantage of host eicosanoid production to modulate the immune response. *P. aeruginosa* secretes a 15-LOX homolog which regulates the host response through the production of anti-inflammatory 15-HETE molecules (Vance *et al.*, 2004). *Listeria monocytogenes* infection of macrophages activates host cPLA<sub>2</sub> and COX-2 activity leading to increased production of PGs. The resulting downregulation of TNF $\alpha$  by the PGs helps *L. monocytogenes* survive (Noor *et al.*, 2008). As these mechanisms for immune regulation are studied further, the roles of microbial PLPs in eicosanoid production will likely be elucidated.

### Interplay of host and parasitic PLA<sub>2</sub> activity during infection

Eicosanoids produced by pathogens often play a dual role in metabolism or maturation of the organism and cross-talk with the host inflammatory response (Noverr *et al.*, 2003). In protozoan parasites specifically, the PLA<sub>2</sub> family of enzymes have been implicated in invasion, membrane remodeling, virulence, and disease progression. PGE<sub>2</sub> inhibition of IL-12 plays a critical role in disease progression of *Leishmania major* (Passero *et al.*, 2008). These intracellular parasites are cholesterol auxotrophs and salvage lipids from the host during infection. An *L. major*-derived PLA<sub>2</sub> is responsible for hydrolyzing platelet-activating factor and contributes to virulence *in vivo* (Pawlowic & Zhang, 2012). Ca<sup>2+</sup>-dependent PLA<sub>2</sub> produced by *Trypanosoma brucei* releases AA and stimulates Ca<sup>2+</sup> influx into the parasite, which has been associated with control of infection (Eintracht *et al.*, 1998). Similar AA-regulated Ca<sup>2+</sup> influx was seen in *T. cruzi* and *L. donovani* (Catisti *et al.*, 2000). *T. brucei* also has a lysoPLA that can release AA by sequentially hydrolyzing the sn1 and sn2 acyl chains in phospholipids (Ridgley & Ruben, 2001). Activation of *T. cruzi*-infection macrophages by LTB<sub>4</sub> induces the production of TNF $\alpha$ . This pro-inflammatory cytokine drives the release of NO, which mediates parasite killing (Talvani *et al.*, 2002). A lytic factor important for the virulence of *Trichomonas vaginalis* was determined to be a PLA<sub>2</sub> and

contributes to tissue damage and inflammation during infection through the downstream production of PGs and LTs (Lubick & Burgess, 2004).

PLA<sub>2</sub>s have been emerging as critical enzymes in the pathogenesis of apicomplexans in recent years as well. *T. gondii* secretes both a Ca<sup>2+</sup>-dependent and -independent PLA<sub>2</sub> that are involved in host cell penetration by facilitating membrane fusion during invasion and synthesis of LOX and COX eicosanoid products (Saffer *et al.*, 1989; Saffer & Schwartzman, 1991; Thardin *et al.*, 1993). The Ca<sup>2+</sup>-independent PLA<sub>2</sub> is resistant to most PLA<sub>2</sub> inhibitors tested unlike the host enzymes, which could be exploited for drug development (Cassaing *et al.*, 2000). The released PUFAs themselves could also aid host cell invasion by increasing the fluidity and permeability of the host cell membrane (Li *et al.*, 2008). IFN $\gamma$  blocks the activities of the *T. gondii* PLA<sub>2</sub>s, suggesting another mechanism of protection for this Th1-type cytokine against active invasion by *T. gondii* (Gomez-Marín *et al.*, 2002). While the Th1 immune response is used by the host to clear parasitic infection, the cytokines from this immune response signals *T. gondii* to shift into the chronic bradyzoite stage suggesting that both stimulation and resolution of the inflammatory response aid survival of *T. gondii* to its chronic stage. Fatty acids from *T. gondii* reduce the secretion of TNF $\alpha$ , which is normally induced by protozoan glycolipids, through the inhibition of NF- $\kappa$ B activation in the host (Debierre-Grockieo *et al.*, 2007).

### Phospholipases in lipid remodeling and scavenging in Apicomplexa

Apicomplexans are auxotrophs for many lipid species such as cholesterol and phospholipids (Gupta *et al.*, 2005; Milovanovi *et al.*, 2017). Phospholipids are important components of membranes and are also involved in signaling, protein turnover and attachment to membranes, and membrane fluidity (Ramakrishnan *et al.*, 2013). Apicomplexans exploit the host lipidome through a variety of mechanisms (Rub *et al.*, 2013). *T. gondii* can acquire lipid precursors from its environment and use them to synthesize all of its major glycerophospholipids (Charron & Sibley, 2002). Previous studies suggest that the parasite is capable of synthesizing only 50% of the phosphatidylserine (PS) and less than 10% of the phosphatidylcholine (PC) necessary to maintain the rate of replication (Gupta *et al.*, 2005). Accumulating enough phospholipids for replication of the parasitic membranes requires both internal synthesis and scavenging from the host and is likely a rate-limiting step in replication. The high abundance of PC in the *T. gondii* membrane, about 75%, increases membrane fluidity, which may help the parasite accommodate a wide range of hosts and environments (Gupta *et al.*, 2005; Seeber *et al.*, 2008). All of Apicomplexa have much higher levels of PC than other eukaryotic cells, which typically have 30–40% of their phospholipids comprised of PC (Mitschler *et al.*, 1994).

