

Cloning, Sequencing, and Role in Virulence of Two Phospholipases (A1 and C) from Mesophilic *Aeromonas* sp. Serogroup O:34

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Two different representative recombinant clones encoding *Aeromonas hydrophila* lipases were found upon screening on tributyrin (phospholipase A1) and egg yolk agar (lecithinase-phospholipase C) plates of a cosmid-based genomic library of *Aeromonas hydrophila* AH-3 (serogroup O34) introduced into *Escherichia coli* DH5 α . Subcloning, nucleotide sequencing, and in vitro-coupled transcription-translation experiments showed that the phospholipase A1 (*pla*) and C (*plc*) genes code for an 83-kDa putative lipoprotein and a 65-kDa protein, respectively. Defined insertion mutants of *A. hydrophila* AH-3 defective in either *pla* or *plc* genes were defective in phospholipase A1 and C activities, respectively. Lecithinase (phospholipase C) was shown to be cytotoxic but non-hemolytic or poorly hemolytic. *A. hydrophila* AH-3 *plc* mutants showed a more than 10-fold increase in their 50% lethal dose on fish and mice, and complementation of the *plc* single gene on these mutants abolished this effect, suggesting that Plc protein is a virulence factor in the mesophilic *Aeromonas* sp. serogroup O:34 infection process.

Mesophilic motile *Aeromonas* species are opportunistic and primary pathogens of a variety of aquatic and terrestrial animals, including humans; the clinical manifestations range from gastroenteritis to soft tissue infections, including septicemia and meningitis (19). Serogroup O:34 strains of mesophilic *Aeromonas* spp. have been recovered from moribund fish (36) and from clinical specimens (40); O:34 is the most common *Aeromonas* serogroup (31), accounting for 26.4% of all infections. Previous investigations have documented O:34 strains as important causes of infections in humans (30, 31). The varied clinical picture of *Aeromonas* infections, and gastroenteritic illness in particular, suggests that complex pathogenic mechanisms occur in aeromonads.

Most aeromonads elaborate a variety of extracellular enzymes: proteases, DNase, RNase, elastase, lecithinase, amylase, lipases, gelatinase, and chitinases; some of them are now confirmed as toxins (32, 38, 42): the cytotoxic/cytolytic enterotoxin (10), three different hemolysins (24, 25, 27) and cytotoxic enterotoxins (34, 46, 48). Some of these toxins (for instance the aerolysin) are involved in septicemic infection (8). However, no clear information is available, to our knowledge, about the possible role of other extracellular enzymes (elastase, amylase, gelatinase, and chitinases) in *Aeromonas* pathogenesis. Clearly, it seems that the extracellular lipases play an important role in pathogenesis, for instance the glycerophospholipid-cholesterol acyltransferases from *A. hydrophila* and *A. salmonicida* (15, 53), which are implicated in the pathogenesis of this bacterium.

Phospholipases (PL) produced by bacteria are involved in different pathogenic process (14, 52) and are often associated with intestinal damage (5, 22, 54). Members of the family *Vibrionaceae* produced secreted PL, some of which act as he-

molysins and some of which act as glycerophospholipid-cholesterol acyltransferases (47, 50, 53). Some of these PL have been cloned and sequenced (18, 49, 51), for instance the alpha-hemolysin (glycerophospholipid-cholesterol acyltransferase) of *A. hydrophila* (53). We report here the cloning, sequencing, identification of gene product, and role in virulence of two different genes of *A. hydrophila* AH-3 (serogroup O:34 [33]) encoding two different PL (PLA1 and PLC [lecithinase]).

MATERIALS AND METHODS

Bacterial strains, plasmids, and growth conditions. The bacterial strains and plasmids used in this study are listed in Table 1. *Escherichia coli* strains were grown on Luria-Bertani LB Miller broth and LB Miller agar (6), while *Aeromonas* strains were grown on tryptic soy broth or agar (TSB and TSA) (37). Tributyrin-agar and egg yolk-agar were prepared as described in reference 6. Ampicillin (50 μ g/ml), chloramphenicol (50 μ g/ml), kanamycin (30 μ g/ml), and/or tetracycline (20 μ l/ml) was added to the different media when needed.

General DNA methods. DNA manipulations were carried out essentially as previously described (44). DNA restriction endonucleases, T4 DNA ligase, *E. coli* DNA polymerase (Klenow fragment), and alkaline phosphatase were used as recommended by the suppliers.

