A phospholipase (PLase) gene of Vibrio vulnificus was cloned in Escherichia coli and the properties of the gene product were investigated. The PLase structural gene was composed of 1,251 bp, encoding 417 amino acids for a protein with a predicted molecular mass of 47,187 Da including a putative signal sequence. The predicted protein sequence was 87 and 82% identical to those of hemolysins from Vibrio spp. and that of lecithinase from V. cholerae, respectively. A lipid binding motif, GDSL, conserved among various PLases and lipases was also observed. Over-expression of PLase caused inclusion body formation in E. coli, but not that of the PLase subclone without the signal sequence (45 kDa). Purified PLase exhibited hemolytic activity on red blood cells and hydrolyzed phosphatidylcholine, phosphatidylethanolamine, phosphatidylinositol, and soya-lecithin mainly to fatty acid and 1,2-diacylglycerol, indicating that it was a PLase with unique catalytic activity. PLase from V. vulnificus had temperature and pH optimum at 45°C and 7.0 in 50 mM Tris-HCl buffer, respectively, but was quite active at temperatures up to 55°C and in a broad range of pH 5 to 10. The activity of the enzyme was enhanced by divalent cations such as Ca²⁺, Co²⁺, Mg²⁺, and Mn²⁺, but not by ethylenediaminetetraacetic acid (EDTA).

Key words: Phospholipase, Vibrio vulnificus, hemolytic, VplA.

INTRODUCTION

Vibrio vulnificus is a Gram negative marine bacterium that is pathogenic to both human and marine animals. The bacterium has become a great concern during summer time in Korea due to the increase of serious wound infections and fatal septicemia with high mortalities (>50%; Blake et al., 1979). The life cycle of V. vulnificus between marine environment and human hosts implies that the pathogen has delicate regulatory systems sensing and responding to environmental changes and that there is a close inter-relationship among the systems that affect the survival of the pathogen. Virulence of the bacterium is likely to be controlled by such complicate and delicate networks of various regulatory systems.

V. vulnificus produces various virulent factors such as polysaccharide capsules (Simpson et al., 1987), cytolytic hemolysins (Chang et al., 1997; Lee et al., 2004), elastolytic protease (Kothary and Kreger, 1987), siderophore (Simpson and Oliver, 1983), collagenase (Smith and Merkel, 1982), and phospholipase (PLase; Testa et al., 1984) etc. Among them, PLases are known to be associated with virulence in many pathogens (Titball, 1993; Mengaud et al., 1991; Portnoy et al., 1981; Gustafson and Tagesson, 1990). Due to their catalytic capability, PLases may also be involved in scavenging phosphate when it became a factor limiting bacterial growth. PLase C of Pseudomonas aeruginosa has well been characterized for its role in phosphate scavenging and pathogenesis (Gray et al., 1982). Many members of the family Vibrionaceae produce and secrete PLases,
some of which have been shown to be hemolysins (Testa et al., 1984; McCarter and Silverman, 1987; Pal et al., 1997; Shinoda et al., 1991) and others glycerophospholipid-cholesterol acyltransferases (Shaw et al., 1994; Thornton et al., 1988). PLases from other families also have been reported to be involved in the induction of apoptosis (Kirschnek and Gulbins, 2006) or in the regulation of flagella (Schmiele et al., 2000), indicating that their expression might be under the control of multiple regulatory systems.

In previous studies, the PLase activity in the lysate of _V. vulnificus_ was shown to be dependent on phosphate concentration, temperature, pH, osmotic pressure, and also subjected to catabolite repression by glucose (Oh et al., 2007). Therefore, PLase that is controlled by multiple environment factors would make a good system to investigate inter-relationship among various regulatory systems. As the first step toward such research goal, a gene encoding PLase of _V. vulnificus_ was cloned based on its capability of forming hemolytic zone on a blood agar plate and over-expressed in _E. coli_. The physico-chemical properties of the purified enzyme were also characterized in this study.