A mechanism for hijacking host resources involves accumulation of lipid droplets in host cells during infection and the concomitant downregulation of host genes involved in lipid metabolism, such as the mammalian patatin-like phospholipase ATGL (Hu *et al.*, 2017). In human mast cells, silencing ATGL caused an increase in neutral lipids in lipid droplets as well as a decrease in eicosanoid production (Dichlberger *et al.*, 2014). LOX and COX enzymes have been shown to localize to lipid droplets and are considered to represent a site of prostaglandin and leukotriene synthesis, so ATGL release of arachidonic acid from lipid

droplet-associated triacylglycerol could be a crucial step for eicosanoid production in mast cells (Schreiber & Zechner, 2014). During Apicomplexa infection, host lipid droplets localize near and within the parasitophorous vacuole but are too large for direct endocytosis, so host- and parasite-derived enzymes, such as PLPs, are likely involved in releasing lipids from the droplets (Nolan *et al.*, 2017). In mammalian cells, phospholipids can move freely between membranes without vesicular trafficking using mitochondrial-associated membranes. The PVM of *T. gondii* parasites can associate with the ER and mitochondria of the host, which could allow for easier lipid exchange between the host and parasite (Coppens, 2006).

The most abundant phospholipid in *Plasmodium* membranes is also PC at 40–50% of the total phospholipids (Dechamps *et al.*, 2010) *Plasmodium* cannot synthesize fatty acids or cholesterol de novo (Labaied, 2011; Fish, 1995). They have multiple pathways to overcome this by either scavenging lipid precursors such as choline and ethanolamine to be metabolized further by the parasite or actively taking up FAs and phospholipids from the erythrocyte membranes and human serum (Mitamura & Palacpac, 2003; Krishnegowda & Gowda, 2003) *Plasmodium* parasites induce a 6-fold increase in the overall phospholipid content in the membranes of their host cells, particularly infected erythrocytes (Dechamps *et al.*, 2010). The membranes become highly susceptible to phospholipase activity due to a rearrangement of those phospholipids to the outer leaflet of the host cell membrane bilayer (Joshi & Gupta, 1988). Of note, lipid metabolism is effectively absent in uninfected mature erythrocytes, so the parasite must rely on its own phospholipid synthetic machinery to meet its requirements for replication (Hsiao *et al.*, 1991) *P. berghei* PLA<sub>2</sub> contributes to several life cycle transitions. PLA<sub>2</sub> activity is involved in oocyst rupture and release of sporozoites, epithelial cell membrane penetration for migration to the liver, and finally PVM rupture in the infected hepatocyte (Burda *et al.*, 2015) and egress of merozoites into the blood stream (Bhanot *et al.*, 2005). Regulation of the immune response is also critical in the pathogenesis of cerebral malaria (CM). Patients who died or developed long-term side effects from CM had higher plasma PLA<sub>2</sub> levels than those who recovered. This increase in PLA<sub>2</sub> was also associated with excessive production of pro-inflammatory cytokines, likely leading to the severe pathogenesis (Gupta *et al.*, 2017). The PUFAs docosahexaenoic acid, eicosapentaenoic acid, AA, and linoleic acid were able to inhibit *P. falciparum* growth, but oleic acid and docosanoic acid did not inhibit growth. Addition of the oxidized derivatives of the PUFAs led to direct killing of the parasites (Kumaratilake *et al.*, 1992). PUFAs, but not their hydroperoxy derivatives, markedly increased neutrophil-mediated killing of parasites (Kumaratilake *et al.*, 1997).

A PLA<sub>2</sub> secreted by *Cryptosporidium parvum* is critical for host cell invasion, but the specific gene has not yet been identified (Pollok *et al.*, 2003). In *C. parvum*, PC was 65% of the total phospholipids (Mitschler *et al.*, 1994). These high levels of PC in the parasitophorous vacuole may help avoid fusion with the lysosome, as PC is more stable as a bilayer than other phospholipids. While *T. gondii* has similarly high levels of PC, *Plasmodium* may not require such high levels during the intraerythrocytic stages as red blood cells lack most fusogenic organelles. *Eimeria neischulzi* has 75–85% PC in both sporulated and unsporulated oocysts and the aqueous insolubility and relative inertness may contribute to their resistant nature (Mitschler, 1994).



