Molecular Mechanism of Lipase Activator Protein from Pseudomonas aeruginosa (Dissertation_全文)

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Molecular Mechanism of Lipase Activator Protein
from *Pseudomonas aeruginosa*

HIROYUKI SHIBATA
1998
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Lipase (triacylglycerol acylhydrolase, EC 3.1.1.3) catalyzes hydrolysis of triacylglycerol into fatty acids and glycerol. This enzyme is distributed among a number of organisms from bacteria to mammalians. In general, lipases possess characteristic properties most enzymes do not. First, their natural substrates, long-chain fatty acyl esters, are usually insoluble. Second, lipases remain stable and active in a variety of organic solvent (Zaks and Klibanov, 1984), so that catalyze reverse reactions in the ester synthetic direction. Third, reactions catalyzed by lipases show high enantioselectivity around alcohol leaving group of substrate. For these reasons, lipases are expected as a versatile catalyst for potential applications such as food industry, detergent formulation, and medicinal chemistry. Particularly, lipases produced from Gram-negative bacterial genus *Pseudomonas* possess not only the above features, but also practical availability as follows (Jaeger et al., 1994). *Pseudomonas* lipase is one of the extracellular enzymes, thus the purified sample can be easily prepared from culture medium (Stuer et al., 1986, Gilbert et al., 1991, Chihara-Sio mi et al., 1992, Sugihara et al., 1992, Taipa et al., 1992). In addition, enzymatic characteristics of the lipase such as thermostability (Iizumi et al., 1990, Sugihara et al., 1992) or substrate specificity (Inagaki et al., 1989a, Ihara et al., 1991) vary according to its producing species of *Pseudomonas*. Typically, LipA (molecular weight of 30,100), an extracellular lipase from *P. aeruginosa* TE3285, expresses a characteristic substrate specificity, and can be utilized for kinetic resolution to obtain optically active chemicals. Namely, LipA catalyzes the stereoselective acylation of [1,1'-binaphthyl]-2,2'-diol (binaphthol) (Inagaki et al., 1989a), benzaldehyde cyanohydrin (mandelonitrile) (Inagaki et al., 1989b), and a-aminonitrile (Nakai et al., 1992) (Fig. 1-1). Notably, the kinetic resolution of binaphthol through acylation was accomplished only by *P. aeruginosa* LipA, but not by lipases from other organisms such as *P. cepacia* M-12-33 (Inagaki et al., 1989a, Nishioka et al., 1991). This result suggests that LipA possesses a substrate recognition site distinct from that of the other lipases. Therefore, it is expected that analyses of LipA based on...
protein structure could elucidate this substrate recognition mechanism, and to give an insight into design of a noble enzyme to catalyze a particular reaction.

For this purpose, at the beginning, the structural gene (lipA) of the P. aeruginosa LipA has been cloned and sequenced (Chihara-Siomi et al., 1992) (Fig. 1-2). The lipA gene consists of an open reading frame of 936 bases, and encodes a polypeptide of 311 amino acid residues containing a signal sequence of 26 residues at the N-terminus. However, when only the lipA gene was introduced into E. coli host-vector system, no detectable lipase activity was observed. This observation caused by a fact that an additional DNA region at closely downstream of lipA was essential for the production of the active LipA protein (Chihara-Siomi et al., 1992). This region includes another set of Shine-Dalgarno sequence and subsequent open reading frame (lipB) of 1,023 bases, which is deduced to encode 340-residue polypeptide. On the basis of the gene structure, lipA and lipB are likely to form a single bicistronic operon. These features suggest that the lipB gene product (LipB, molecular weight of 37,700) specifically acts on active LipA production system. However, even in the presence of lipB, remarkable fractions of the LipA polypeptide are produced as inactive inclusion bodies in E. coli. In order to establish more effective production system of LipA, it is important to understand function of LipB in molecular level.

It has been found by in vitro experiments that LipB assists folding of LipA into its active conformation (Oshima-Hirayama et al., 1993). In this study, LipB was prepared as a recombinant fusion protein with glutathione transferase. This fusion protein recovered the lipase activity of two preparations of inactive LipA, that is, recombinant LipA solubilized from inclusion bodies accumulated in E. coli, and denatured LipA purified from the culture medium of Pseudomonas. These results suggest that LipB refolds and reactivates LipA losing the active structure at a post-translational event in the cell. This function seems to be similar to molecular chaperones, which act on a number of non-native polypeptides so as to mediate their folding at stages of biosynthesis and translocation in the cell (Ellis, 1987, Hartl, 1996). One of the common characteristics of the chaperones is that their binding of the substrate polypeptide is coupled with their ATP hydrolytic activity. On the other hand, LipB-assisted reactivation was not affected by ATP or magnesium ion (Oshima-Hirayama et al., 1993). Thus, LipB is a different type of folding factor from general molecular chaperones. So far, protein folding factors similar to LipB have been found only from Pseudomonas species (Gilbert, 1993) and Acinetobacter, that is, LimL from Pseudomonas sp. 109 (Ihara et al., 1992, Ihara et al., 1995), LipH from P. aeruginosa PA01 (Wohlfarth et al., 1992), LimA from P. cepacia DSM3959 (Jørgensen et al., 1991, Hobson et al., 1993, Aamand et al., 1994, Hobson et al., 1995), Act from Pseudomonas sp. KWI-56 (Iizumi et al., 1991, Iizumi and Fukase, 1994), LipX from P. cepacia M-12-33 (Nakanishi et al., 1991), LipB from P. glumae PG1 (Frenken et al., 1993a, Frenken et al., 1993b), and LipB from A. calcoaceticus BD413 (Kok et al., 1995). All of these proteins are encoded closely to the gene of the corresponding lipase. Amino acid sequences of the lipase activator proteins from Pseudomonas species are aligned in Fig. 1-3. LimL and LipH show more than 90% sequence identities against P. aeruginosa LipB, whereas the other four activator proteins show less than 30% identities. This propensity among the activator proteins is applied to that among the corresponding lipases from the respective species (Fig. 1-4). In any case, these activator proteins

![Fig. 1-1. Stereoselective acylation catalyzed by LipA, lipase from Pseudomonas aeruginosa TE3285.](image)
CHAPTER 1

Fig. 1-2. Nucleotide sequence of lipA and lipB genes from Pseudomonas aeruginosa TE3285. Putative Shine-Dalgarno sequences are boxed. Filled triangle indicates the position of the release of the signal peptide. Horizontal arrows indicate palindromic sequences, which are putative termination signals. The sequences reported by Chihara-Sioni et al. (1992) has been corrected, and new sequence has been incorporated into the DDBJ/EMBL/databases with accession number of AB008452.
### Amino Acid Sequence Alignment among Pseudomonas Lipase Activator Proteins

<table>
<thead>
<tr>
<th>Species</th>
<th>Lipase Activator Protein</th>
<th>Accession Number</th>
<th>Sequence</th>
</tr>
</thead>
<tbody>
<tr>
<td>Pseudomonas cepacia M-12-33</td>
<td>LipB</td>
<td>M-12-33</td>
<td></td>
</tr>
<tr>
<td>Pseudomonas cepacia TE3285</td>
<td>LipB</td>
<td>TE3285</td>
<td></td>
</tr>
<tr>
<td>Pseudomonas cepacia DSM3959</td>
<td>LipB</td>
<td>DSM3959</td>
<td></td>
</tr>
<tr>
<td>Pseudomonas cepacia PA01</td>
<td>LipB</td>
<td>PA01</td>
<td></td>
</tr>
<tr>
<td>Pseudomonas cepacia DSM109</td>
<td>LipB</td>
<td>DSM109</td>
<td></td>
</tr>
<tr>
<td>Pseudomonas cepacia KWI156</td>
<td>LipB</td>
<td>KWI156</td>
<td></td>
</tr>
<tr>
<td>Pseudomonas cepacia KWI56</td>
<td>LipB</td>
<td>KWI56</td>
<td></td>
</tr>
<tr>
<td>Pseudomonas aeruginosa DSM3959</td>
<td>LipB</td>
<td>DSM3959</td>
<td></td>
</tr>
<tr>
<td>Pseudomonas aeruginosa PA01</td>
<td>LipB</td>
<td>PA01</td>
<td></td>
</tr>
<tr>
<td>Pseudomonas aeruginosa KWI56</td>
<td>LipB</td>
<td>KWI56</td>
<td></td>
</tr>
<tr>
<td>Pseudomonas aeruginosa DSM109</td>
<td>LipB</td>
<td>DSM109</td>
<td></td>
</tr>
</tbody>
</table>

**Conserved Residues:** Conserved residues are indicated with asterisk. The numbering of amino acids is given for P. aeruginosa TE3285 lipase activator protein (LipB) of P. aeruginosa TE3285 (Ichihara-Siomi et al., 1992). P. aeruginosa DSM3959 (Jørgensen et al., 1991); P. cepacia M-12-33 (Nakanishi et al., 1991); P. glumae PG1 (Frenken et al., 1992).