### MATERIALS AND METHODS

#### Bacteria, plasmids and media

_V. vulnificus_ ATCC29307 was cultivated either in Luria-Bertani broth (LB; 0.5% yeast extract, 1% bacto tryptone, Difco, USA) containing 2.5% NaCl or heart infusion broth (beef heart infusion 1% and 2.5% NaCl or heart infusion broth (beef heart infusion 1% and 2.5% NaCl), or _V. vulnificus_ ATCC29307 was cultivated in LB broth containing 100 µg/ml of ampicillin. However, PLase with the signal sequence from pVPL10 was found in the insoluble fraction as inclusion body and the enzyme was refolded and purified according to Wingfield et al. (1995). The cell extract in the Histag binding buffer containing 8 M urea was subjected to chromatography using a Ni-NTA column (Qiagen, Germany) after sonication in the presence of 1 mM phenylmethylsulfonyl fluoride (PMSF) and filtration of the supernatant through 3M paper (Whatman, USA). The enzyme bound to the resin was renaturated by sequential wash and incubation with renaturation buffers [100 mM NaCl, 20% glycerol, 20 mM Tris-HCl (pH 7.4)] containing 6, 4, 2, 1, and 0 M urea. Finally, the enzyme was washed with 20 mM Tris-HCl (pH 8.0) and eluted with 20 mM Tris-HCl (pH 8.0) containing 100 mM imidazole. PLase without the signal sequence from pVPL11 was purified from the supernatant of the cell lysis using regular buffers for Ni-NTA chromatography. Protein concentration was determined by the Bradford method (Bradford, 1976) and the purified enzyme was analyzed by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) using 10% polyacrylamide gel.

#### Cloning of the PLase gene

The PLase gene of _V. vulnificus_ ATCC29307 was cloned in _E. coli_ MC1061 by shotgun cloning. The _V. vulnificus_ genomic DNA was digested partially with either Sau3AI or HindII and the DNA fragments in the range of 2.0 to 9.4 kb were isolated from agarose gel by electro-blotting onto DEAE membrane. Isolated DNA fragments were ligated to pUC119 at the BamHI or HindIII site to construct a sub-genomic DNA library and the resulting library was transformed into _E. coli_ MC1061. Putative PLase clones were isolated based on their hemolytic activity on sheep blood agar plates. Nucleotide sequence analysis of the insert on the positive clone (pHPLC3) was determined by the dideoxy chain termination sequencing method using an ABI377 PRISM DNA sequencer (Perkin-Elmer, USA). Nucleotide sequence was analyzed using Lasergene (DNASTAR Inc., USA) and putative signal sequence was predicted using SignalP 3.0 Server (Technical University of Denmark).

#### Over-expression of the PLase gene

The PLase structural gene (Vp1A) cloned on pHPLC3 was subcloned onto pET22b(+ / pET22b) for over-expression in _E. coli_. The structural gene was amplified by polymerase chain reaction (PCR) using two primers, VPLF2 (5′-GAAGATATGCTATAGGAAGAGATA-3′) and VPLR1 (5′-GTGGACCTCGAGATTTAAGC-3′), carrying a Ndel and a Xhol site (underlined), respectively. In order to remove the signal sequence from the gene another primer set, VPLF3 (5′-AAACATATGGATGACGCGCCTCTC-3′) and VPL4 (5′-AAAGTCAGCTGAAATAAAATGCGTTGC-3′), carrying an Ndel and a SalI site (underlined), respectively, was used. The 1.25 kb long PCR product was digested with Ndel and Xhol (or SalI) and ligated to the corresponding sites on pET22b(+ / pET22b) to place the Vp1A gene under the control of the T7 promoter and to tag the 3′ end of the gene with the sequence encoding 6xHis. Putative subclones were screened for their capability of forming clear zone around the colony by producing hemolysin and/or PLase activities upon induction with 0.5 mM Isopropyl-β-D-thiogalactopyranoside (IPTG) on a blood agar plate and a lecithin agar plate containing 1% lecithin, respectively. The subclone of PLase with or without the signal sequence was designated as pVPL10 and pVPL11, respectively.