## Apicomplexa-derived patatin-like phospholipases

A *T. gondii* PLP, named TgPL1, was discovered during a mutagenesis screen to identify genes important for the inhibition of NO production from activated macrophages (Mordue *et al.*, 2007). This mutant had a defect in its ability to survive in active macrophages and increased cytokines with fewer inflammatory lesions in late chronic infection compared to wild type. TgPL1 localizes within the parasite during the tachyzoite stage but moves out to the PV and cyst wall during the bradyzoite stage, further supporting its role in late chronic infection (Tobin *et al.*, 2014). TgPL1 lacks the predicted catalytic serine essential for PLA<sub>2</sub> activity, so its effects are likely not due to PLA<sub>2</sub> activity (Tobin & Knoll, 2012). This led to a screen of the *T. gondii* genome where six potential PLP enzymes were found, four of which had retained the catalytic serine (Fig. 4). Recently TgPL2 was shown to be critical in maintaining membrane integrity of the apicoplast (Lévêque *et al.*, 2017). Lipid analysis revealed that TgPL2 is important for maintaining levels of apicoplast-generated fatty acids and regulating PC and LPC levels in the parasite. A third PLP, TgPL3, was previously identified in a screen for *T. gondii* virulence *in vivo* and is currently under investigation (Frankel *et al.*, 2007). In *P. falciparum*, the localization of a putative PLP, Pf3D7\_0209100, was shown to be cytosolic during all asexual and gametocyte stages with additional nuclear localization during the trophozoite and gametocyte stages (Pappa *et al.*, 2017). Another predicted *Plasmodium* PLP, Pf3D7\_092400, was downregulated in response to choline kinase inhibition. Choline kinase is a key enzyme in the synthesis of PC, a phospholipid comprising a large portion of the parasitophorous vacuole membrane, and is critical for *Plasmodium* replication during the asexual stages. Pf3D7\_092400 inhibition in response to reduced PC synthesis could indicate a role for the PLP in maintaining membrane lipid homeostasis (Ridzuan *et al.*, 2014).

A search of Apicomplexa genomes reveals that these PLP domains are present broadly and in high numbers across the phylum. In addition to the 6 putative PLPs found in the *T. gondii* genome, there are 6 in *Cryptosporidium* and *Hammondia*, 5 in *Eimeria* and *Neospora*, and 4 in *Plasmodium* and *Sarcocystis*. Most PLPs contain a conserved proline between the lipase domain and the catalytic aspartate. The proline motif in bacterial PLPs was typically ASxxxP, whereas in mammalian PLPs, the motif was AAP (Banerji & Flieger, 2004). An alignment of the *Toxoplasma*, *Plasmodium* and *Cryptosporidium* PLPs revealed a mixture of both motifs but the majority aligned with ASxxxP, suggesting these PLPs have a bacterial origin (Fig. 4). TgPL2 and its *Plasmodium* ortholog, Pf3D7\_1358000, notably contained the AAP motif. As discussed earlier, mammalian PLPs contribute mainly to lipid metabolism and turnover, similar to the role TgPL2 plays in the apicoplast. It will be intriguing to see if this motif distinction predicts the role of the apicomplexan PLPs in either lipid metabolism or inflammation. The Apicomplexa PLPs fall roughly into 6 ortholog groups with an additional 5 ortholog groups specific for *Cryptosporidium* or *Eimeria* species and a handful of PLPs that did not fall into any of the ortholog groups (Fig. 5). Several ortholog groups contain signal peptides and/or transmembrane domains that will direct the localization and specialized activities of the PLPs. For example, TgPL1 has a signal peptide that may be responsible for the localization shift of the protein out to the cyst wall during chronic infection. PLPs in the ortholog group named OG5\_129101 have signal peptides, multiple transmembrane domains, and a domain of unknown function (DUF3336). While

functionally uncharacterized, this domain has been described adjacent to the GxSxG lipase domain in Tgl3 Tgl4 and Tgl5 in *Saccharomyces cerevisiae*. All three have triacylglycerol lipase activity and localize to lipid particles (Athenstaedt & Daum, 2003; Athenstaedt & Duam, 2005). Tgl4 is a functional ortholog of mammalian ATGL and has additional steryl ester hydrolase and phospholipase activities (Rajakumari & Duam 2010). These data give insight into the potential role of this Apicomplexa PLP ortholog group and will help guide the enzymatic assays and conditions used during further experiments. The conservation of multiple PLPs across the phylum suggests these enzymes play a critical role for the parasites. Based on the diversity, these enzymes are likely to fill unique roles to address the changing needs across the life cycle of the parasites in both lipid metabolism and host immune regulation.