**Fig. 1-3.** Amino acid sequence alignment among Pseudomonas lipase activator proteins. Conserved residues are indicated with asterisk. The numbering of amino acids is given for P. aeruginosa TE3285 lipase activator protein (LipB) of P. aeruginosa TE3285 (Ichihara-Siomi et al., 1992); P. aeruginosa DSM3959 (Jørgensen et al., 1991); P. cepacia M-12-33 (Nakanishi et al., 1991); P. glumae PG1 (Frenken et al., 1992).
then this polypeptide is refolded by LipB in the periplasm following secretion into the extracellular medium.

With respect to genetic structure and in vivo function, LipB is likely to be similar to N-terminal propeptide of several proteases, such as subtilisin (Ikemura et al., 1987), carboxypeptidase Y (Winther and Sørensen, 1991), and α-lytic protease (Silen et al., 1989). These propeptides are synthesized as a single polypeptide with its mature protease region, and specifically mediate folding of the protease after translocation through cellular membrane (Shinde and Inouye, 1993, Eder and Fersht, 1995). From the crystallographic analysis of the complex between subtilisin and its propeptide (Gallagher et al., 1995), the propeptide is likely to recognize specific structural elements of the mature region through the refolding process. Considering the functional similarity to the propeptides, also LipB could recognize some structural segments of LipA. Candidates of such substructures can be presumed by three-dimensional structures of bacterial lipases (Noble et al., 1994, Lang et al., 1996, Schrag et al., 1997, Kim et al., 1997). From these analyses, common structural features of bacterial lipases have been found, that is, (1) serine protease-like active site including catalytic triad and oxyanion hole, (2) hydrophobic surface on the walls of the active site cleft and helical lid structure for masking the hydrophobic site, and (3) calcium binding site. The first two features are also applicable to eukaryotic lipases according to their crystal structures, whereas the third one is fit to only bacterial lipases. Although three-dimensional structure of LipA from P. aeruginosa TE3285 has not been resolved, LipA is expected to possess the above three features. Thus, LipB could mediate construction of such structural features of LipA in its folding process. However, properties of LipB such as reactivation kinetics, requirements, and functional amino acid residues have been unknown because purification of LipB is difficult. It is considered that elucidation of its properties enables us to understand key process of protein folding in a molecular level. Furthermore, this could contribute to give an important insight into the protein translocation in the cell.

In the present study, the LipA reactivation mediated by LipB was analyzed in the molecular level by protein engineering techniques. In Chapter 2, LipB was overproduced in E. coli, and purified in the presence of detergent. By using this LipB sample, fundamental characteristics of LipB were investigated by kinetic analysis of LipA reactivation and chemical cross-linking (Jaenicke and Rudolph, 1989) with denatured LipA. In Chapter 3, to investigate the characteristics of N-terminal region of LipB, two forms of N-terminal truncated LipBs were prepared, and their molecular properties and reactivation activity were compared with those of full-length form. In Chapter 4, to find important amino acid residues of LipB in reactivation, random mutagenesis using error-prone PCR (Leung et al., 1989) was performed on a gene encoding the functional region of LipB. Given DNA library was introduced into lipase expression system using E. coli, and mutant LipB losing its activity was selected by two simple screening procedures. Consequently, five single-residue substituted LipBs were newly prepared, and their properties were compared with that of wild-type LipB.
CHAPTER 2

Overexpression, Purification, and Characterization of LipB, Lipase Activator Protein from Pseudomonas aeruginosa TE3285

2-1. Introduction

LipB, the lipase activator protein from Pseudomonas aeruginosa TE3285, is encoded at the position adjacent to the gene of its substrate LipA. Therefore, LipB would be a specific folding factor for LipA. In this respect, LipB seems to be more similar to N-terminal propeptide of several proteases such as subtilisin (Ikemura et al., 1987) than to general molecular chaperones. In the case of subtilisin, calcium ion plays an important role in the propeptide-mediated folding. It has been considered that calcium binding to subtilisin during folding process is regulated by its propeptide (Gallagher et al., 1995). This calcium binding contributes to the stability of the subtilisin structure, and so to the expression of its enzymatic activity. Bacterial lipases also have a calcium binding site that is important for maintaining their structure (Noble et al., 1994, Lang et al., 1996, Schrag et al., 1997, Kim et al., 1997). Thus, it could be presumed that LipB participates in this calcium binding during the reactivation process of LipA. However, the characteristics of LipB during reactivation have been little elucidated.

In this chapter, the recombinant full-length LipB was purified, and its function was kinetically analyzed in vitro. The purified LipB reactivated denatured LipA, but did not dissociate from the reactivated LipA in vitro. Furthermore, the effect of calcium ion on the LipB-assisted reactivation was examined, and it is proposed that LipB specifically assists the binding of calcium ion to LipA.
2-2. Experimental Procedures

Materials. Bacterial strain *Escherichia coli* BL21(DE3) [F', *ompT*, *hsdS* (rB−mB−), *gal*, *dcm*, (DE3)] and plasmid pET-3d (Novagen Inc., Madison, WI) were used as a host and a vector (Studier et al., 1990) for expression of *lipB*, respectively. Bacterial strain *E. coli* BW313 (dut, ung, thi-1, relA, spoT1/F'lysA) was used for the preparation of single strand DNA including uracil on site-directed mutagenesis (Kunkel, 1985). Plasmid pUL11 is a pUC19 derivative carrying both *lipA* and *lipB* from *Pseudomonas aeruginosa* TE3285 (Chihara-Siomi et al., 1992). M13mp19 was provided by Takara Shuzo Co., Ltd. (Kyoto, Japan). Synthetic oligonucleotide was a gift from Toyobo Co., Ltd. (Osaka, Japan). Restriction enzymes and DNA modifying enzymes were obtained from Toyobo Co., Ltd. and Takara Shuzo Co., Ltd. The LipA protein purified from culture medium of *P. aeruginosa* TE3285 (Chihara-Siomi et al., 1992) was a special gift from Toyobo Co., Ltd. The purified lipases from *Pseudomonas* sp. 109 (Ihara et al., 1991) and *P. cepacia* M-12-33 were generous gifts from Nagase Biochemicals Ltd. (Tokyo, Japan) and Amano Pharmaceutical Co., Ltd. (Nagoya, Japan), respectively. The purified lipases from *Candida cylindracea* and porcine pancreas were obtained from Sigma Chemical Co (St. Louis, Missouri). Cellulofine GCL-1000m was a gift from Chisso Co. Ltd. (Tokyo, Japan). All other chemicals used in the present work were of the purest grade commercially available.

Plasmid construction. An expression plasmid of *lipB*, pELB10, was constructed as shown in Fig. 2-1. A *Kpn I*-BanHI fragment of pUL11 containing *lipA* and *lipB* was inserted into M13mp19. By use of the given phage vector (M13D1) as a template, a new *Nco I* site was introduced at the position of the initiation codon of *lipB* by site-directed mutagenesis according to the method of Kunkel (1985). The mutational primer consists of the sequence 5′-GCCCCCTCCCATGGGAAAATCTCCCTGC-3′. The plasmid pELB10 was prepared by isolating an *Nco I*-Hind III fragment including *lipB* from the resulting phage vector (M13LB10), and inserting the fragment at the position downstream of the T7 promoter in pET-3d.