DNA sequencing. The primers used for DNA sequencing were purchased from Pharmacia LKB Biotechnology. Double-stranded-DNA sequencing was performed by the dideoxy-chain termination method of Sanger et al. (45) with the Abi Prism dye terminator cycle-sequencing kit (Perkin-Elmer).

DNA and protein sequence analysis. The DNA sequence was translated in all six frames, and all open reading frames longer than 100 bp were inspected. Deduced amino acid sequences were compared with those of DNA translated in all six frames from the nonredundant GenBank and EMBL databases by using the BLAST network service at the National Center for Biotechnology Information (2). Multiple-sequence alignments and determination of putative terminator sequences were done with the PileUp and Terminator programs from the Genetics Computer Group package (GCG, Madison, Wis.) on a VAX 4300.

Construction of *pla* and *plc* mutant strains. To obtain mutants with defined insertion mutations in the *pla* and *plc* genes, a method based on the use of the suicide plasmid pFS100 was applied (43). Plasmid pBR-PLA2 was *Bgl*II digested and blunt ended by treatment with the Klenow fragment of DNA polymerase, and a *pla* internal DNA fragment (1,230 bp) was isolated, ligated to *Eco*RV-digested and dephosphorylated pFS100, and transformed into *E. coli* MC1061 (λ pir) to generate plasmid pFS-PLA.

Plasmid pBR-PLC was double digested with *Sal*I and *Kpn*I and blunt ended, and a *plc* internal DNA fragment (697 bp) was isolated, ligated to *Eco*RV-

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TABLE 1. Bacterial strains, cosmids, and plasmids used in this study

Strain, cosmid, or plasmid	Relevant characteristics	Source or reference
<i>E. coli</i>		
DH5 α	F ⁻ <i>endA hsdR17</i> (r _k ⁻ m _k ⁺) <i>supE44 thi-1 recA1 gyrA96 ϕ80lacZ</i>	23
XL1-Blue	<i>recA1 endA1 gyrA96 thi-1 hsdR17 supE44 relA1 lac</i> (F' <i>proAB lacIZ ΔM15 Tn10</i>)	Stratagene
MC1061	(λ <i>pir</i>), <i>thi thr-1 leu6 proA2 his-4 argE2 lacY1 galK2 ara14 xyl5 supE44, λpir</i>	43
SM10	(λ <i>pir</i>), <i>thi thr leu tonA lacY supE recA::RP4-2-Tc::Mu, Km^r, λ pir</i>	43
<i>A. hydrophila</i>		
AH-3	Wild type, serogroup O:34	36
AH-405	Rifampin-resistant mutant derived from AH-3	39
AH-3PLA1	<i>pla</i> insertion AH-405 mutant obtained with pFS-PLA	This work
AH-3PLA4	<i>pla</i> insertion AH-405 mutant obtained with pFS-PLA	This work
AH-3PLC2	<i>plc</i> insertion AH-405 mutant obtained with pFS-PLC	This work
AH-3PLC3	<i>plc</i> insertion AH-405 mutant obtained with pFS-PLC	This work
Cosmids		
pLA2917	Tc ^r Km ^r	1
COS-PLA	pLA2917 with 20-kb chromosomal AH-3 <i>Sau3A</i> insert (<i>pla</i> gene)	This work
COS-PLC	pLA2917 with 20-kb chromosomal AH-3 <i>Sau3A</i> insert (<i>plc</i> gene)	This work
Plasmids		
pBR328	Ap ^r Cm ^r Tc ^r	44
pBR-PLA1	pBR328 with 8.3-kb <i>HindIII</i> insert from COS-PLA (<i>pla</i> gene)	This work
pBR-PLA2	<i>HpaI-EcoRV</i> 4.5-kb insert of <i>pla</i> gene derived from pBR-PLA1	This work
pBR-PLC	pBR328 with 3-kb <i>HindIII</i> insert from COS-PLC (<i>plc</i> gene)	This work
pBluescript SK	Ap ^r <i>ori</i> of ColE1	Stratagene
pSK-PLA	pBluescript SK with insert of pBR-PLA2 (<i>pla</i> gene)	This work
pSK-PLC	pBluescript SK with insert of pBR-PLC (<i>plc</i> gene)	This work
pACYC184	Cm ^r Tc ^r	44
pACYC-PLA	pACYC184 with insert of pBR-PLA2 (<i>pla</i> gene)	This work
pACYC-PLC	pACYC184 with insert of pBR-PLC (<i>plc</i> gene)	This work
pFS100	pGP704 suicide plasmid, λ <i>pir</i> dependent, Km ^r	43
pFS-PLA	pFS100 with an internal fragment (1,230 bp) of <i>pla</i>	This work
pFS-PLC	pFS100 with an internal fragment (697 bp) of <i>plc</i>	This work