### Future perspectives

As seen in the PLP sequence alignments, Apicomplexa PLPs more closely resemble bacterial PLPs than eukaryotic PLPs. Additionally, compounds identified as potent inhibitors of ExoU PLA<sub>2</sub> activity did not inhibit the activity of mammalian-derived PLA<sub>2</sub>s (Lee *et al.*, 2007). These parasite PLPs will likely be excellent drug targets as TgPL2 has already been characterized as a critical gene to parasite growth and replication (Lévêque *et al.*, 2017). Treatment of *T. gondii* with atglistatin, an inhibitor of ATGL, led to a decrease in parasite replication proportional to drug concentration and disorganization of the parasites within the PV. There was also accumulation of lipids in the lumen of the PV and between the parasites, indicative of dysfunctional lipid metabolism (Nolan *et al.*, 2017). This paper suggested the effects of the drug were based solely on the mammalian ATGL, however the drug could also be acting on one or more of the six parasite-derived PLPs. Anti-bacterial drugs gentamicin and amikacin have modest effects on Plasmodium development from the ring stage to mature trophozoites and schizonts. While the ring stage matures in erythrocytes, it ingests host cell cytoplasm through endocytosis. The endocytic vesicle fuses with the parasite food vacuole and phospholipases contribute to the digestion of its contents. Drug treatment resulted in reduced host cytosol digestion concurrent with reduced PLA<sub>2</sub> activity in the parasite cytosol, suggesting these drugs may function through the inhibition of a parasite-derived PLA<sub>2</sub> (Krugliak *et al.*, 1987). Anti-malarials chloroquine, quinine and arteether also produce minor inhibition of PLA<sub>2</sub> activity associated with *P. falciparum* infection of erythrocytes with IC<sub>50</sub>s of 1.3, 1.0 and 1.8 mM, respectively (Zidovetzki *et al.*, 1993). Arteether and quinine have been shown to disrupt the structure of lipid membranes, which could alter the ability of PLA<sub>2</sub>s to access their substrates leading to reduced activity. In chloroquine-sensitive parasites, the drug enters the parasite in a neutral form that can move freely across the food vacuole membrane, but in this acidic environment, it becomes charged and can no longer diffuse out of the vacuole (Saliba *et al.*, 1998). The accumulation of chloroquine to higher concentrations within the food vacuole compared to the rest of the parasite may give some therapeutic potential for the current IC<sub>50</sub> of this drug on PLA<sub>2</sub> activity. However, these drugs are likely more useful as a starting point in designing more specific and potent drugs against the parasitic PLA<sub>2</sub> enzymes. A mammalian PLA<sub>2</sub> inhibitor, AACOCF<sub>3</sub>, had an inhibitory anti-malarial effect at low μM concentrations, but whether this AA analogue is targeting host or parasite-derived PLA<sub>2</sub> is not yet known (Pappa *et al.*, 2017). An alternative route to fight the spread of malaria is to target the mosquito vector

where oocyst formation occurs. When active or inactive PLA<sub>2</sub> from snake and bee venoms was fed to mosquitoes, the protein associated with the midgut surface and prevented ookinete attachment and invasion of the midgut epithelium, critical for oocyst formation (Zieler *et al.*, 2001). Further, mosquitoes were genetically manipulated to express an inactive form of PLA<sub>2</sub> under the control of a midgut-specific promoter and showed similar inhibition of oocyst development (Rodrigues *et al.*, 2008).

There is crosstalk among the many pathways discussed here and inhibition of one enzyme can stimulate activity in another pathway to maintain a balance (Buczynski *et al.*, 2009; Quehenberger & Dennis, 2011; Norris & Dennis, 2012). A systemic approach is needed to fully understand the entire lipidomic response to host and pathogen interactions. The emerging field of lipidomics is largely driven by the improving mass spectrometry methods integrated with better detection and characterization of the enzymes involved in lipid anabolism and catabolism. In addition to the lipidomics advancements, Apicomplexa have become more genetically manipulatable through new methods such as CRISPR/Cas9 (Sidik *et al.*, 2014; Brown *et al.*, 2014). Combining drug development with lipidomics and targeted parasite genetic manipulation will allow for a better understanding of the interwoven roles these PLPs play in parasite development and survival in the host.