Overproduction and purification of LipB. *E. coli* BL21(DE3) was transformed with the expression plasmid pELB10 and was cultured at 37 °C in 1 liter of Luria-Bertani broth (1% Bacto tryptone, 0.5% Bacto yeast extract, and 1% NaCl) containing 50 μg/ml ampicillin. Expression of *lipB* was induced by addition of 1 mM isopropyl β-D-thiogalactopyranoside when the absorbance at 600 nm of the growing culture reached 0.7. After a total 5 h culture, bacterial cells were harvested by centrifugation at 7,000 × g, and cell pellets (3.5 g) were resuspended in 30 ml of the extraction buffer (20 mM Tris-HCl, pH 8.0, 0.5 mM CaCl₂, and 0.5 mM EDTA). The cell suspension was sonicated 20 times for 30 s at 0 °C using a Branson Sonifier 250, then centrifuged at 25,000 × g for 30 min at 4 °C, and the supernatant was recovered as crude extract. The fraction containing LipB was precipitated from the crude extract with 20 to 30% saturated ammonium sulfate. The precipitates were separated by centrifugation at 25,000 × g for 30 min at 4 °C and resuspended in the buffer (20 mM Tris-HCl, pH 8.0, 0.1 M NaCl, and 0.5 mM EDTA). The solution was dialyzed against the same buffer. The dialyze was mixed with one-fourth volume of 10% SDS and applied to a Cellulofine GCL-1000m gel filtration column (2.6 x 90 cm) equilibrated with the eluent (20 mM Tris-HCl, pH 8.0, 0.1 M NaCl, 0.5 mM EDTA, and 1% SDS) at room temperature. The ac-
tive fractions including 1.5 mg proteins were applied to SDS polyacrylamide gels (180 x 180 x 2 mm) and electrophoresed as described by Laemmli (Laemmli, 1970) at 20 °C. The gels were stained with Copper Stain (Bio-Rad Laboratories, Inc., Hercules, CA) (Lee et al., 1987), and a band including LipB was excised from the gels. The purified protein was recovered by electroelution (Findlay, 1990). The eluate was applied to an Extracti-Gel D column (Pierce Chemical Co., Rockford, IL) to remove SDS.

Denaturation of LipA. Denatured LipA was prepared by addition of 48 μM native LipA solution (20 mM Tris-HCl, pH 8.0 and 0.2 M NaCl) to three volumes of the same buffer containing 8 M guanidine hydrochloride, followed by incubation for more than 1 h at room temperature. The denaturation of LipA was checked by examination of the circular dichroism in the range between 200 and 240 nm.

Assay of lipase activity. Protein concentration was determined with BCA Protein Assay Reagent (Pierce Chemical Co.) (Smith et al., 1985). Bovine serum albumin was used as a standard. Lipase activity was measured with Lipase Kit S (Dainippon Pharmaceutical Co., Ltd., Osaka), in which 2,3-dimercaptopropan-1-ol tributyrate was used as a substrate and Gly-Lys-Ile-Leu, as predicted from the DNA sequence of lipB (37.7 kDa). The 37-kDa protein fraction was blotted onto a polyvinylidene fluoride membrane, and its N-terminal amino acid sequence was analyzed by a gas-phase sequencer (Applied Biosystems Model 477A). This protein has the N-terminal sequence Met-Gly-Lys-Ile-Leu, as predicted from the DNA sequence of lipB (Fig. 1-2) except for the second Gly; this Gly is substituted for Lys of the native LipB owing to the site-directed mutagenesis. The expression level of LipB was estimated as 25% of the total cell proteins on the basis of densitometric analysis of the gels stained with Coomassie Brilliant Blue R-250.

Overexpression of lipB in E. coli. LipB was overproduced by using the T7 expression system (Studier et al., 1990). An expression plasmid for lipB, pELB10, was constructed by inserting lipB at the position downstream of the T7 promoter in pET-3d (Fig. 2-1). The plasmid pELB10 was introduced into E. coli BL21(DE3), and the transformant was grown with induction by isopropyl β-D-thiogalactopyranoside. Crude extract of the cultured cells was analyzed by SDS-PAGE (Fig. 2-2, lane 2). A 37-kDa protein was detected only for the induced cells, and its molecular weight is consistent with that calculated from the DNA sequence of lipB (37.7 kDa). The 37-kDa protein fraction was blotted onto a polyvinylidene difluoride membrane, and its N-terminal amino acid sequence was analyzed by a gas-phase sequencer (Applied Biosystems Model 477A). This protein has the N-terminal sequence Met-Gly-Lys-Ile-Leu, as predicted from the DNA sequence of lipB (Fig. 1-2) except for the second Gly; this Gly is substituted for Lys of the native LipB owing to the site-directed mutagenesis. The expression level of LipB was estimated as 25% of the total cell proteins on the basis of densitometric analysis of the gels stained with Coomassie Brilliant Blue R-250.

Purification of LipB. LipB was purified 4.9-fold from the crude extract in three steps; ammonium sulfate fractionation, gel filtration chromatography, and polyacrylamide gel electrophoresis (Table 2-1). The SDS-PAGE analysis of each purification step is shown in Fig. 2-2.
Table 2-1. Purification of recombinant full-length LipB. Specific activity of LipB was determined from the initial rate of reactivation of denatured LipA. One unit of LipB was defined as the amount of LipB reactivating one unit of the denatured LipA per minute under the standard assay conditions.

<table>
<thead>
<tr>
<th>Purification step</th>
<th>Total protein (mg)</th>
<th>Total activity (U)</th>
<th>Yield (%)</th>
<th>Specific activity (U/mg)</th>
<th>Purity (-fold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crude extract</td>
<td>310</td>
<td>827</td>
<td>100</td>
<td>2.64</td>
<td>1.0</td>
</tr>
<tr>
<td>Salting-out</td>
<td>80</td>
<td>483</td>
<td>58</td>
<td>6.05</td>
<td>2.3</td>
</tr>
<tr>
<td>Gel filtration</td>
<td>38</td>
<td>421</td>
<td>51</td>
<td>11.0</td>
<td>4.2</td>
</tr>
<tr>
<td>SDS-PAGE</td>
<td>5.8</td>
<td>75.1</td>
<td>9.1</td>
<td>12.9</td>
<td>4.9</td>
</tr>
</tbody>
</table>

SDS was added to protein solutions and buffers at the steps of gel filtration and electrophoresis during the purification process. Without SDS, LipB was eluted in the void volume on gel filtration using Cellulofine GCL-1000m, of which the exclusion limit is 500 kDa, and it could not be separated from the other proteins. These results indicate that LipB readily forms large soluble aggregates. When LipB solution containing 1% SDS was diluted 500-fold into the reactivation buffer, its reactivation activity was the same as that of LipB without SDS treatment. Thus, it is likely that SDS effectively disperses the aggregates and does not inactivate LipB irreversibly.

**Reactivation kinetics of LipB.** Denatured LipA gradually recovered its lipase activity in the presence of LipB, whereas no lipase activity was recovered without LipB (Fig. 2-3). In the presence of 0.28 μM LipB (at the LipB/LipA molar ratio of 1:1), the recovery of the lipase activity reached maximum at least 1 h after the initiation of the reactivation. When the concentration of LipB was lower than that of the denatured LipA, the maximum recovery increased with the amount of LipB. However, the maximum recovery of the lipase activity was inhibited by an excess amount of LipB. At LipB concentrations lower than 8.8 nM (at a LipB/LipA molar ratio of 1:30), no more than 14.7 U of the lipase activity was recovered by one nanomole of LipB. Since the activity of 1 nM native LipA is 34.3 U/l, LipB was expected to reactivate less than an equimolar amount of the denatured LipA. Thus, multiple turnover is not involved in the LipB-assisted reactivation of the denatured LipA. Moreover, reactivation was observed in the same manner when the purified LipA denatured with additional thiol reagents or the recombinant LipA produced as inclusion bodies in *E. coli* (Oshima-Hirayama et al., 1993) was used for a substrate of LipB (data not shown). In addition, it was observed that the reactivated LipA possesses hydrolytic activity for triolein as well as 2,3-dimercapto-propan-1-ol used as the standard substrate in the present study.
Cross-linking between LipB and reactivated LipA. It was thought that LipB would still be bound to LipA after the reactivation, since no multiple turnover was observed in the LipB-assisted reactivation (Fig. 2-3). To detect this LipA-LipB complex, chemical cross-linking experiments were carried out. A mixture of LipB and the denatured LipA was incubated for 4 h, then glutaraldehyde was added to the solution for cross-linking. The products were analyzed by SDS-PAGE (Fig. 2-4). A 68-kDa protein was newly observed (lanes 3-6), corresponding in size to the sum of LipA (30.1 kDa) and LipB (37.7 kDa). When either LipB or the denatured LipA was alone, no intermolecular cross-linked product was detected around the position of the 68 kDa protein (lane 1 or 2, respectively). These results indicate that the 68-kDa protein is the cross-linked 1:1 complex between LipB and LipA. This cross-linked product increased with the LipB concentration (lanes 3-5), but diminished with an excess amount of LipB (lane 6). These effects of the LipB concentration on the amount of the cross-linked product seem to be compatible with the effect of the LipB concentration on the recovery of lipase activity described above (Fig. 2-3). Thus, it is suggested that this complex detected by cross-linking expresses the lipase activity recovered with LipB.