digested and dephosphorylated pFS100, and transformed into *E. coli* MC1061 (λ *pir*) to generate plasmid pFS-PLC. Plasmid pFS-PLA and plasmid pFS-PLC were isolated, transformed into *E. coli* SM10(λ *pir*), and transferred by conjugation to *A. hydrophila* AH-405 (rifampin resistant) to obtain mutants with defined insertion mutations in the *pla* and *plc* genes, respectively.

Substrate specificity and enzyme activity measurements. The substrate specificity with neutral glycerides and glycerophospholipids was determined as previously described (16, 17). Lipase activity was initially determined with tributyrin by the method of Ihara et al. (28). PLC activity was tested initially with p-nitrophenylphosphorylcholine as described by Ingham and Pemberton (29).

Determination of extracellular activities. Hemolysin and cytotoxin assays were performed as previously described (37). Briefly, hemolysin activity was assayed with a 1% suspension of sheep, bovine, or rainbow trout erythrocytes (4) and cytotoxin activity was assayed on Vero cell monolayers (7) and EPC (epithelioma papulosum of carp, *Cyprinus carpio*) monolayers (57). Enterotoxin activity was assayed by the rabbit ligated ileal loop assay as described by Nishibuchi et al. (41). In some *E. coli* strains, these activities were also assayed with the periplasmic proteins released by osmotic shock (56).

Virulence for fish and mice. The virulence of the strains grown at 20°C was measured by monitoring their 50% lethal dose (LD₅₀) by the method of Reed and Muench, as previously described (37).

(i) **Fish.** Rainbow trout (12 to 20 g) were maintained in 20-liter static tanks at 17 to 18°C. The fish were injected intraperitoneally with 0.05 ml of the test samples (approximately 10⁹ viable cells). Mortality was recorded up to 2 weeks; all the deaths occurred within 2 to 8 days.

(ii) **Mice.** Albino Swiss female mice (5 to 7 weeks old) were injected intraperitoneally with 0.25 ml of the test samples (approximately 5 × 10⁹ viable cells). Mortality was recorded up to 1 week; all the deaths occurred within 2 to 5 days.

Nucleotide sequence accession numbers. The nucleotide sequences of the genes described here have been assigned the following GenBank accession numbers: *pla*, AF092033; *plc*, AF092034.

RESULTS AND DISCUSSION

Mesophilic *Aeromonas* strains from different O serogroups, but mainly from serogroup O:34, seem to produce more than

one enzyme with lipolytic activity when grown on egg yolk medium according to Matos et al. (35). It is clear that in this medium these strains produce a precipitate zone (lecithinase reaction) and an iridescent film or "pearly layer," visible by reflected light, with lipase activity (35). Furthermore, O:34 strains were able to degrade tributyrin in a solid medium (lipolytic activity). We decided initially to call PLA the lipase activity on tributyrin medium and PLC the lecithinase activity on egg yolk medium. We decided to clone the corresponding genes from a single O:34 strain (AH-3) and see if they encoded two different PL activities.

Cloning of two *A. hydrophila* AH-3 genomic regions encoding PLA and PLC activities. *A. hydrophila* AH-3 (serogroup O:34) produces PLA and PLC activities. To determine the basis for these activities, a cosmid-based genomic library of *A. hydrophila* AH-3 was constructed and introduced into *E. coli* DH5 α (21). Tetracycline-resistant (20 μ g/ml) clones were screened independently on tributyrin and egg yolk-agar plates. We found two representative recombinant clones, COS-PLA and COS-PLC, with lipase activity on tributyrin and lecithinase activity on egg yolk-agar plates, respectively. It is important to note that COS-PLC showed only the precipitation zone, not the possible lipase activity (iridescent film) on egg yolk-agar plates.

