



## Identification of a secretory phospholipase A<sub>2</sub> from *Papaver somniferum* L. that transforms membrane phospholipids

Veronika Jablonická<sup>a</sup>, Johanna Mansfeld<sup>b</sup>, Ingo Heilmann<sup>b</sup>, Marek Obložinský<sup>a,\*</sup>,  
Mareike Heilmann<sup>b</sup>

<sup>a</sup> Department of Cell and Molecular Biology of Drugs, Faculty of Pharmacy, Comenius University in Bratislava, Kalinčiaková 8, 832 32 Bratislava, Slovakia

<sup>b</sup> Department of Cellular Biochemistry, Institute of Biochemistry and Biotechnology, Martin-Luther-University Halle-Wittenberg, Kurt-Mothes-Str.3, 06120 Halle (Saale), Germany

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### ABSTRACT

The full-length sequence of a new secretory phospholipase A<sub>2</sub> was identified in opium poppy seedlings (*Papaver somniferum* L.). The cDNA of poppy phospholipase A<sub>2</sub>, denoted as *pspla*<sub>2</sub>, encodes a protein of 159 amino acids with a 31 amino acid long signal peptide at the N-terminus. *PsPLA*<sub>2</sub> contains a PLA<sub>2</sub> signature domain (PA2c), including the Ca<sup>2+</sup>-binding loop (YGKYCGxxxxGC) and the catalytic site motif (DACCxxHDxC) with the conserved catalytic histidine and the calcium-coordinating aspartate residues. The aspartate of the His/Asp dyad playing an important role in animal sPLA<sub>2</sub> catalysis is substituted by a serine residue. Furthermore, the *PsPLA*<sub>2</sub> sequence contains 12 conserved cysteine residues to form 6 structural disulfide bonds. The calculated molecular weight of the mature *PsPLA*<sub>2</sub> is 14.0 kDa. Based on the primary structure *PsPLA*<sub>2</sub> belongs to the XIB group of PLA<sub>2</sub>s. Untagged recombinant *PsPLA*<sub>2</sub> obtained by expression in *Escherichia coli*, renaturation from inclusion bodies and purification by cation-exchange chromatography was characterized *in vitro*. The pH optimum for activity of *PsPLA*<sub>2</sub> was found to be pH 7, when using mixed micelles of 1,2-dioleoyl-*sn*-glycero-3-phosphocholine (DOPC) and Triton X-100. *PsPLA*<sub>2</sub> specifically cleaves fatty acids from the *sn*-2 position of 1-palmitoyl-2-oleoyl-*sn*-glycero-3-phosphocholine and shows a pronounced preference for PC over phosphatidyl ethanolamine, -glycerol and -inositol. The active recombinant enzyme was tested *in vitro* against natural phospholipids isolated from poppy plants and preferably released the unsaturated fatty acids, linoleic acid and linolenic acid, from the naturally occurring mixture of substrate lipids.

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### 1. Introduction

In recent years, an appreciation of phospholipids as more than just passive structural components of biological membranes has grown. Phospholipids play important roles in many biochemical and physiological processes in plants, including cell-to-cell communication or responses to external stimuli. Phospholipid-derived molecules with roles in plant signaling and communication can be generated by phospholipases (Canonne et al., 2011). While phospholipases C and D have been extensively characterized over the past decades (Janda et al., 2015; Zhao, 2015), there is still a lack of information about phospholipases A<sub>2</sub> (PLA<sub>2</sub>s). PLA<sub>2</sub> (phosphatide 2-acylhydrolase, EC 3.1.1.4) catalyzes the stereospecific

