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## Crystallization and preliminary X-ray diffraction studies of a toxic phospholipase A<sub>2</sub> from the venom of *Vipera ammodytes meridionalis* complexed to a synthetic inhibitor

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## Abstract

A toxic phospholipase  $A_2$  (PLA<sub>2</sub>) is isolated from the neurotoxic complex Vipoxin, the major lethal component of the venom of *Vipera* anmodytes meridionalis. The enzyme is complexed to the synthetic inhibitor elaidoylamide and crystallized. The crystals belong to the space group  $P2_12_12_1$ , with unit cell dimensions a = 46.57 Å, b = 82.68 Å, c = 119.47 Å and  $\beta = 90^{\circ}$ . Initial diffraction data to 3.3 Å resolution are collected.

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Phospholipase A<sub>2</sub>s (PLA<sub>2</sub>, phosphatide 2-acylhydrolase, EC 3.1.1.4) are a fast expanding family of enzymes that specifically catalyze the hydrolysis of the *sn*-2 acyl ester bond of 1,2-diacyl-3-*sn*-phosphoglycerides releasing fatty acids and lysophospholipids [1]. The released arachidonic acid has an important physiological function as a precursor of eicosanoid mediators of inflammation: prostaglandins, leukotriens and tromboxanes. In this way, PLA<sub>2</sub> is involved in human diseases, such as rheumatoid arthritis, asthma and septic shock [2,3]. Lysophospholipids participate in phospholipids remodelling, cell signalling and membrane perturbation [1, and references therein]. Lypolitic enzymes influence a number of cellular functions: chemotaxis, cytotoxicity and cell differentiation [4].

PLA<sub>2</sub>s are widely distributed in animal organs and physiological fluids: mammalian pancreas, snake venom,

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lung, gastric mucosa, liver, spleen, brain, heart, alveolar macrophages, intestine, membranes, placenta and synovial fluid. These enzymes are the major toxic components of the snake venom and display a wide variety of pharmacological activities such as neurotoxicity, cardiotoxicity, myotoxicity, anticoagulant, antiplatelet, hypotensive, haemolytic, hemorrhagic and edema-inducing effects [5]. The venomous snakes in Europe are representatives of the genera Vipera and three species, Vipera ammodytes, Vipera aspis and *Vipera berus* are of public health significance [6]. The snakes of the first species are the most toxic in Europe. Two subspecies of V. ammodytes, V. ammodytes ammodytes and V. ammodytes meridionalis, inhabit the Balkan peninsula. Envenomation of humans by these snakes is often lethal. The major toxic component of the venom from V. a. meridionalis is Vipoxin, a heterodimeric postsynaptic neurotoxin. It is a representative of a group of heterodimeric toxins found in the venom of snakes inhabiting widely separated regions of the world. Analogues of this neurotoxin were isolated from the venom of European vipers, Vipera aspis zinnikeri [7] and Vipera aspis aspis [6], as well as

Abbreviations: PLA2, phospholipase A2

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from the Taiwan (Asia) viper Vipera russeli formosensis [8]. Vipoxin is a non-covalent complex between two oppositely charged subunits: a basic, strongly toxic Asp49 PLA<sub>2</sub> with a pI of 10.4 and an acidic non-toxic and catalytically inactive PLA<sub>2</sub>-like (Gln48 PLA<sub>2</sub>) component with a pI of 4.6 [9]. Both subunits are closely related proteins with 62% sequence identity and the same length of the polypeptide chain, 122 residues [10]. Gln48 PLA<sub>2</sub> component lacks catalytic activity due to the substitution of the active site His48 by a glutamine residue and reduces both the catalytic activity and toxicity of Asp49 PLA<sub>2</sub>. This is the first reported example of regulation of the toxic function generated by molecular evolution. Probably, the non-toxic subunit evolved from the toxic PLA<sub>2</sub> and acquired a chaperone function to avoid non-specific targeting of the toxic component. Vipoxin is an example of evolution of the toxic and phospholipolytic activities into non-toxic and inhibitory functions. In this paper, we report the crystallization and preliminary X-ray diffraction studies of the toxic Asp49 PLA<sub>2</sub> separated from the heterodimer and complexed to the synthetic inhibitor elaidoylamide (the amide of trans-9octadecenoic acid).