#### Purification of recombinant PLase

PLase was over-expressed in _E. coli_ BL21 (DE3) carrying one of the subclones, pVPL10 or pVPL11 from the T7 promoter by inducing with 0.5 mM IPTG during early exponential growth phase in LB broth containing 100 µg/ml of ampicillin. However, PLase from pVPL10 was found in the insoluble fraction as inclusion body and the enzyme was refolded and purified according to Wingfield et al. (1995). The cell extract in the -Tag binding buffer containing 8 M urea was subjected to chromatography using a Ni-NTA column (Qiagen, Germany) after sonication in the presence of 1 mM phenylmethylsulfonyl fluoride (PMSF) and filtration of the supernatant through 3M paper (Whatman, USA). The enzyme bound to the resin was renaturated by sequential wash and incubation with renaturation buffers [100 mM NaCl, 20% glycerol, 20 mM Tris-HCl (pH 7.4)] containing 6, 4, 2, 1, and 0 M urea. Finally, the enzyme was washed with 20 mM Tris-HCl (pH 8.0) and eluted with 20 mM Tris-HCl (pH 8.0) containing 100 mM imidazole. PLase without the signal sequence from pVPL11 was purified from the supernatant of the cell lysis using regular buffers for Ni-NTA chromatography. Protein concentration was determined by the Bradford method (Bradford, 1976) and the purified enzyme was analyzed by sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE) using 10% polyacrylamide gel.

#### Enzyme assay

PLase activity was determined using an artificial substrate, ρ-nitrophenylphosphorylcholine (pNPC; Sigma Co., USA; Kurioka and Matsuda, 1976). Enzyme solution (200 ng/100 µL) was mixed with pre-warmed 50 mM pNPC (60 µL) dissolved in D2O and 2 M Tris-HCl (pH 7.0) containing 1 mM ZnCl2 (140 µL). The reaction mixture was incubated at 37°C for 10 min or until yellow color was developed. The reaction was stopped by boiling for 3 min and mixing with 800 µL of ethanol and 200 µL of 2 M Tris-HCl (pH 7.0). Optical density of the supernatant was measured at 420 nm. One PLase unit was defined as the amount of enzyme that released 1 mmol of p-nitrophenol at 37°C for 1 h (Kuroshima and Hayano, 1982). Moreover, hemolytic activity of PLase was analyzed using sheep red blood cells according to Lee et al. (2002a) or on sheep blood agar plates for the capability of the clone forming clear zone. Lecithinase activity of PLase was examined using agar plates containing 1% lecithin based on the formation of clear zone around colonies (Sibinovic et al., 1971).
Figure 1. Agar plate assay of hemolytic (A) and lecithinase (B) activities of the VplA clones. Panel A represents a blood agar plate inoculated with V. vulnificus 29307 (1), E. coli BL21 (2), E. coli MC1061 harboring pHPLC3 (3), and E. coli BL21 harboring pVPL10 (4 to 7). Panel B represents a lecithin (egg yolk) agar plate inoculated with E. coli BL21 (1) and E. coli BL21 harboring pVPL10 (2 to 4).

**RESULTS AND DISCUSSION**

**Screening of the sub-genomic DNA libraries for the putative PLase gene**

From the two sub-genomic DNA libraries of V. vulnificus, several putative clones were isolated based on their capability of hemolyzing red blood cells. Five hemolytic clones from the Sau3AI sub-genomic DNA library (pSPLC1-5) had inserts of different lengths but with a common open reading frame (ORF) for the zinc metalloprotease gene of V. vulnificus (Chuang et al., 1997). The hemolytic zone of the clones on the blood agar plate was hazy and small. Three hemolytic clones from the HindIII sub-genomic DNA library (pHPLC1-3) carried an identical insert of 3.5 kb long (Supplementary data). E. coli MC1061 carrying pHPLC3 formed a clearer hemolytic zone than V. vulnificus (Figure 1a) and the metalloprotease clones (data not shown) on blood agar plates. They also showed small clear zone around the colonies on a lecithin agar plate (Figure 1b). The coding region for the hemolytic and pNPPC hydrolyzing activities was defined to the 2.5 kb HindIII fragment by deletion mapping (data not shown). Therefore, nucleotide sequence analysis of the DNA fragment was carried out to determine the primary structure of the PLase gene.

**Primary structure of the PLase gene**

Nucleotide sequence analysis of the insert revealed an open reading frame (ORF) of 417 amino acid residues for a protein with a predicted molecular mass of 47,187 Da (Figure 2). The ORF was preceded by a putative ribosome binding site and potential promoter sequences at the 5’ upstream region and followed by an inverted repeat for transcriptional termination at the 3’ downstream. The gene was designated as VplA. The first 19 amino acids of the ORF with a stretch of hydrophobic residues were typical of a signal sequence for secretion, correlating well with the secreted nature of PLase in V. vulnificus.