Effect of calcium ion. The effects of divalent cations on the LipB-assisted reactivation of the denatured LipA were examined. CaCl\(_2\) was the most effective cation for the reactivation among those examined. The recovery of the lipase activity with 5 mM MnCl\(_2\) was 59% of that with 5 mM CaCl\(_2\), but in the presence of 5 mM MgCl\(_2\), the reactivation was not observed. In the absence of divalent cations, the recovery of activity was undetectable. When 10 mM EDTA was added to the reaction mixture after 4.5-h reactivation, the recovered lipase activity was completely lost within 5 min (Fig. 2-5). In contrast, the native LipA was inactivated more slowly by the addition of EDTA; the activity of 3 nM LipA was reduced by half during 2-h incubation in the reactivation buffer with 10 mM EDTA (data not shown). Thus, LipA reactivated with LipB is more sensitive to inactivation by EDTA addition than the native LipA. Therefore, the effect of calcium ion on the complex formation between LipB and LipA was analyzed by cross-linking (Fig. 2-6). Without CaCl\(_2\) the cross-linked band was not clearly detected (lane 2), indicating that calcium ion also affected the complex formation between
Substrate specificity of LipB.

The substrate specificity of LipB in the reactivation was examined using denatured lipases from *Pseudomonas* sp. 109, *P. cepacia* M-12-33, *Candida cylindracea* and porcine pancreas. The final concentration of LipB was 14.2 nM, and that of the denatured lipase corresponded to 490 U/1 of the native lipase. The denatured lipase from *Pseudomonas* sp. 109 was reactivated with LipB up to 205 U/1 during 4-h incubation at 20 °C (without LipB: 2.0 U/1). In contrast, the denatured lipases from *P. cepacia* M-12-33, *Candida cylindracea* and porcine pancreas were little reactivated with LipB; the values of recovery (U/1) with LipB (without LipB) were 1.8 (5.7), 0.4 (0.0), and 0.7 (0.9), respectively.

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2-4. Discussion

The full-length LipB of *P. aeruginosa* TE3285 has been purified, and the isolation of the purified LipB allowed the analysis of its molecular properties in the reactivation of LipA. The kinetic observations suggested that the reactivation reaction with LipB does not involve multiple turnover. The formation of the stoichiometric (1:1) complex between LipB and LipA was demonstrated by cross-linking experiments. By the addition of EDTA, this complex was readily dissociated, and its lipase activity was simultaneously lost. These phenomena suggested that LipA in the active form seems not to be released from LipB after reactivation in vitro, unlike molecular chaperones. Accordingly, some additional factors appear to be necessary for the release of the active LipA. To find such factors, the effects of several coenzymes on the LipB-assisted reactivation of the denatured LipA were examined. Neither the initial rate nor the maximum recovery in the reactivation was influenced by coenzymes such as ATP, GTP, NAD(P)H, and NAD(P)⁺ (data not shown). However, the active LipA unbound with LipB is secreted into the extracellular medium of *Pseudomonas*. Consequently an unknown factor is anticipated to mediate the release of the active LipA from LipB during the secretion process in *Pseudomonas* cells. *Pseudomonas* has a characteristic complex of membrane proteins, Xcp proteins, which is considered to be an apparatus for the permeation of extracellular proteins through the outer cellular membrane (Tommassen et al., 1992). Secretion of *Pseudomonas* lipase is also proposed to be mediated by Xcp proteins (Filloux et al., 1987). Furthermore, it is observed that the lipase activator protein is located in periplasm (Frenken et al., 1993a, Ihara et al., 1995). Thus, one or more Xcp proteins are candidates for direct participation in the dissociation of the complex between LipB and the active LipA in periplasm.

It has been observed that the LipB-assisted reactivation is significantly stimulated by calcium ion. The complex formation of LipB with denatured LipA was found also to require calcium ion, since the cross-linked product between LipA and LipB was not detected in the absence of calcium ion. The LipA reactivated with LipB rapidly lost its enzymatic activity upon the addition of EDTA. These results suggest two possibilities for the function of calcium ion in the LipB-assisted reactivation of denatured LipA; one is that calcium ion is necessary for the interaction between LipA and LipB, and the other is that calcium ion is required
for the enzymatic activity of the reactivated LipA. Regarding the first possibility, calcium ion seems to participate in the formation of the LipA-LipB complex during the reactivation process. However, the removal of calcium ion by EDTA seems not necessarily to cause the dissociation of the complex, because the cross-linked product between LipA and LipB was not lost completely at a lower concentration (0.05%) of Triton X-100. Thus, calcium ion may indirectly play a role in the control of association and dissociation of the complex. On the other hand, the second possibility would be rather plausible, that is, calcium ion is needed to express the enzymatic activity of LipA refolded with LipB. It has been reported that the active conformation of Pseudomonas lipases is stabilized by calcium ion (Svendsen et al., 1995). The calcium binding site of other bacterial lipases was determined by crystal structure analyses (Noble et al., 1994, Lang et al., 1996, Schrag et al., 1997, Kim et al., 1997). These lipases have two aspartic acid residues coordinated to the calcium ion. These residues are also conserved in LipA. Thus, LipA is believed to have a calcium binding site similar to that of the above bacterial lipases. In this respect, the reactivated LipA forming the complex with LipB is expected to differ from the native LipA in structure, because the reactivated complex was more rapidly inactivated by EDTA addition than the native LipA. Thus, it is suggested that LipB could affect this calcium binding to LipA in the reactivation process. This proposed function of LipB seems to be similar to that of the subtilisin propeptide as a protein-folding factor, since its refolding is also accompanied by calcium binding to the enzyme. The crystal structure of the propeptide-subtilisin complex suggests that the propeptide prevents the complete formation of the high-affinity calcium binding site of subtilisin until folding has occurred (Gallagher et al., 1995).

It was found that LipB specifically recognizes and reactivates the denatured lipase from the same source. The lipase specificity of LipB appears to be related to the amino acid sequence of lipases since LipB also reactivates the Pseudomonas sp. 109 lipase, of which the amino acid sequence is 98% identical with that of LipA, but does not reactivate the denatured lipase from P. cepacia M-12-33 with 36% sequence identity to LipA. LipB reactivated neither of two eukaryotic lipases with little similarity to LipA in amino acid sequence. This strict specificity suggests that LipB recognizes a unique structural element of LipA during its folding process. In addition, regarding the sequence identity of the activator proteins, LimL from Pseudomonas sp. 109 and LipX from P. cepacia M-12-33 are 98% and 37% identical with LipB, respectively. The extent of the identity among the activator proteins is similar to that among the corresponding lipases. Thus, the other lipase activator proteins could also essentially recognize and activate their own lipase. Hobson et al. (1993) suggested that lipase activator proteins function as a private chaperone for the Pseudomonas lipases based on their gene construction. The present results experimentally confirmed this idea of the specificity of the lipase activator protein.