To localize the genes involved in PLA (COS-PLA) and PLC (COS-PLC) activities, different subcloning experiments with some plasmid vectors were performed and the recombinant transformants were screened for the lipase (tributyrin) and lecithinase (egg yolk) activities, respectively. The strains and plasmids obtained are described in Table 1.

TABLE 2. Identity and similarity of the amino acid sequence of Pla1 and Plc proteins from *A. hydrophila* AH-3 to other proteins

Protein ^a and bacterium of origin	No. of amino acids	% identity	Overlap (amino acids)	Accession no.	Reference
Pla-1 (PLA1), <i>A. hydrophila</i> AH-3	805			AF092033	
LipE (extracellular lipase), <i>A. hydrophila</i>	684	52.1	696	P40600	3
Lip (extracellular lipase), <i>A. hydrophila</i>	751	50.4	746	O05484	12
Apl-1 (PLC), <i>A. hydrophila</i>	684	48.5	671	Q44055	29
Alt (cytotoxic enterotoxin), <i>A. hydrophila</i>	368	96.0	326	Q44061	11
Plc (lecithinase, PLC), <i>A. hydrophila</i> AH-3	572			AF092034	
Hly1 (hemolysin), <i>A. salmonicida</i>	572	99.1	572	Q08675	26
LecD (PLD), <i>Vibrio damsela</i>	573	61.4	570	Q60079	Unpublished

^a The percentages were obtained from pair comparisons, using the Gap program. Gap program settings: gap weight 12 and length weight 12.

Sequencing of the DNAs conferring PLA and PLC activities.

The nucleotide sequences of 2,602 and 2,868 bp were determined in both directions from plasmid pSK-PLA (*pla*) and pSK-PLC (*plc*), respectively; oligonucleotides M13 universal, reverse M13, SK, and other sequence-derived oligonucleotides were used to complete the nucleotide sequence.

Analysis of the deduced sequence of pSK-PLA showed a potential ORF (*pla*) (nucleotides 176 to 2591), encoding a putative protein of 805 amino acid residues with a predicted molecular mass of 82.7 kDa. Sequence analysis of pSK-PLC showed a potential ORF (*plc*) (nucleotides 885 to 2691), encoding a putative protein of 572 amino acid residues with a predicted molecular mass of 64.8 kDa. Upstream of the *pla* and *plc* genes, sequences similar to the ribosomal binding site were found. Sequences similar to the -10 and -35 consensus sequences of *E. coli* promoter were found upstream of *plc* gene, and a palindromic sequence, which could be involved in transcription termination, was found downstream from *plc* gene.

Analysis of the *pla* and *plc* deduced amino acid sequences. The deduced 805-amino-acid sequence from *pla* showed amino acid similarities to three extracellular lipases (LipE, Lip, and Apl-1) and a heat-labile cytotoxic enterotoxin (Alt) from *A. hydrophila* (Table 2). All five proteins show the lipase substrate binding signature sequence VHFLGHSL (13). Analyses of the Pla-1 amino acid sequence showed a putative lipoprotein signal sequence (residues 1 to 17) and a putative lipoprotein signal sequence cleavage site between residues 17 and 18. Another putative signal peptidase cleavage site was found between residues 48 and 49. Taken together, these two features strongly suggest that the Pla-1 is a secreted protein. Similar signal sequences and cleavage sites were previously found in the three extracellular lipases similar to Pla-1 but not in the heat-labile cytotoxic enterotoxin. These results are in agreement with the previously reported similarity (47 to 51%) between Apl-1 and Alt (11). Furthermore, Alt also showed 54 and 52% of similarity to Lip (12) and LipE (3) extracellular lipases, respectively.

The putative Pla-1 lipoprotein had an apparent molecular mass of 83 kDa on sodium dodecyl sulfate-polyacrylamide gel electrophoresis analysis of plasmid pBR-PLA2 gene products with an *E. coli* S30 coupled transcription-translation system (Amersham) and [³⁵S]methionine (Amersham) (Fig. 1).