## Supplementary Material

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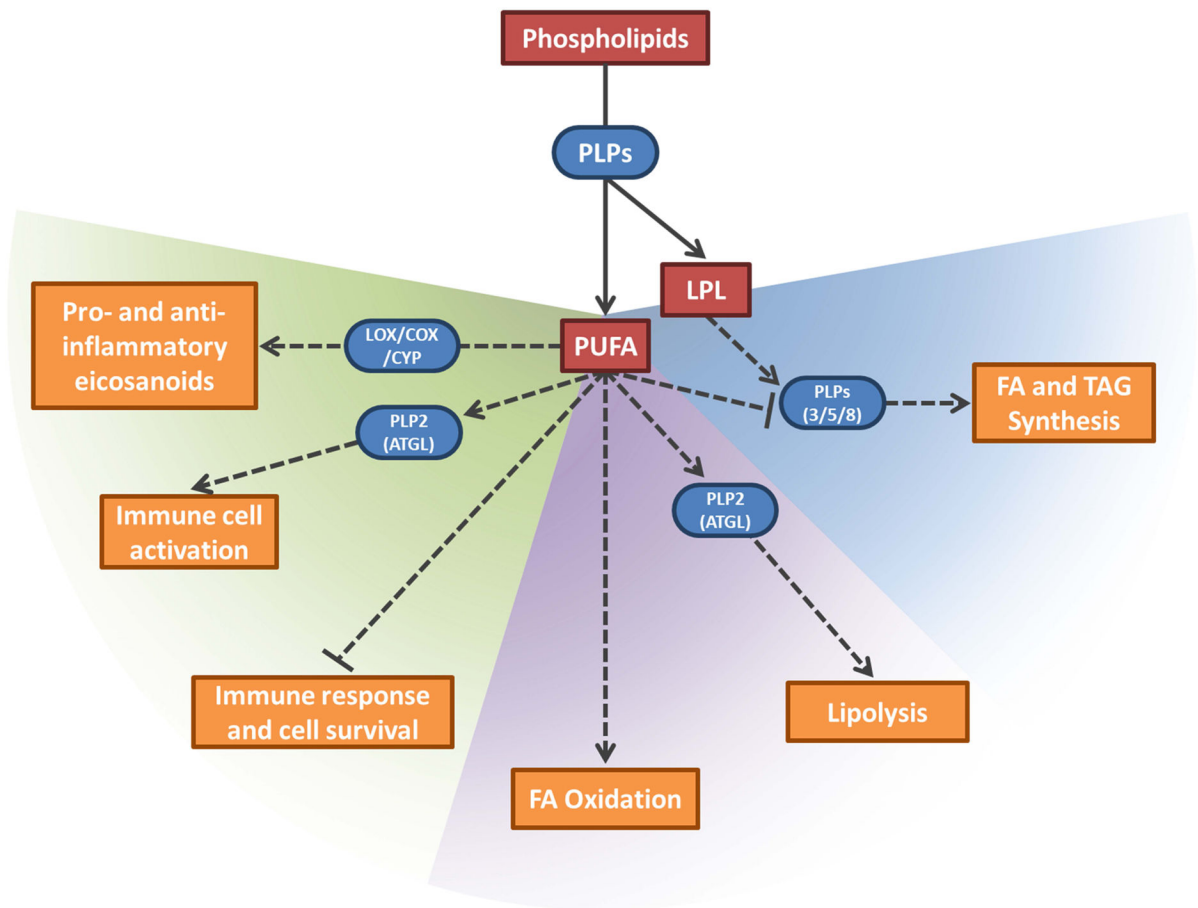
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