A homology search of the GenBank/EMBL database revealed that the ORF shared homology with various PLases and hemolysins. The ORF was 99% identical to the PLase encoded by a gene (Gene ID 1181413, VV2_1483) on chromosome II of V. vulnificus CMCP6 strain. It also shared 87% identity with hemolysin of Vibrio harveyi (Zhang et al., 2001), 83% with thermolabile hemolysin of Vibrio parahaemolyticus (Taniguchi et al., 1986), 82% with lecithinase of V. cholerae (Fiore et al., 1997), and 69% with hemolysin of Vibrio campbellii (Luis and Hedreyda, 2006), and 64% with PLase A of Vibrio mimicus (Kang et al., 1998; Lee et al., 2002b) at the amino
Figure 2. DNA and predicted amino acid sequences of the VplA gene and its flanking regions. The sequences of putative promoters are boxed and ribosome binding sites (rbs) are shown in a black box. A transcription terminator-like sequence was underlined. Putative signal sequence was also underlined with a cleavage site indicated by an arrow. The conserved blocks for lipolytic enzymes are shown in shaded boxes and the residues constituting an active site were marked with asterisks.

acid sequence level. The ORF carried conserved sequences (Block I-V, Figure 3) frequently observed among various lipases/acyltransferases in their active sites (Thornton et al., 1988; Brumlik and Buckley, 1996). The catalytic signature for lipolytic enzymes, GDSL, was observed in Block I and the residues constituting the active site are all conserved except one in Block V, in which a D residue was substituted with a G at residue 386 (Figure 3). The significance of the substitution is yet to be elucidated. Based on the results of the comparative analysis, the cloned DNA fragment was likely to carry a putative hemolytic PLase gene (VplA). Southern blot analysis confirmed that the insert was originated from the chromosomal DNA of V. vulnificus (data not shown).

Expression of the VplA gene in E. coli

The VplA gene cloned on pHPLC3 was subcloned onto an expression vector, pET22b(+), since it expressed the PLase activity poorly in E. coli when pNPPC was used as the substrate (Supplementary data). The structural VplA gene amplified by PCR was placed under the control of T7 promoter and fused to six histidine residues at the carboxyl terminus on the expression vector. The resulting recombinant DNA was designated as pVPL10 and E. coli carrying the subclone formed even clearer and larger zones on both blood and lecithin agar plates than those carrying pHPLC3 (Figure 1). However, purification of VplA from the supernatant of the E. coli cell lysate using a Ni-NTA column was not successful, since the protein induced by the addition of IPTG was precipitated forming inclusion body (Figure 4a, lanes 3 and 4). Therefore, in order to recover active VplA from the insoluble fraction of the cell lysate, the proteins in the precipitate was solubilized in the presence of 8 M urea (Figure 4a, lane 5) and mixed with Ni-NTA agarose before being packed into a column. Then, the enzyme was refolded before eluted by sequential removal of urea as described above. Renatured VplA was present in the soluble fraction and purified to an apparent homogeneity (Figure 4a, lane 6).

Substrate specificity of VplA

Substrate specificity of purified VplA was analyzed using 0.5% (w/v) phosphatidylcholine, phosphatidylethanolamine, phosphatidylinositol, phosphatidylserine, and soya-lecithin homogenized in 50 mM Tris-maleic acid-NaOH buffer (pH 7.0) at 37°C for 1 h. TLC analysis of apolar lipids in the reaction mixtures indicated that the
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**Figure 3.** Comparison of conserved blocks among various lipolytic enzymes harboring the GDSL motif. Amino acid residues that are conserved in at least six of the enzymes are presented in shade and those constituting the catalytic sites are underlined. Numbers in parentheses represent the spacing between the conserved blocks (Brumlik and Buckley, 1996).

![Figure 3](image-url)

**Figure 4.** SDS-PAGE analysis of the purified VplA enzymes from *E. coli* BL21 harboring pVPL10 (A) or pVPL11 (B). Proteins were subjected to 10% SDS-polyacrylamide gel and visualized by staining Coomassie-blue. A). Lane 1 was loaded with standard markers; lane 2, *E. coli* cell lysate without induction; lane 3, *E. coli* cell lysate that had been induced by 0.5 mM IPTG; lane 4, supernatant of the induced *E. coli* cell lysate; lane 5, denaturated VplA using 8 M urea; lane 6, purified VplA using a Ni-NTA column. B) Lane 1 was loaded with purified VplA without the signal sequence; lane 2, standard markers.