The deduced 572-amino-acid Plc protein was found to be nearly identical to hemolysin ASH1 from *A. salmonicida* ATCC14174 (26), and furthermore there were only four different nucleotides between the *plc* and this hemolysin structural gene, showing that the *plc* gene is practically identical in both *Aeromonas* species. The Plc protein was also found to be similar to the unpublished PLD from *Vibrio damsela* (Table 2). However, no significant similarity was detected between Plc

and a previously reported PLC from *A. hydrophila* (Apl-1), which is similar to Pla-1 (Table 2). Analyses of the Plc amino acid sequence showed a putative signal sequence (residues 1 to 19) and a putative signal sequence cleavage site between residues 19 and 20. In vitro coupled transcription-translation experiments on plasmid pBR-PLC showed a polypeptide of about 65 kDa, similar in size to the expected *plc* mature product (Fig. 1).

PLA and PLC are two different enzymes with PL activity.

E. coli strains harboring the *pla* gene in the COS-PLA, pBR-PLA1, pBR-PLA2, and pSK-PLA plasmids were able to degrade tributyrin but unable to show any lecithinase activity on egg yolk medium. *E. coli* DH5 α and the same strain carrying the same plasmids used as vectors without the DNA insert from AH-3 showed no activity in either tributyrin or egg yolk media. *E. coli* strains harboring COS-PLA, pBR-PLA1, pBR-PLA2, pACYC-PLA, and pSK-PLA plasmids were able to degrade other neutral glycerides (di- or triolein) or natural glycerophospholipids carrying a 1-acyl bond (phosphatidylcholine, phosphatidylinositol, phosphatidylethanolamine, or phosphatidylglycerol) but unable to degrade neutral glycerides like cholesteryloleate or *p*-nitrophenylacetate or substituted (at position 1-acyl) glycerophospholipids like 1-alkyl-2-acyl-*sn*-glycero-3-phosphocholine. For all these reasons, we concluded that this activity found in tributyrin plates is a PLA1 activity (15, 16).

E. coli strains harboring the *plc* gene in the Cos-PLC, pBR-PLC, pACYC-PLC, and pSK-PLC plasmids were able to pre-

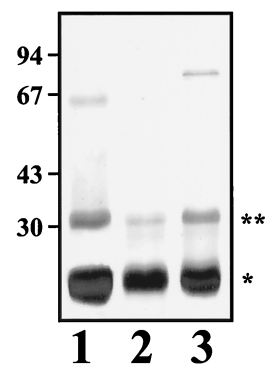


FIG. 1. In vitro *E. coli* S30 coupled transcription-translation system with [³⁵S]methionine performed as specified by the supplier (Amersham). Lanes: 1, pBR-PLC plasmid DNA (*plc* gene); 2, pBR328 plasmid DNA (cloning vector); 3, pBR-PLA2 plasmid DNA (*pla* gene). *, chloramphenicol acetyltransferase (25 kDa) from the Cm^r determinant of pBR328 plasmid DNA; **, β -lactamase (31.5 kDa) from the Ap^r determinant of pBR328 plasmid DNA. Molecular mass standards are shown in kilodaltons.

TABLE 3. Determination of some extracellular and periplasmic activities in different *E. coli* and *A. hydrophila* strains as described in Materials and Methods

Strain	Cellular fraction ^a	Hemolysis on erythrocytes of:			Cytotoxicity on:	
		Sheep	Bovine	Rainbow trout	Vero cells	EPC cells
<i>E. coli</i>						
DH5 α	S	— ^b	—	—	—	—
	P	—	—	—	—	—
DH5 α + pACYC-PLA	S	—	—	—	—	—
	P	—	—	—	—	—
DH5 α + pACYC-PLC	S	—	—	1/8	1/4	1/16
	P	—	—	1/16	1/64	1/128
<i>A. hydrophila</i>						
AH-405 (AH-3 Rif ^r)	S	1/64	1/64	1/128	1/64	1/128
AH-3PLA1; <i>pla</i> insertion mutant from AH-405	S	1/64	1/64	1/128	1/64	1/128
AH-3PLA4; <i>pla</i> insertion mutant from AH-405	S	1/64	1/64	1/128	1/64	1/128
AH-3PLA1(pACYC-PLA); mutant <i>pla</i> complemented	S	1/64	1/64	1/128	1/64	1/128
AH-3PLA4(pACYC-PLA); mutant <i>pla</i> complemented	S	1/64	1/64	1/128	1/64	1/128
AH-3PLC2; <i>plc</i> insertion mutant from AH-405	S	1/64	1/64	1/128	1/4	1/16
AH-3PLC3; <i>plc</i> insertion mutant from AH-405	S	1/64	1/64	1/128	1/4	1/16
AH-3PLC2(pACYC-PLC); mutant <i>plc</i> complemented	S	1/64	1/64	1/128	1/32	1/64
AH-3PLC3(pACYC-PLC); mutant <i>plc</i> complemented	S	1/64	1/64	1/128	1/32	1/128

^a S, supernatant; P, periplasmic fraction.