LipB is considered to form soluble aggregates in buffer solution without detergents. By the addition of detergents to disperse the aggregates, the property of LipB was altered during the process of purification and during reactivation of the denatured LipA. These alterations seem to be attributed to an N-terminal hydrophobic segment of LipB, of which first 20 amino acid residues contain 17 hydrophobic residues. It is known that the LipB protein from P. glumae PG1 is anchored into the inner cellular membrane by its N-terminal hydrophobic segment (Frenken et al., 1993a). In the case of the LimL protein from Pseudomonas sp. 109, its mutant protein lacking an N-terminal hydrophobic region can be separated by conventional chromatographic techniques without a detergent (Ihara et al., 1995). On the basis of these observations, LipB from P. aeruginosa TE3285 is also expected to be buried in the cellular membrane at the hydrophobic N-terminal region. In vitro, LipB would be anchored by its N-terminal segment into detergent micelles, so that it would effectively disperse and reactivate the denatured LipA.
CHAPTER 3

Molecular Properties and Activity of Amino-Terminal Truncated Forms of LipB

3.1. Introduction

In the purification of full-length LipB, SDS was necessary for separating LipB from other proteins. Purified LipB did not reactivate even an equimolar amount of denatured LipA. From these observations it was suspected that full-length LipB readily forms soluble aggregates. It is considered that the N-terminal hydrophobic region of LipB cause aggregation, because in other lipase activator proteins, this N-terminal hydrophobic region is associated with the inner cellular membrane, and the main part of the molecule is in the periplasm, helping to refold the transported lipase (Frenken et al., 1993a, Ihara et al., 1995).

To identify characteristics of the N-terminal region, in this chapter, two forms of truncated LipB mutant proteins: Δ21LipB (LipB lacking the N-terminal 21 residues) and Δ61LipB (LipB lacking the N-terminal 61 residues) were prepared. Differences in the original and mutant proteins are shown in Fig. 3-1. It was observed that when N-terminal 21 residues were lacking, LipB was dispersed in solution and reactivated denatured LipA more effectively than full-length LipB. Furthermore, it was found that Δ61LipB reactivated denatured LipA.

Fig. 3-1. N-terminal amino acid sequences of full-length and truncated LipBs.
3-2. Experimental Procedures

Materials. Bacterial strain Escherichia coli BL21(DE3) and plasmid pET-3d (Studier et al., 1990) were used as the host and vector for production of the N-terminal truncated mutants of LipB, respectively. Synthetic oligonucleotides were obtained from Takara Shuzo Co., Ltd.

Plasmid construction. For expression of the gene of Δ61LipB, a plasmid named pELB31 was constructed. A new initiation codon with an *Nco* I site was introduced into the position encoding Lys62 of LipB by site-directed mutagenesis. The mutagenesis was done by the method of Eckstein (Taylor et al., 1985) with the Sculptor *in vitro* mutagenesis system (Amersham, Buckinghamshire, UK). The mutational primer consists of the sequence 5'-GGCCTGGTTCGTCTCCATGGGCCGGCCATGGTCGCGCC-3'. M13D1 was used as a template for the mutagenesis (Fig. 2-1). The gene of pET-3d was isolated from the resulting phage vector (M13LB30) digested by *Nco* I and *Hind* III. The plasmid pELB31 was prepared by insertion of this fragment into pET-3d.

pELB20, an expression plasmid for the gene of Δ21LipB, was designed in a similar way to pELB31. A new initiation codon was introduced into the position encoding Leu22 of LipB. The mutational primer consists of the sequence 5'-GGCCCTGGTTCGTCTCCATGGGCCGGCCATGGTCGCGCC-3'.

Production and purification of truncated LipBs. *E. coli* BL21(DE3) pELB31 was cultured for the production of Δ61LipB in the same way as for overproduction of full-length LipB in Chapter 2. From 6 liters of culture fluid, 20.4 g of cell pellets was obtained. These pellets were resuspended in 100 ml of the extraction buffer containing 20 mM Tris-HCl, pH 7.5, 0.2 M NaCl, 0.5 mM EDTA, and 0.5 mM phenylmethylsulfonyl fluoride (PMSF), and were sonicated 20 times for 30 s at 0 °C with a Branson Sonifier 250. By centrifugation at 25,000 x g for 30 min at 4 °C, the supernatant was recovered as crude extract for later steps of purification.

Column chromatography was performed at 4 °C. The crude extract was mixed with an equal volume of the extraction buffer, which contains 2.0 M (NH₄)₂SO₄, and the mixture was centrifuged at 25,000 x g for 30 min at 4 °C. The supernatant was applied to a Butyl-

Toyopearl 650M column (2.6 x 30 cm) equilibrated with the starting buffer (20 mM Tris-HCl, pH 7.5, 0.5 mM EDTA, 1.0 M (NH₄)₂SO₄, and 0.5 mM PMSF). Proteins were eluted with a linear gradient from 1.0 to 0.0 M (NH₄)₂SO₄, and the active fraction was dialyzed against a mixture of 20 mM MES-NaOH, pH 6.5, 0.5 mM EDTA, and 0.5 mM PMSF. The dialyze (12 ml) was mixed with 60 ml of 1 M MnCl₂, and applied to an AF-Red Toyopearl 650M column (1.6 x 7.5 cm) equilibrated with the starting buffer (20 mM MES-NaOH, pH 6.5, 0.5 mM EDTA, 5 mM MnCl₂, and 0.5 mM PMSF). After the column was washed with the same buffer for removal of unbound proteins, the active fraction was eluted stepwise with 20 mM MES-NaOH, pH 6.5, 10 mM EDTA, and 0.5 mM PMSF. The eluate was dialyzed against a mixture of 20 mM Tris-HCl, pH 7.5, 0.5 mM EDTA, and 0.5 mM PMSF, and applied to a Q Sepharose FF column (2.6 x 20 cm) equilibrated with the same buffer. The active fraction was eluted with a linear gradient from 0.0 to 0.5 M NaCl. The purity of Δ61LipB in each step was checked by SDS-PAGE (Laemmli, 1970).

Δ21LipB was overproduced by the culture of *E. coli* BL21(DE3) pELB20, and purified from crude extract of the cells by the same protocol as Δ61LipB. However, for Δ21LipB, conditions for Butyl-Toyopearl column chromatography were slightly different: the crude extract was mixed with an extraction buffer that contains 1.6 M (NH₄)₂SO₄, and the Butyl-Toyopearl column was equilibrated with a buffer that contains 0.8 M (NH₄)₂SO₄.

The purified full-length LipB was prepared as described in Chapter 2.

Gel filtration analysis. HPLC gel filtration was done with a Tosoh instrument using a TSKgel G3000SW XL PEEK column at 25 °C. The running buffer consists of 20 mM Tris-HCl, pH 7.5, 0.2 M NaCl, 0.5 mM EDTA, and 0.02% NaN₃. The flow rate was 0.5 ml/min, and the elution of protein was detected by absorbance at 280 nm. The column was calibrated using Calibration proteins for gel chromatography (Boehringer Mannheim, Mannheim, Germany).

Assay of denatured LipA reactivation. The LipB-assisted reactivation of denatured LipA was carried out as described in Chapter 2.
3-3. Results

Overproduction and purification of truncated LipBs. Δ21LipB was overproduced with use of the T7 expression system in the same way as full-length LipB. Detergent was not required for the purification of Δ21LipB in any column chromatography, whereas SDS was necessary for the separation of full-length LipB from the other proteins.

When the purified Δ21LipB was stored without PMSF at 0 °C, Δ21LipB was readily digested, and a 30-kDa fragment was accumulated (data not shown). This fragment also reactivated denatured LipA. It was found that this fragment has an N-terminal sequence, Val-Ala-Pro-Leu-Pro, which is consistent with the sequence Val63-Pro67 of full-length LipB. Accordingly, a gene of LipB lacking the N-terminal 61 residues (Fig. 3-1) was prepared by site-directed mutagenesis. This mutant form, Δ61LipB, was overproduced and purified in the similar procedure as Δ21LipB. The SDS-PAGE after each purification step on Δ61LipB is shown in Fig. 3-2. The Δ61LipB was purified 35-fold with a yield of 20% (Table 3-1).

Molecular dispersion of truncated LipBs. Because detergent was not needed in the purification of Δ21LipB or Δ61LipB, the molecular dispersion of these proteins in solution was examined by gel filtration analysis using TSKgel G3000SWXL PEEK column (Fig. 3-3). The exclusion limit of the column is 500 kDa. Full-length LipB was eluted in the void volume (6.5 ml) with a broad peak although monomers of this LipB have the molecular mass of 37.5 kDa. This finding indicates that full-length LipB forms large soluble aggregates. In contrast, Δ21LipB (35.3 kDa) was eluted in a sharp peak from gel filtration at the elution volume of 9.3 ml. This location corresponds to a molecular mass of 63 kDa, which is close to a dimeric size. Similarly, Δ61LipB (31.5 kDa) was sharply eluted at the elution volume of 9.9 ml, which corresponds to 50 kDa, close to a dimeric size. These results suggest that the truncation of at least the N-terminal 21 residues allows homogeneous dispersion of the molecules in solution.