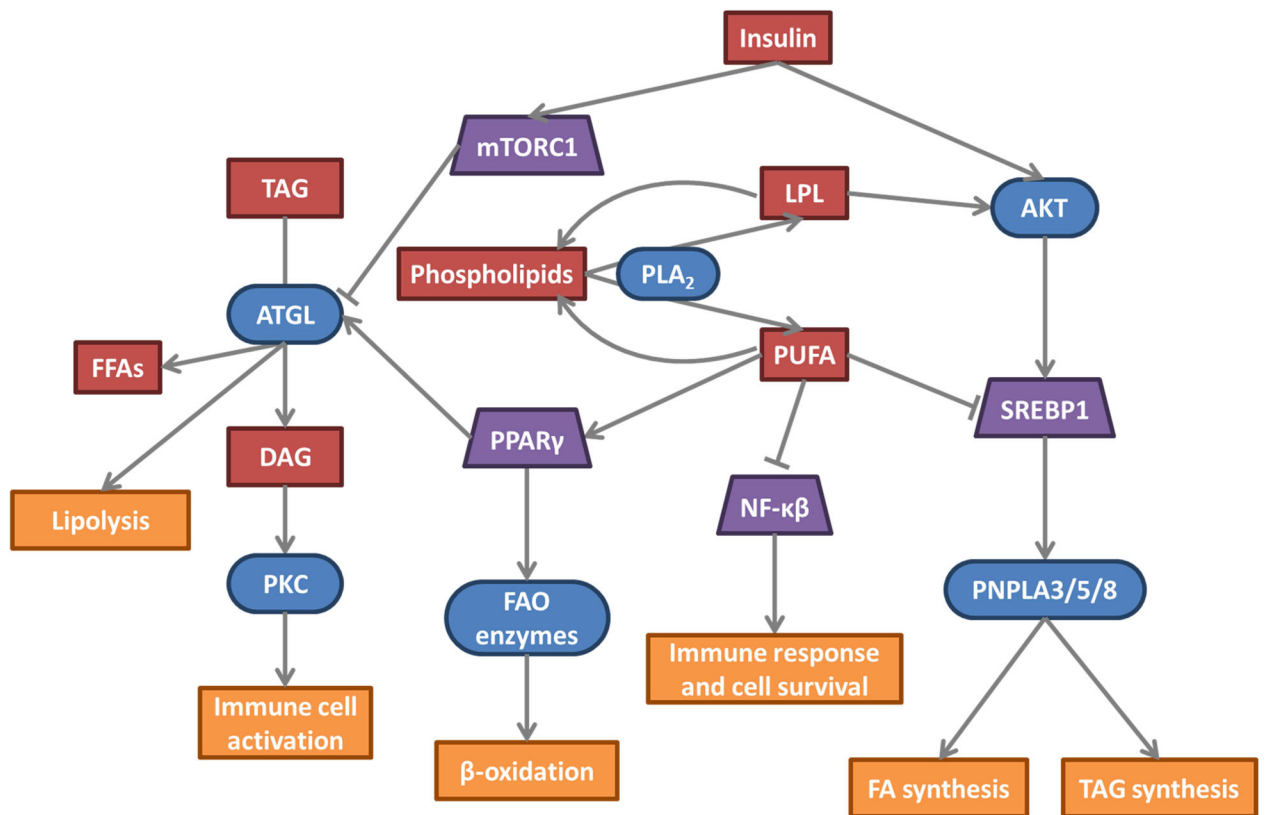
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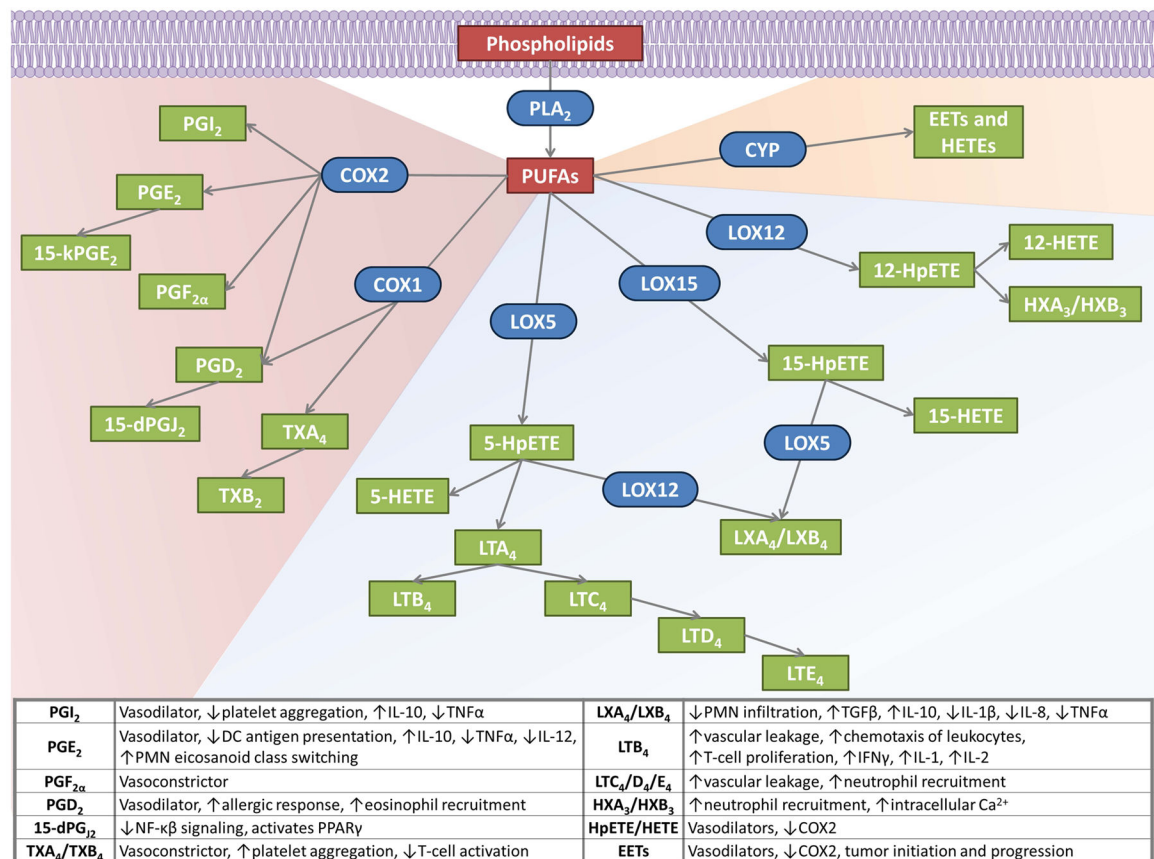