^b —, not detected.

precipitate the egg yolk medium (lecithinase activity) but unable to degrade tributyrin. Also, these strains were able to rapidly degrade the typical synthetic substrate for PLC, *p*-nitrophenylphosphorylcholine, at pH 7.2 with 2 mM CaCl₂, and this activity was inhibited by spermine tetrahydrochloride (Calbiochem). The PL activity was dramatically reduced (<5% of the activity) on the same substrate at pH = 5.7 and 0.5 M CaCl₂ (typical conditions for measuring PLD activity [20]). Two different assays were performed to differentiate PLC and PLD activities, and the PL activity determined by the *plc* gene showed (i) the presence of the diglyceride when incubated with lecithin as determined by thin-layer chromatography (petroleum ether-diethyleter-acetic acid [90:10:1, vol/vol]) and visualized by UV light as described by Grossman et al. (20) and (ii) hydrolysis of phosphatidylcholine and release of P_i in a low-P_i medium (33). The release of P_i was measured spectrophotometrically by the method of Chen et al. (9), in either concentrated supernatants (AH-3 = 18 μ g of P_i; AH-3PLC2 [*plc* insertion mutant] = 0.15 μ g of P_i) or periplasmic fractions (DH5 α = 0.3 μ g of P_i; DH5 α with the pACYC-PLC plasmid [*plc*] = 22 μ g of P_i). From these results, we concluded that the lecithinase activity in these strains on egg yolk medium is mainly a PLC activity.

Construction of defined *pla* and *plc* insertion mutants. Plasmid pFS-PLA, a replication *pir*-dependent plasmid, carrying an internal fragment of the *pla* gene was transferred by mating to a rifampin-resistant *A. hydrophila* strain, AH-3 (AH-405 [39]), and Rif^r and Km^r colonies were selected. We obtained mutants AH-3PLA1 and AH-3PLA4 unable to degrade tributyrin but still able to show lecithinase (PLC) activity. The insertion of plasmid pFS-PLA in these mutants was confirmed by Southern blot analysis with appropriate DNA probes. Complementation of these mutants with COS-PLA or pACYC-PLA restored the PLA1 activity on tributyrin medium.

Plasmid pFS-PLC carrying a *plc* gene internal fragment was used in identical way to that mentioned above to generate mutants AH-3PLC2 and AH-3PLC3 (also confirmed by Southern blot analyses), which were unable to show any lecithinase (PLC) activity on egg yolk medium but were able to degrade

tributyrin (PLA1 activity). Complementation of these mutants with COS-PLC or pACYC-PLC restored the lecithinase activity on egg yolk medium. All these results indicate that *pla* and *plc* are different genes in *A. hydrophila* AH-3 and also are unique genes for PLA1 and PLC activities in this strain.

PLC (lecithinase) is cytotoxic. As we previously shown *A. hydrophila* AH-3, as well as other strains from serogroup O:34, are hemolytic, cytotoxic, and enterotoxic (37, 38). As shown in Table 3, neither *E. coli* strains carrying *pla* nor *A. hydrophila* AH-3 *pla* insertion mutants were altered in their hemolytic or cytotoxic activities (no activities found for *E. coli* strains in either supernatants or periplasmic cellular fractions). Also, nonenterotoxic activity was found in *E. coli* strains carrying the *pla* gene and reduced enterotoxicity was found in *pla* insertion mutants of *A. hydrophila* AH-3, despite the high homology between Alt (heat-labile cytotoxic enterotoxin [11]) and Pla in 33% of the last protein. Then, we concluded that Pla is an extracellular lipase with PLA1 activity but is nonhemolytic, noncytotoxic, and nonenterotoxic.