Reactivation of denatured LipA with truncated LipBs. The reactivation of denatured LipA with full-length and two truncated LipBs was kinetically analyzed. Reactivation reached a maximum with 1 h of incubation with the truncated LipBs as with full-length LipB (Fig. 2-3). The maximum concentration of the reactivated LipA, which was determined after 4 h of incubation, is

![Fig. 3-2. SDS-PAGE analysis of the purification of Δ61LipB. A 12.5% polyacrylamide gel was used, and proteins were stained with Coomassie Brilliant Blue R-250. Lane 1, total cells; lane 2, crude extract; lane 3, Butyl-Toyopearl 650M eluate; lane 4, AF-Red Toyopearl 650M eluate; lane 5, Q Sepharose FF eluate.](image)

![Fig. 3-3. Gel filtration of full-length and truncated LipBs. Ten microliters of purified LipB proteins (1 mg/ml) was applied to TSKgel G3000SWXL PEEK column. Elution of the proteins at the flow rate of 0.5 ml/min was monitored by the absorption at 280 nm.](image)

Table 3-1. Purification of Δ61LipB. The specific activity of LipB was determined from the initial rate of reactivation of denatured LipA. One unit was defined as the amount of LipB reactivating one unit of denatured LipA per minute at 20 °C.

<table>
<thead>
<tr>
<th>Purification step</th>
<th>Total protein (mg)</th>
<th>Total activity (U)</th>
<th>Yield (%)</th>
<th>Specific activity (U/mg)</th>
<th>Purity (fold)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crude extract</td>
<td>982</td>
<td>3660</td>
<td>100</td>
<td>3.73</td>
<td>1.0</td>
</tr>
<tr>
<td>Butyl-Toyopearl</td>
<td>38.9</td>
<td>2700</td>
<td>74</td>
<td>69.4</td>
<td>18.6</td>
</tr>
<tr>
<td>AF-Red Toyopearl</td>
<td>15.5</td>
<td>1480</td>
<td>40</td>
<td>95.5</td>
<td>25.6</td>
</tr>
<tr>
<td>Q Sepharose FF</td>
<td>5.57</td>
<td>727</td>
<td>20</td>
<td>131</td>
<td>35.1</td>
</tr>
</tbody>
</table>
plotted against the LipB concentration in Fig. 3-4. In all concentrations tested, either truncated LipBs recovered lipase activity much more effectively than the full-length LipB. When the concentration of the truncated LipB was less than 5.9 nM, 1 mole of LipA was fully reactivated per mole of LipB. In contrast, only 0.4 mole of LipA was reactivated per mole of full-length LipB even under the most suitable conditions with the LipB concentration less than 8.8 nM. These results indicate that the N-terminal 21 residues prevent LipB from the stoichiometric reactivation of the denatured LipA. This reactivation with truncated LipBs would involve no multiple turnover in the same way as full-length LipB.

Fig. 3-4. Effects of the concentration of LipBs on maximum recovery of LipA activity. A solution of denatured LipA was diluted 41-fold in LipB solution (20 mM Tris-HCl, pH 7.5, 0.2 M NaCl, 5 mM CaCl2, 0.5 mM EDTA, and 0.5% Triton X-100) and incubated at 20 °C for 4 h. The final concentration of denatured LipA was 0.29 μM. The solid and dashed lines indicate theoretical results when 1.0 and 0.4 equimolar amounts, respectively, of denatured LipA are reactivated per mole of LipB. Full-length LipB (Δ); Δ21LipB (■); Δ66LipB (○).

3-4. Discussion

It was observed that truncation of the N-terminal region containing 21 residues affects the distribution of apparent molecular weight of LipB. The results of gel filtration suggest that the molecules form soluble aggregates larger than 500 kDa, although the monomeric size is 37.5 kDa. The region containing the N-terminal 21 residues seems to cause aggregation of LipB molecules. In other lipase activator proteins, the N-terminal region of them is also hydrophobic (Jørgensen et al., 1991; Ihara et al., 1992; Frenken et al., 1993a). The lipase activator protein of P. glumae PG1, is anchored in the inner membrane by its N-terminal hydrophobic segment, and acts on the lipase in the periplasm (Frenken et al., 1993a). The N-terminal hydrophobic region of the lipase activator protein from Pseudomonas sp. 109, is considered to be a signal sequence for translocation into the periplasm (Ihara et al., 1995). In this respect, the N-terminal region of LipB would be a similar membrane-associated segment. In vivo, because the N-terminal segment is anchored in the membrane or cleaved off, LipB could be effectively dispersed, and activate LipA in the periplasm.

The results of kinetic analysis show that truncation of the N-terminal 21 residues increases LipB-assisted reactivation of denatured LipA in vitro. Δ21LipB can quantitatively re-activate LipA although full-length LipB reactivated only 0.4 equivalent of LipA at the most. These results indicate that the N-terminal region of full-length LipB inhibits the reactivation activity of LipB in vitro. Thus, LipB would essentially re-activate a stoichiometric amount of denatured LipA. In addition, because the reactivation with Δ21LipB does not involve multiple turnover, Δ21LipB would complex with the reactivated LipA. This reactivated LipA is likely to have the same level of lipase activity as native LipA. In contrast, the lipase activator protein LimL from Pseudomonas sp. 109 was prepared as an N-terminal truncated mutant, and the complex between the lipase and the truncated LimL has a lower specific activity than the native lipase (Ihara et al., 1995). Considering the behavior of LipB in the present study, LimL is expected to recover full activity of the lipase under certain conditions, such as in the presence of calcium ion.
CHAPTER 3

It was further demonstrated that the N-terminal region of LipB containing 61 amino acid residues was not involved in its reactivation activity of denatured LipA. Δ61LipB is capable of reactivating the denatured LipA quantitatively, like Δ21LipB. Δ21LipB is readily digested between Lys62 and Val63, a position that may be exposed into the solvent. Thus, it is proposed that the region containing the N-terminal 62 residues of full-length LipB forms an independent domain from the residual C-terminal segment that reactivates LipA.

CHAPTER 4

Exploring Functional Amino Acid Residues of LipB by Random Mutagenesis

4-1. Introduction

Random mutagenesis is one of the useful methods for exploring functional amino acid residues of a protein. This method includes two processes: introduction of mutation into the gene of target protein, and subsequent screening of objective clones from the given mutational library. It is particularly important to establish a screening system suitable for the purpose to get successful results. Simple and effective screening procedures allow to identify the functional residues of target protein. Even after elucidation of three-dimensional structure of target protein, information deduced by the random mutagenesis must contribute to understanding its functional sites on the basis of the structure.

In Chapter 3, it was described that at least the N-terminal 61 residues of LipB was unnecessary for its reactivation activity. This finding indicates that Δ61LipB contains all of the functional amino acid residues required for the reactivation. For the purpose of exploring the functional residues, in this chapter, random mutagenesis was introduced into the gene coding for Δ61LipB by error-prone PCR (Leung et al., 1989). Subsequently, inactive mutant LipBs losing reactivation activity were selected from the given library by two screening steps: plate assay with the guidance of active LipA secretion (Chihara-Siomi et al., 1992), and detection of the molecular size of LipB by Western blotting to exclude nonsense mutants and frameshift ones. As a result, we found four amino acid residues that play an important role in the reactivation activity of LipB.
4-2. Experimental Procedures

**Materials.** Bacterial strain *Escherichia coli* 1100 (F-, prototrophic, endo I) (Dürwald and Hoffmann-Berling, 1968) was used as the host for screening of inactive LipBs. *E. coli* JM109 (recA1, endA1, gyrA96, thi, hsdR17, supE44, relA1, λ-, Δ(lac-proAB), [F, proAB, lacP2ΔM15, traD36]) and plasmid pRSET B (Invitrogen Co., San Diego, CA) were used for overproduction of mutant LipBs (Kroll et al., 1993). pUL1 is a pUC19 derivative, in which lipA and lipB are cloned (Chihara-Siomi et al., 1992). Synthetic oligonucleotides were obtained from Cruachem. (Kyoto, Japan). Restriction enzymes and DNA modifying enzymes were obtained from Toyobo Co., Ltd., Takara Shuzo Co., Ltd., and New England Biolabs, Inc. (Beverly, MA). Rabbit anti-Δ61LipB was purchased from Sawady Technology Co., Ltd. (Tokyo, Japan). Chelate Cellulofine was a gift from Chisso Co., Ltd.