hydrolysis of membrane glycerophospholipids at the *sn*-2 position to release free fatty acids (FFAs) and lysophospholipids (LPLs). Even though PLA<sub>2</sub>s are rather small proteins, there is a striking structural diversity among representatives of the PLA<sub>2</sub> superfamily. Based on amino acid sequences, molecular weight and biochemical properties, PLA<sub>2</sub>s are classified into five groups: cytosolic Ca<sup>2+</sup>-dependent PLA<sub>2</sub>s (cPLA<sub>2</sub>s) and Ca<sup>2+</sup>-independent PLA<sub>2</sub>s (iPLA<sub>2</sub>s); secretory PLA<sub>2</sub>s (sPLA<sub>2</sub>s); lysosomal PLA<sub>2</sub>s and platelet-activating factor acylhydrolases (Six and Dennis, 2000). In plants, only two groups of PLA<sub>2</sub> have been identified: the low-molecular-weight sPLA<sub>2</sub>, and the less specific patatin-like PLA with a combined PLA<sub>2</sub> and PLA<sub>1</sub> activity (Lee et al., 2005). No cPLA<sub>2</sub> is known to be present in plants. Within the last years full sequences of putative sPLA<sub>2</sub> cDNAs have been cloned from rice (Ståhl et al., 1999), carnation flowers (*Dianthus caryophyllus* L. cv. Degio) (Kim et al., 1999), tobacco (*Nicotiana tabacum*) (Fujikawa et al., 2005, 2012), orange (*Citrus sinensis*) (Liao and Burns, 2010), durum wheat (*Triticum durum*) (Verlotta et al.,

\* Corresponding author.

E-mail address: [oblozinsky@fpharm.uniba.sk](mailto:oblozinsky@fpharm.uniba.sk) (M. Obložinský).

## Abbreviations

AtsPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Arabidopsis thaliana</i>	PA	phosphatidic acid
BIA	benzylisoquinoline alkaloid	PC	phosphatidylcholine
CsPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Citrus sinensis</i>	PE	phosphatidylethanolamine
DcPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Dianthus caryophyllus</i>	PG	phosphatidylglycerol
DOPC	1,2-dioleoyl- <i>sn</i> -glycero-3-phosphocholine	PI	phosphatidylinositol
cPLA <sub>2</sub>	cytosolic phospholipase A <sub>2</sub>	PLA <sub>1</sub>	phospholipase A <sub>1</sub>
FAME	fatty acid methylester	PLA <sub>2</sub>	phospholipase A <sub>2</sub>
FFA	free fatty acid	POPC	1-palmitoyl-2-oleoyl- <i>sn</i> -glycero-3-phosphocholine
GC	gas chromatography	POPE	1-palmitoyl-2-oleoyl- <i>sn</i> -glycero-3-phosphoethanolamine
GmsPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Glycine max</i>	POPG	1-palmitoyl-2-oleoyl- <i>sn</i> -glycero-3-phosphoglycerol
iPLA <sub>2</sub>	Ca <sup>2+</sup> -independent phospholipase A <sub>2</sub>	PsPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Papaver somniferum</i>
IPTG	isopropyl β-D-1-thiogalactopyranoside	PtPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Populus trichocarpa</i>
LPC	lysophosphatidylcholine	RcPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Ricinus communis</i>
LPI	lysophosphatidylinositol	sPLA <sub>2</sub>	secretory PLA <sub>2</sub>
LPL	lysophospholipid	TdsPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Triticum durum</i>
MJ	methyl jasmonate	TLC	thin layer chromatography
NtPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Nicotiana tabacum</i>	VvPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Vitis vinifera</i>
OsPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Oryza sativa</i>	ZmPLA <sub>2</sub>	secretory phospholipase A <sub>2</sub> from <i>Zea mays</i>

2013) and soybean (*Glycine max*) (Mariani et al., 2012). In the *Arabidopsis* genome, genes for four isoforms of sPLA<sub>2</sub> have been identified, denoted AtsPLA<sub>2</sub>-α, AtsPLA<sub>2</sub>-β, AtsPLA<sub>2</sub>-γ, and AtsPLA<sub>2</sub>-δ (Lee et al., 2005). Putative sPLA<sub>2</sub>s have been purified from elm seeds (*Ulmus glabra*) (Stähl et al., 1998) and rice (*Oryza sativa*) (Stähl et al., 1999). Based on their deduced primary structures, plant sPLA<sub>2</sub> have been classified into groups XIA and XIB (Mansfeld et al., 2006; Six and Dennis, 2000).