![Figure 4](image-url)
Figure 5. Substrate specificity of VplA analyzed by TLC. VplA was incubated with 0.5% of each substrate homogenized in 50 mM Tris-HCl (pH 7.0) at 37°C for 30 min and the reaction mixture was subjected to TLC. PC represents phosphatidylcholine; PE, phosphatidylethanolamine; PI, phosphatidylinositol; PS, phosphatidylserine; SO, soya-lecithin. Lanes B were spotted with reactions carried out in the absence of VplA; lanes E, those carried out in the presence of the enzyme.

substrates were hydrolyzed mainly to free fatty acids at various degrees, suggesting that VplA might be a PLase A (Figure 5; Flieger et al., 2000). PLase A has been known to hydrolyze phospholipids into lysophosphatidylcholine and fatty acid (Dessen, 2000). However, significant amounts of 1,2-diacylglycerol were also released, implying that it also had PLase C activity (Flieger et al., 2000). VplA preferentially hydrolyzed various phospholipids in the order of phosphatidylcholine > soya-lecithin > phosphatidylinositol phosphatidylethanolamine > phosphatidylserine. VplA could also hydrolyze pNPPC, an artificial substrate that was specific for PLase C (Figure 6) (Kuroshima and Hayano, 1982). The results, therefore, indicated that VplA seemed to be a unique lecithin-dependent PLase A with PLase C activity.

However, VplA did not share significant homology with any PLase C that has been documented. PLase A has been reported from various pathogenic bacteria such as Mycobacterium tuberculosis (Parker et al., 2007), Legionella pneumophila (Broich et al., 2006) and P. aeruginosa (Kirschnek and Gulbins, 2006) as a potent virulence factor. Recently, Koo et al. (2007) reported that a hemolytic PLase A of V. vulnificus could have a crucial role in the pathogenesis of the bacterial infection using a cytolysin-negative mutant strain, CVD707. However, it is not clear yet whether the PLase A enzyme they reported is a protein identical to VplA, since they did not identify the gene responsible for the activity.

Enzymatic properties of VplA

Temperature and pH optima of purified VplA were investigated using 50 mM pNPPC as the substrate. VplA had the highest activity at 45°C with a broad temperature range for activity between 25 and 80°C in 50 mM Tris-HCl buffer (pH 7.0; Figure 6a). It is interesting to note that PLase from V. vulnificus, a mesophile, is a thermophilic
Figure 6. Effects of various factors on the activity of VplA. (A) Effect of temperature on the enzyme activity was analyzed using 50 mM pNPPC in 50 mM Tris-HCl (pH 7.0) for 30 min. (B) Effect of pH on the activity was analyzed using 50 mM pNPPC in 50 mM sodium acetate for pH 5.0 and 6.0; 50 mM Tris-HCl for pH 7.0-9.0; 50 mM CHES for pH 10.0. The reactions were carried out at 45°C for 30 min. (C) Effect of various divalent cations and EDTA (5 mM) on the activity was analyzed using 50 mM pNPPC in 50 mM Tris-HCl (pH 7.0) at 45°C for 30 min.

Previously, extracellular PLase A2 and Lyso-PLase of *V. vulnificus* E4125 have been characterized by Testa et al. (1984). However, the physico-chemical properties of PLase A2 were different from those of VplA in that it was larger in molecular mass (>80 kDa), heat-labile, and active at pH 5.0 to 5.5. The enzyme was not affected by Ca^{2+}, either. Lyso-PLase was heat-resistant with molecular mass of larger than 80 kDa. Both PLases reported by the group did not seem to be identical to VplA. Moreover, the activity of hemolytic and membranous PLase A reported by Koo et al. (2007) was dependent on Ca^{2+} and exhibited the highest activity at 10 mM. From all these results, *V. vulnificus* was likely to
possess multiple or strain specific PLases with various activities and functions. Further analysis constructing the VplA mutant might prove the existence of multiple PLases in the pathogenic bacterium.

ACKNOWLEDGEMENT

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REFERENCES


Thornton J, Howard SP, Buckley JT (1988). Molecular cloning of a phospholipid-choleterol acyltransferase from Aeromonas hydrophila. sequence homologies with lecithin-cholesterol acyltransferases and