**Plasmid construction.** A plasmid pULB200 was constructed for the template DNA on error-prone PCR for random mutagenesis (Fig. 4-1A). Plasmid pELB31 was digested by Nco I, treated with Klenow fragment, and digested by Hind III. A 900-bp fragment containing Δ61LipB gene was ligated into pUC18 digested by Sma I H ind III to give pULB200.

pUL32 was derived from pUL11 for expression of lipA in E. coli (Fig. 4-1B). First, a DNA fragment containing lipB with an Nco I site was isolated from M13LB30 digested by PpuM I and Hind III. The resulting fragment (1.1 kbp) was substituted for the corresponding segment of pUL11. The given plasmid, named pUL31, has two Nco I sites on lipA and lipB. Second, 430-bp of an Xmn I-Spl I fragment without Nco I site on lipA was isolated from pUL1, and ligated with fragments of pUL31 digested by Xmn I and Spl I. The resulting plasmid, pUL32, contains a single Nco I site on lipB, which encodes K62M mutant LipB.

pRSLB30 was constructed for overproduction of Δ61LipB as a fusion protein containing hexahistidyl leader sequence (Kroll et al., 1993). The gene coding for Δ61LipB was isolated from pUL32 digested by Nco I and Hind III, and inserted into pRSET B to obtain pRSLB30 (Fig. 4-1C).

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**Fig. 4-1. Construction of the plasmids containing the gene coding for Δ61LipB.** (A) pULB200 was used for the template of error-prone PCR on the gene coding for Δ61LipB. (B) pUL32 was the expression plasmid of lipA, and used for tributyrin plate assay, Western blotting for detection of LipB production, and DNA sequencing of the gene coding for Δ61LipB. (C) pRSLB30 was the expression vector for H6-Δ61LipB. Restriction sites are indicated as follows: H, Hind III; N, Nco I; P, Pst I; S, Spl I; and X, Xmn I.
Assay of LipB activity. In vivo Random mutagenesis. was carried out using MnCh, to produce a plasmid library. A x fragment was ligated with the 3.9-kbp fragment of pUL32 digested by HindIII. PCR was carried out using 10 ng of the template DNA, 40 pM each primer, 0.2 mM each dNTP, 1 x PCR buffer (10 mM Tris-HCl, pH 8.3, 50 mM KCl, and 1.5 mM MgCl2), 0.2-0.3 mM MnCl2, 1% dimethyl sulfoxide, and 1.25 unit of Taq DNA polymerase in a total volume of 50 μl. PCR consists of 30 cycles using 30 s of denaturing at 94 °C, followed by annealing at 55 °C for 2 min and extension at 72 °C for 3 min. The PCR product was digested by NcoI and HindIII, and a 900-bp fragment containing the gene coding for Δ61LipB was isolated. This fragment was ligated with the 3.9-kbp fragment of pUL32 digested by NcoI and HindIII to produce a plasmid library.

**Assay of LipB activity. In vivo** activity of LipB produced in *E. coli* 1100 pUL32 was detected with the guidance of Lip A secretion. Activity of secreted Lip A was detected by hydrolysis of tributyryin on agar plate as described by Chihara-Siomi et al. (1992). In the present study, agar plates contain no isopropyl β-D-thiogalactopyranoside. To detect *in vitro* activity of LipB, two kinds of assays; reactivation of denatured LipA and cross-linking with LipA by glutaraldehyde, were carried out as described in Chapter 2.

**Western blotting.** Cell harvest of 1 ml culture of *E. coli* 1100 pUL32 was solubilized and applied to SDS-PAGE according to Laemmli (1970). After the electrophoresis, separated proteins in the gel were blotted to polyvinylidene difluoride membrane. Then, the membrane was treated with Immun-Blot Assay Kit (Bio-Rad Laboratories). Rabbit anti-Δ61LipB and goat anti-rabbit IgG conjugated with horseradish peroxidase (Blake et al., 1984) were used for the first and second antibody, respectively. Activity staining for peroxidase was performed with 4-chloro-1-naphthol and hydrogen peroxide as substrates.

**DNA sequencing.** Plasmids isolated from cell harvest of 3 ml culture of *E. coli* 1100 pUL32 were used for DNA sequencing on the gene coding for Δ61LipB. The sequencing was carried out by use of ABI PRISM Dye Terminator Cycle Sequencing Kit With AmpliTaq DNA Polymerase, FS. DNA encoding C-terminal half and N-terminal half of Δ61LipB was sequenced with primer I (5′-TGTAAACGACGGCCAGT-3′) and II (5′-AGCAGCCTCC-GCGGAGAA-3′), respectively (Fig. 4-2). Electrophoresis and sequence analysis of the resulting samples were carried out by ABI PRISM 377 DNA sequencer.

**Site-directed mutagenesis.** Site-directed mutagenesis was carried out on the basis of the modification of the overlap extension PCR method (Ito et al., 1991). Mutagenized pUL32 plasmid was used as the template. Primers described below are named according to Ito et al. (1991), and are schematically represented in Fig. 4-2. Primers I and II in the sequencing experiments were used for both rounds of PCR. Primer III (5′-CCTAGCTTTGCATGCCG-AGG-3′) corresponds to the sequence located between primer I and the gene coding for Δ61LipB with one mismatched base that destroys the HindIII site. Primers IV-a (5′-CGGA-ACCTGCTGCCTAAGC-3′) or IV-b (5′-GAACCCCTTCAGCAAGCCTG-3′) were used for mutation in which the region encoding the amino acid residue of Arg94-Ser113 is replaced by the wild-type sequence, respectively. These primers are designed to introduce a silent mutation with a restriction site: a BspE I site for primer IV-a, and an Xmn I site for primer IV-b. On the first PCR, two DNA fragments were amplified using either primers I and IV or primers II and III. After these products were mixed and annealed, the second PCR was performed with primers I and II. The resulting product was digested with NcoI and HindIII, and then was substituted for the corresponding segment of pUL32.

**Construction of plasmids encoding single-residue substituted Δ61LipB.** From multiple-residue mutagenized plasmids, five single-residue substituted mutants (D76G, Y99C, Y99H, S125R, and R115C) were prepared as follows. The mutational sites of each mutant and restriction sites are illustrated in Fig.4-2.

1. D76G. pUL32 (D76G/F100Y/F195L/1256T/R261H/D277G/R309C) was digested by NcoI and Pml I, and a 360-bp fragment containing the region of D76G/F100Y was inserted into the corresponding position of wild-type pUL32. Next, Tyr100 in the resulting plasmid was returned to phenylalanine residue by site-directed mutagenesis using the primer IV-a, so that pUL32 (D76G) was constructed.
bp fragment was once inserted into the corresponding position of wild-type was digested by Overproduction and purification of (Ll09Q/Rl15C) using the primer IV-b. Gln109 was then replaced by leucine residue. was cultured in containing the region of Cys99 was inserted into the corresponding region of the corresponding segment of wild-type (Y99H/E107G) using the primer IV-b. Gly was then substituted for the corresponding segment of wild-type sequence of (Y99C). (2) Y99C. pUL32 (V75A/Y99C) was digested by Acc I, and an 820-bp fragment containing the region of Cys99 was inserted into the corresponding region of pULB200 with wild-type sequence of Δ61LipB. Then, a 900-bp Neo I-Hind III fragment from the resulting plasmid was substituted for the corresponding segment of wild-type pUL32 to give pUL32 (Y99C).

(3) Y99H. pUL32 (Y99H) was prepared by site-directed mutagenesis of pUL32 (Y99H/E107G) using the primer IV-b. Gly107 was then replaced by glutamic acid residue.