FFA and LPLs, the enzymatic products of PLA<sub>2</sub> catalysis, can serve as precursors of signaling messengers involved in various physiological and pathological processes. In animals, arachidonic acid released from membrane lipids by PLA<sub>2</sub> action is metabolized into prostaglandins and leukotrienes that play an important role in inflammation (Clark et al., 1995). For plants, LPLs, such as lysophosphatidylcholine, have been demonstrated to have a role in host-symbiont communication during plant-microbe interactions in soil, suggesting that PLA<sub>2</sub>s are important players in plant-microbe interactions (Drissner et al., 2007). FFAs released by PLA<sub>2</sub>s in plants can be precursors for the enzymatic or chemical production of a multitude of oxylipins with signaling and defensive functionalities (Mosblech et al., 2009). Moreover, PLA<sub>2</sub>s have also been reported to be biologically active in the control of various biological processes in plants, such as cell growth (Scherer et al., 2007), cell elongation (Lee et al., 2003), stomatal opening (Seo et al., 2008) or defence and stress responses (Canonne et al., 2011). From the available data it can be concluded that PLA<sub>2</sub>s have a role in lipid signaling events mediating plant defense responses.

Opium poppy belongs to the world's oldest and most prominent medicinal plants due to the production of therapeutically important secondary metabolites, in particular benzylisoquinoline alkaloids (BIAs). Opium – the dried latex obtained from unripe poppy seed pods – is the source of analgesic morphine, the cough suppressant codeine, the vasodilator papaverine, the potential anticancer drug noscapine, or the antimicrobial agent, sanguinarine (Beaudoin and Facchini, 2014). It is a paradox, that much more is known about the pharmacological effects of BIAs than about their biological role in the poppy plants in which they naturally occur. Secondary metabolites are not essential in maintaining normal physiological processes in plants; however, they might be

important under special conditions, for instance during plant defence reactions (Hagel and Facchini, 2013) or for communication between plants and their microbiotic surroundings. Several BIAs are known to be involved in chemical defence responses against microorganisms and herbivores (Schmeller et al., 1997). For instance, the production of sanguinarine was rapidly induced in suspension cultures of *Papaver somniferum* L. (Holková et al., 2010) or *Eschscholtzia californica* Cham. after elicitation with the necrotrophic fungal pathogen, *Botrytis cinerea*, or with methyl jasmonate (MJ), respectively (Kollárová et al., 2014). Plants accumulate jasmonates in response to many biotic and abiotic stresses, particularly after herbivore attack and wounding and, therefore, jasmonate signaling might be involved in the control of defense responses (Okada et al., 2015), in poppy possibly including the production of BIAs.

Until now, opium poppy is the only commercial source for morphine, codeine and semi-synthetic derivatives such as oxycodone and naltrexone (Beaudoin and Facchini, 2014), even though several protocols for the chemical synthesis of morphine and its derivatives have been published (Rinner and Hudicky, 2012) and their production via microbial biomanufacturing seems to be promising (Fossati et al., 2015; Thodey et al., 2014). Despite all these efforts, the extraction of morphinan from poppy plants as a natural resource is still far more economical. Therefore, the study of signaling pathways controlling the biosynthesis of alkaloids in poppy plants remains a current topic of research in the field of plant alkaloid metabolism.

It has been shown that the production of BIA in poppy plants is stimulated by exposure of the plants to exogenous stresses, such as wounding (Mishra et al., 2013). From other plant model systems, such as *Arabidopsis*, it is known that the same wounding stress triggers responses that are mediated by lipid signaling cascades involving phospholipases (Mosblech et al., 2008; Munnik, 2001). To understand the molecular players involved in the control of alkaloid accumulation, we have started to analyze possible connections between phospholipid signaling and plant defence response mechanisms in opium poppy. A better understanding of the players and principles of regulation of BIA biosynthesis might be the basis for the future genetic modification of opium poppy to optimize BIA production. It is therefore important, to analyze the background of

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