**Fig. 1.** Diverse roles of patatin-like phospholipases (PLPs) and their products in immune regulation (left/green region), lipolysis (middle/purple region), and lipogenesis (right/blue region). PLPs release polyunsaturated fatty acids (PUFA) and lysophospholipids (LPL) from phospholipids. These products can directly alter membrane fluidity and can also act as signaling molecules to regulate lipid metabolism and cellular signaling pathways. PUFAs can be oxidized by LOX, COX, and CYP to form both pro- and anti-inflammatory eicosanoids (figure 3 for details). Some PLPs (e.g. PNPL2/ATGL, PNPLA3, PNPLA5, and PNPLA8 in mammals) can be regulated by PUFAs and LPLs to maintain stringent control over immune responses and lipid homeostasis (figure 2 for details). Substrates and signaling molecules are red, enzymes are blue and rounded, and altered downstream processes are orange. Activation and inhibition are indicated with arrows and bar-headed lines, respectively. Dashed lines indicate indirect pathways.



**Fig. 2.**

PLA<sub>2</sub> enzymes in lipid metabolism and cellular signaling. PUFAs and lysophospholipids (LPLs) are cleaved from phospholipids by PLA<sub>2</sub>. These products can be recycled back into the lipid membrane or serve as signaling molecules to regulate lipolysis, lipogenesis, and the immune responses. Downstream patatin-like PLA<sub>2</sub>s (ATGL, PNPLA3, PNPLA5, and PNPLA8) respond to insulin levels, adding another layer of regulation on these lipid metabolism and cellular signaling pathways. Substrates and signaling molecules are red, enzymes are blue and rounded, transcription factors are purple trapezoids, and altered downstream processes are orange. Activation and inhibition are indicated with arrows and bar-headed lines, respectively. mTORC1 (mammalian target of rapamycin complex 1), Akt (Protein kinase B), PKC (Protein kinase C), DAG (diacylglycerol), PPAR $\gamma$  (Peroxisome proliferator-activated receptor gamma)



**Fig. 3.**

Eicosanoid production and inflammatory roles. PUFAs, released from phospholipids by PLA<sub>2</sub>, are oxidized by three main pathways to form both pro- and anti-inflammatory eicosanoids. COX pathways to produce PGs and TXs are shown in the red-shaded region. LOX production of HETEs, HXs, LTs, and LXs are shown in the blue-shaded region. Cytochrome P450 (CYP) products are shown in the orange-shaded region. Substrates are red, products are green, and enzymes are blue and rounded. The table summarizes some of the discussed downstream pro- and anti-inflammatory effects of the eicosanoids.