However, *E. coli* strains carrying the *plc* gene showed a clear cytotoxic activity on Vero and EPC cells (by assaying either supernatant or periplasmic fraction). Furthermore, *plc* insertion mutants of *A. hydrophila* AH-3 were reduced in their cytotoxic activity, and this activity was fully restored in these mutants by complementation with COS-PLC or pACYC-PLC (Table 3). These results for the cytotoxicity of Plc suggested that the wild-type *A. hydrophila* strain has several cytotoxic factors, with Plc being one of them. The results observed for the hemolytic activity of *E. coli* strains carrying the *plc* gene, *plc* insertion mutants of *A. hydrophila* AH-3, and the mutants complemented with COS-PLC or pACYC-PLC (Table 3) suggested the following. (i) Plc is nonhemolytic on sheep or bovine erythrocytes and only slightly on rainbow trout erythrocytes. These results are mainly in agreement with those reported for Hly1 of *A. salmonicida* (26), which has 99% identity to Plc (Table 2). The authors concluded that Hly1 (termed "hemolysin" despite its poorly hemolytic activity) found in *A. salmonicida* ATCC 14174 did not originate from this bacterium because of its low GC content, the codon usage frequency, and

TABLE 4. Virulence for rainbow trout and mice of *A. hydrophila* AH-3 (serogroup O:34), defined insertion mutants, and mutants complemented by *pla* or *plc*

Strain and main characteristics	LD ₅₀ ^a for:	
	Rainbow trout	Mice
AH-3; wild-type	0 ^{5.3}	10 ^{7.4}
AH-405; AH-3 rifampin-resistant mutant	10 ^{5.4}	10 ^{7.6}
AH-3PLA1; <i>pla</i> insertion mutant from AH-405	10 ^{5.6}	10 ^{7.7}
AH-3PLA4; <i>pla</i> insertion mutant from AH-405	10 ^{5.5}	10 ^{7.5}
AH-3PLA1(pACYC-PLA); mutant <i>pla</i> complemented	10 ^{5.7}	10 ^{7.5}
AH-3PLA4(pACYC-PLA); mutant <i>pla</i> complemented	10 ^{5.5}	10 ^{7.6}
AH-3PLC2; <i>plc</i> insertion mutant from AH-405	10 ^{7.4}	>10 ^{9.0}
AH-3PLC3; <i>plc</i> insertion mutant from AH-405	10 ^{7.3}	>10 ^{9.0}
AH-3PLC2(pACYC-PLC); mutant <i>plc</i> complemented	10 ^{5.6}	10 ^{7.7}
AH-3PLC3(pACYC-PLC); mutant <i>plc</i> complemented	10 ^{5.7}	10 ^{7.6}

^a The values are the averages of three independent experiments, and the maximum deviation was always <10^{0.4}.

the negative results obtained by a DNA probe for this gene; unfortunately, they did not test if this protein showed any lecithinase activity (26). We suggest that this gene originates from *A. hydrophila*. (ii) Plc is not a major hemolytic factor on *A. hydrophila* AH-3, because no major differences could be observed between the *plc* insertion mutants and the wild-type strain.

Finally, nonenterotoxic activity was found in *E. coli* strains carrying the *plc* gene and reduced enterotoxicity was found in *plc* insertion mutants of *A. hydrophila* AH-3. We therefore concluded that Plc is nonenterotoxic.

PLC (lecithinase) is an important virulence factor. As pointed out by Vipond et al. (55), the major *A. salmonicida* secreted proteins (toxins) are not essential for the virulence of this bacterium, as they demonstrated with defined deletion mutants. We therefore decided to study the contribution to *A. hydrophila* pathogenesis of our defined *pla* and *plc* insertion mutants. We tested the virulence of the wild-type strain and the corresponding *pla* and *plc* insertion mutants (LD₅₀), as shown in Table 4. As can be observed, no differences were found in mortality between the wild-type strain (or they rifampin-resistant mutant) and mutants AH-3PLA1 and AH-3PLA4, which suggests that the PLA1 activity is not essential for virulence on these strains or that the mutation is unstable in vivo. However, mutants AH-3PLC2 and AH-3PLC3 showed a higher LD₅₀ (an increase of 1 to 2 log units) in both fish and mice than the wild-type strain did. Complementation of these insertion mutants with COS-PLC or just with pACYC-PLC (carrying the single *plc* gene) completely restored their virulence for fish or mice (similar LD₅₀ to the wild-type strain [Table 4]). These results suggested that Plc (lecithinase) is an important virulence factor for mesophilic *Aeromonas* (serogroup O:34) pathogenesis.

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