The heterodimeric complex Vipoxin was dissociated to subunits and the two components, Asp49 PLA<sub>2</sub> and Gln48 PLA<sub>2</sub>, were isolated in homogeneous state as described in Ref. [10]. A 10-fold molar excess of elaidoylamide inhibited almost all catalytic activity of the Vipoxin PLA<sub>2</sub> towards the major structural phospholipid in the brain phosphatidylcholine. The lyophilized toxic component was dissolved in distilled water at a concentration of 20 mg/ml. Crystallization conditions were screened by the hanging drop vapourdiffusion method using Jena Bioscience screening kits 1-5. Typically, a 2-µl drop of the protein solution was mixed with  $2 \mu$ l of the screening agent. In condition D2 of kit 5 (20%) PEG-10000, 50 mM HEPES, pH 7.5), small needle crystals were obtained. These conditions were further optimised and crystals suitable for X-ray analysis of the Vipoxin Asp49 PLA<sub>2</sub> in a complex with elaidoylamide were obtained as follows: 2 µl of the protein solution with a concentration of 20 mg/ml were mixed with 2 µl of elaidoylamide (10 mg/ml stock solution) and 2  $\mu$ l of a precipitant solution containing 24% PEG-10000 and 50 mM HEPES, pH 7.5. The mixture was equilibrated against 1 ml of the same precipitant solution. Crystals were grown within 3 days at room temperature and for initial test experiments mounted in quartz capillaries. Diffraction data to 3.3 Å were obtained from a flash-frozen crystal at 100 K using synchrotron radiation ( $\lambda = 0.802$  Å) at the consortiums beamline X13 at HASYLAB/DESY-Hamburg. A non-protein electron density corresponding to the inhibitor was observed. The preliminary X-ray data show that the crystal contains a non-covalently bound elaidoylamide. Evidently, the inhibitor possesses a high binding affinity towards the Vipoxin PLA<sub>2</sub>.

The programs DENZO, SCALEPACK [11] were used for data processing and analysis. Autoindexing yielded unit-cell

Table 1	
Data collection	etatistics

Data collection statistics		
Space group	P212121	
Unit cell parameters		
<i>a</i> (Å)	46.57	
<i>b</i> (Å)	82.68	
<i>c</i> (Å)	119.47	
Crystal volume per Dalton ( $V_{\rm M}$ ) (Å <sup>3</sup> Da <sup>-1</sup> )	2.13	
Wavelength used (Å)	0.802	
Resolution (Å)	20.0-3.3	
Completeness (%)	99 (99)	
Average $I/\sigma$	14 (3)	
Number of images	127	
Raw measurements used	69.923	
Unique reflections	7.251	
R <sup>a</sup> <sub>merge</sub>	0.117 (0.573)	
Subunits per asymmetric unit	4	

Values in parentheses are for the high resolution bin.

<sup>a</sup>  $R_{\text{merge}} = \sum |I - \langle I \rangle | / \sum I$ , where  $\langle I \rangle$  is the average intensity and the summation is done for all reflections.

parameters of a=46.6 Å, b=82.7 Å, c=199.5 Å, This crystal lattice is orthorhombic and belongs to the space group  $P2_12_12_1$ . Packing parameter calculations based on a molecular weight indicate the presence of 4 subunits of the inhibited PLA<sub>2</sub> in the asymmetric unit. This corresponds to a typical Matthews coefficient  $V_{\rm M}$  of 2.1 Å<sup>3</sup> Da<sup>-1</sup> [12] and a solvent content of 40%. The data collection parameters and statistics are summarised in Table 1.