| No. | Gene ID              | % identity | Δ AA | Oxanyon hole                | Δ AA | Serine lipase motif | Δ AA | Conserved proline       | Δ AA | Catalytic aspartate | Protein Length |
|-----|----------------------|------------|------|-----------------------------|------|---------------------|------|-------------------------|------|---------------------|----------------|
| 1   | LOWK: Patatin        | 100        | 14   | EMVTVLSIDGGGIRGIPATILFLE    | 20   | VIGGTSSTGGLLTAMIST  | 90   | ARMYDISYSTAAAPTYFPPHYF  | 14   | LVDGAVTVADFA        | 373 AA         |
| 2   | 4QMK: ExoU           | 21         | 65   | PPPAHLVLSSGGAKGTAFFPMVQALE  | 10   | VVSGSSAGAICAALLAS   | 153  | MDIGRALISGALPGLFKSPTE   | 14   | FQDGGLLL-NTFA       | 677 AA         |
| 3   | TgPL1: TgME49_232600 | 29         | 283  | GVCHILVLSSGGARSFAFAGGIVGL-  | 15   | VVTGVGGVQAAFGGLP    | 151  | APVLVAMATAAIPGTFPPVAL   | 10   | MIDGAVNS-FLNV       | 665 AA         |
| 4   | TgPL2: TgME49_231370 | 31         | 2028 | RGLRILCFDGGGTRGVLSLALKQIM   | 13   | IICGTSSTGGVIAALLGL  | 244  | ILVKDALRATAAIPGTFSPVFW  | 5    | FSDGALLA-NNPT       | 2904 AA        |
| 5   | TgPL3: TgME49_305140 | 22         | 1369 | RSPLGFSFSPAGLIGPYHLGVLISLLC | 10   | PVAGSAGLAAAAGVL     | 77   | SDMIDCLIASCNIPFYLTKWPT  | 10   | CVDGFAT-KHKA        | 2579 AA        |
| 6   | TgME49_212130        | 28         | 619  | WGVTVLILSSGASLGHHPGVLELL    | 13   | VIGGCSAGAVVAAWLCT   | 95   | VLIWSAILCSCAFPLSLPLPL   | 20   | FHDGSLSG-DIPT       | 994 AA         |
| 7   | TgME49_254420        | 26         | 795  | DRCTMLTDDGGALTFVSLFVLRLE    | 20   | LVAGSGGGLVALGL--    | 91   | ALHARAYRGTARVPLWVAGWAT  | 12   | KSDFSSLGYQLEP       | 1173 AA        |
| 8   | TgME49_273730        | 26         | 208  | QHRALALIEGGAMRCVTFAGMAVALH  | 10   | AVFGSSAGSLIGAYFIS   | 111  | PSLMACVRASMLLPLGLAGPVVH | 39   | LADALLEY-PVPF       | 656 AA         |
| 9   | Pf3D7_0924000        | 19         | 270  | WGNLALFLSSGAILLGHHPGVLEVL   | 315  | IICGTSAGSIVAAWICT   | 102  | VLIYTAVLASCSEFPYLQPFKL  | 5    | YNKENVYR-FMSI       | 1292 AA        |
| 10  | Pf3D7_1358000        | 29         | 1125 | RKRLILCFDGGGIRGLSLIEILKYIN  | 13   | IICGTSSTGAIISLILGL  | 185  | IFVKYVLRCTAAGFFNPFSP    | 5    | YADGAI CF-NNPT      | 2012 AA        |
| 11  | Pf3D7_0209100        | 37         | 333  | KPVSILSLDGGGILITSTLLVLRLE   | 20   | MVCGTSAGLISLAL--    | 100  | VPLWLAAWATASAPTYLKGPSA  | 16   | LVDGALKA-SNPA       | 679 AA         |
| 12  | Pf3D7_0218600        | 15         | 655  | PMNLGISFSFAGLILPYHLGVSSLLI  | 10   | SIAGSSAGSICACCLSV   | 77   | NDLISAIIASCNIPVLLSSNFI  | 8    | CIDGFFST-KKKD       | 2380 AA        |
| 13  | Cgd7_3390            | 19         | 41   | NICYALIMSFGSNKGPWQAGVVRGL-  | 15   | LVGTSVGGAINALASQF   | 103  | EETIEAVIGSGTIPGIFPIKYL  | 6    | HVDGFIA-AGDL        | 794 AA         |
| 14  | Cgd1_3610            | 23         | 144  | SKCYLITVSSGAKGSPSAGLINGL-   | 15   | VTSVIGTILNTIWSQF    | 101  | SIIPSIIRSSSAFPLVLEPAEI  | 6    | FGDGAI SK-TIDL      | 935 AA         |
| 15  | Cgd2_4050            | 23         | 471  | TGKLAFLSSGGALAMYHLGVVKVLL   | 8    | INTSSGSIVAAILAT     | 97   | ILLWSAVSASCALPGLMPVAREL | 20   | WMDGSI SQ-DIPH      | 821 AA         |
| 16  | Cgd7_2630            | 17         | 139  | KIPLGFSFVSAMLIPIYHLGVILEIQ  | 10   | PLSAGSSIAAICCAL     | 80   | DDLIECLIASSTIPLFVSV--   | 10   | CVDGYFAV-GRGE       | 484 AA         |
| 17  | Cgd8_3870            | 32         | 111  | DKCYVLLSSGANRCAWQTVLRGLL    | 15   | VIGVSIIGLALAGLF     | 127  | PDLINATLASSVPGAFSPVLI   | 5    | YMDGQVVM-NHNI       | 482 AA         |
| 18  | Cgd8_4130            | 29         | 112  | DKCYVLLSSGNRAMEVAALRGL-     | 15   | VISGVVGAIGAYSALF    | 103  | DELLDAVFASLAPLVVRYPIYV  | 5    | YMDGIRG-NANL        | 457 AA         |
|     | consensus sequence   |            |      | xkcxILSLSSGGaXGpyhLGVLRgLe  |      | vixGTSa@gixAaalxx   |      | vdlixAVLAScAIPglfppvxI  |      | LxDGalsa-nxP-       |                |
|     | secondary structure  |            |      | eeeee hhhhhhhhhhhhhhh       |      | eeee hhhhhhhhh      |      | hhhhhhhhh eee           |      | eee                 | h              |

Fig. 4.

Alignment of conserved patatin domains in Apicomplexa PLPs. 16 *Toxoplasma*, *Plasmodium*, and *Cryptosporidium* PLP genes were aligned to PDB structures of Patatin and *P. aeruginosa* ExoU using the CLUSTAL Omega and MAFFT methods in MegAlign Pro (DNASTAR). PROMALS3D and SWISS-MODEL were used to confirm the predicted secondary and tertiary structures aligned with the known PLP structures. The known conserved patatin motifs are underlined and residues conserved in more than 60% of the sequences are colored red. Arrows indicate the catalytic S/A dyad. % identity = 100\*(1 – distance) where distance is the uncorrected pairwise distance between the full sequence of each gene compared to patatin. AA is the number of residues before and after each motif.