In conclusion, for the first time, an isolated toxic component of Viperidae snake venom heterodimeric neurotoxin, complexed to a synthetic inhibitor, has been crystallized and preliminary X-ray data are collected. The separated PLA<sub>2</sub> changes the target of the physiological attack and the type of toxicity: from the post- to the presynaptic membranes of the neuromuscular junctions. Most probably, Vipoxin exerts its toxicity through dissociation to subunits. The neurotoxic chain binds to the target membrane and the non-toxic component (chaperone subunit) remains in solution. The modulation of PLA<sub>2</sub> activity is of pharmacological interest and the 3-D structure of the enzyme-inhibitor complex can be used for structure-based drug design. Initial calculations to solve the phase problem by molecular replacement methods are in progress, as well as attempts to optimise the crystals for high-resolution data collection.

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## References

 D.A. Six, E.A. Dennis, The expanding superfamily of phospholipase A<sub>2</sub> enzymes: classification and characterization, Biochim. Biophys. Acta 1488 (2000) 1–19.

- [2] D.L. Scott, S.P. White, J.L. Browning, J.J. Rosa, M.H. Gelb, P.B. Sigler, Structures of free and inhibited human secretory phospholipase A<sub>2</sub> from inflammatory exudates, Science 254 (1991) 1007–1010.
- [3] D.L. Scott, S.P. White, Z. Otwinowski, W. Yuan, M.H. Gelb, P.B. Sigler, Interfacial catalysis: the mechanism of phospholipase A<sub>2</sub>, Science 250 (1990) 1541–1546.
- [4] Ch. Betzel, N. Genov, K.R. Rajashankar, T.P. Singh, Modulation of phospholipase A<sub>2</sub> activity generated by molecular evolution, Cell. Mol. Life Sci. 56 (1999) 384–397.
- [5] M.Z. Huang, P. Gopalakrishnakone, M.C.M. Chung, R.M. Kini, Complete amino acid sequence of an acidic, cardiotoxic phospholipase A<sub>2</sub> from the venom of *Ophiophagus hannah* (king cobra): a novel cobra venom enzyme with 'pancreatic loop', Arch. Biochem. Biophys. 338 (1997) 150–156.
- [6] V. Jan, R.C. Maroun, A. Robbe-Vincent, L. de Haro, V. Choumet, Toxicity evolution of *Vipera aspis aspis* venom: identification and molecular modelling of a novel phospholipase A<sub>2</sub> heterodimer neurotoxin, FEBS Lett. 527 (2002) 263–268.
- [7] Y. Komori, K. Masuda, T. Nikai, H. Sugihara, Complete primary

structure of the subunits of heterodimeric phospholipase  $A_2$  from *Vipera a. zinnikeri* venom, Arch. Biochem. Biophys. 327 (1996) 303-307.

- [8] Y.-M. Wang, P.-J. Lu, C.-L. Ho, I.-H. Tsai, Characterization and molecular cloning of neurotoxic phospholipases A<sub>2</sub> from Taiwan viper (*Vipera russeli formosensis*), Eur. J. Biochem. 209 (1992) 635–641.
- [9] B. Tchorbanov, E. Grishin, B. Aleksiev, Y. Ovchinnikov, A neurotoxic complex from the venom of the Bulgarian viper (*Vipera ammodytes meridionalis*) and a partial amino acid sequence of the toxic phospholipase A<sub>2</sub>, Toxicon 16 (1978) 37–44.
- [10] I. Mancheva, T. Kleinschmidt, B. Aleksiev, G. Braunitzer, The primary structure of phospholipase A<sub>2</sub> of Vipoxin from the venom of the Bulgarian viper (*Vipera ammodytes meridionalis*), Biol. Chem. Hoppe-Seyler 368 (1987) 343–352.
- [11] Z. Otwinowski, W. Minor, Processing of X-ray diffraction data collected in oscillation mode, Methods Enzymol. 276 (1997) 307–326.
- [12] B.W. Matthews, Solvent content of protein crystals, J. Mol. Biol. 33 (1968) 491–497.