(4) S102R. pUL32 (S102R/E126G) was digested by Neo I and Hind III, and a 900-bp fragment was once inserted into the corresponding position of pULB200. This plasmid was digested by Ban II, and a 150-bp fragment with the region of Arg102 was substituted for the corresponding segment of wild-type pULB200. The resulting plasmid was then digested by Neo I and Hind III, and a 900-bp fragment was replaced by the corresponding region of wild-type pUL32 to obtain pUL32 (S102R).

(5) R115C. pUL32 (R115C) was prepared by site-directed mutagenesis of pUL32 (L109Q/R115C) using the primer IV-b. Gln109 was then replaced by leucine residue.

Overproduction and purification of H6-Δ61LipB. For preparation of H6-Δ61LipB (Δ61LipB fusion protein containing hexahistidyl leader sequence), E. coli JM109 pRSLB30 was cultured in 100 ml of SOB medium (2% Bacto tryptone, 0.5% Bacto yeast extract, 0.05% NaCl, 2.5 mM KCl, and 10 mM MgCl2) containing 50 μg/ml ampicillin at 37 °C. When absorbance at 600 nm reached 0.3, 1 mM of isopropyl β-D-thiogalactopyranoside was added. After further 1-h culture, M13 phage including the gene of T7 RNA polymerase was mixed with the culture, and the cells were grown for 5 h.

Pellets of the cells were suspended in 10 ml of the extraction buffer containing 20 mM sodium phosphate buffer, pH 7.5, 0.2 M NaCl, 10 mM imidazole, 0.02% NaN3, and 0.5 mM PMSF, and sonicated 10 times for 30 s at 0 °C with a Branson Sonifier 250. After centrifugation at 20,000 × g for 20 min at 4 °C, the supernatant was applied to a Ni2+ -bound Chelate Cellulofine affinity chromatography column (1.1 × 5 cm) equilibrated with the starting buffer (20 mM sodium phosphate buffer, pH 7.5, 0.5 M NaCl, 30 mM imidazole, 0.5 mM PMSF, and 0.02% NaN3). The active fraction was eluted with 300 mM imidazole.

4-3. Results

Random mutagenesis and screening of inactive LipBs. To explore amino acid residues of LipB required for reactivation of LipA, random mutagenesis was carried out on the gene coding for Δ61LipB, and inactive LipB mutants were selected by two steps of screening, as summarized in Fig. 4-3. The mutation was introduced by error-prone PCR method (Leung et al., 1989) using pULB200 as the template. Addition of 0.2-0.3 mM MnCl2 to the PCR reaction mixture stimulated incorporation of incorrect nucleotides during the polymerization. The PCR products were inserted at immediate downstream of the N-terminal 61-residue region of LipB into pUL32 to prepare plasmid library (Fig. 4-1).
Fig. 4-4. Tributyrin plate assay for determining LipB activity in \textit{E. coli} 1100 pUL32. (A) Clear zone-positive colonies that possess wild-type \textit{lipB} sequence in pUL32. (B) Clear zone-negative colonies. These clones are expected not to produce active LipB.

Fig. 4-5. Western blotting analysis of LipB production in \textit{E. coli} 1100 pUL32. Lane 1, wild-type LipB; lanes 2-6, LipB from clear zone-negative clones. Sample on lane 6 was selected as a clone with producing a normal size LipB. Digested product was always detected even in the wild-type (lane 1).

\textit{E. coli} 1100 was transformed with this pUL32 library, and was cultured on tributyrin agar plate for the first screening of inactive LipBs (Fig. 4-4). Colony of \textit{E. coli} 1100 pUL32 with wild-type LipB formed clear zone due to hydrolysis of tributyrin by secreted active LipA. In the case of mutational library of pUL32, up to 20 colonies formed no clear zone out of about 3000 colonies from one plate (15 cm of diameter). Then, 175 of colonies without clear zone were picked up and cultured for the second screening to exclude frameshift mutants and nonsense ones. This screening was carried out by Western blotting with anti-\Delta61LipB to detect the molecular weight of produced LipB in each cell. Some examples of this Western blotting analysis are shown in Fig. 4-5. On lane 6, a band was detected at the same position as wild-type LipB on lane 1. As a result, 27 types of such samples that contain the normal size of LipB were selected. Plasmids were isolated from these selected mutant cells, and were sequenced on the gene coding for \Delta61LipB. In all of these mutants, multiple amino acids (2-16 residues) were replaced (Table 4-1).

<table>
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<tr>
<th>No.</th>
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<th>Mutational sites</th>
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<td>30B</td>
<td>2 (2)</td>
<td>V75A Y99C</td>
</tr>
<tr>
<td>29A</td>
<td>2 (2)</td>
<td>Y99H E107G</td>
</tr>
<tr>
<td>30C</td>
<td>2 (3)</td>
<td>S102R E126G</td>
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<tr>
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<td>L109Q R115C</td>
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<tr>
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<td>3 (3)</td>
<td>S69P L146Q D289V</td>
</tr>
<tr>
<td>26E</td>
<td>3 (6)</td>
<td>F80S L287P E293G</td>
</tr>
<tr>
<td>26K</td>
<td>3 (5)</td>
<td>D98G F186L E317V</td>
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<td>19G</td>
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<tr>
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</tr>
<tr>
<td>26L</td>
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<td>E107V L146R K207V E305G</td>
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<tr>
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<td>5 (5)</td>
<td>V63A G77S T210I I257T E317V</td>
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Preparation of single-residue substituted inactive LipBs. Preparation of single-residue substituted LipBs from above mutants was attempted by genetic engineering techniques to determine functional residue for activity of LipB. A DNA fragment containing a part of the mutational sites was substituted for the corresponding segment of wild-type pUL32 to obtain a new plasmid with the other part of the mutational sites. In other cases, site-directed mutagenesis was performed to replace one of the mutational sites by wild-type sequence. New plasmids prepared in these procedures were introduced into E. coli 1100, and the clones of inactive LipB were further selected by tributyrin plate assay. The constructed plasmid was checked again by DNA sequencing. As a result, five genes of single-residue substituted mutants missing their in vivo activity (D76G, Y99C, Y99H, S102R, and R115C) were obtained from multiple-residue mutagenized plasmids, pUL32 (D76G/F100Y/F195L/I256T/R261H/D277G/R309C), pUL32 (V75A/Y99C), pUL32 (Y99H/E107G), pUL32 (S102R/E126G), and pUL32 (L109Q/R115C), respectively. The mutational positions of single-residue or double-residue substituted LipB finally obtained are illustrated in Fig. 4-6.

Preparation of the purified H6-Δ61LipB mutants. Purified samples of the five single-residue substituted mutants were prepared as hexahistidyl fusion proteins (H6-Δ61LipB) for examination of their in vitro properties. A DNA fragment encoding Δ61LipB mutant from pUL32 was inserted into an expression plasmid pRSET B. The resulting plasmid was introduced into E. coli JM109, and H6-Δ61LipB was overproduced. Five mutants of H6-Δ61LipB as well as the wild-type were readily purified with the Ni²⁺-bound Chelate Cellulofine. Five mutant H6-Δ61LipBs were observed to show similar circular dichroism spectra to wild-type H6-Δ61LipB. Typical examples are shown in Fig. 4-7. Thus, the folding of each mutant LipB would not be significantly changed by substitution of the amino acid residue.

In the case of Y99C and R115C, effect of the substitution of cysteine residue on molecular assembly was analyzed by SDS-PAGE with or without 2-mercaptoethanol (Fig. 4-8). Without the reductant, both mutants appeared as two bands, which are close to the sizes of monomer (36 kDa) and dimer (72 kDa). In contrast, dimeric size of the band disappeared by addition of 2-mercaptoethanol. Because these mutants have only one cysteine residue introduced by the mutagenesis, parts of molecules of Y99C and R115C are likely to form dimers by the disulfide bond with the substituted cysteine residue, Cys99 and Cys 115, respectively.

Fig. 4-6. Mutational sites of single- or double-residue substituted mutants of Δ61LipB. Substituted residues are identified by DNA sequencing of the gene coding for Δ61LipB.

Fig. 4-7. Circular dichroism spectra of the wild-type and mutant H6-Δ61LipBs. (A) Wild-type; (B) Y99C; (C) S102R; (D) R115C.
In vitro reactivation of mutant LipBs. Activity of single-residue substituted H6-Δ61LipB was determined by measurement of reactivation of denatured LipA. H6-Δ61LipB with the wild-type sequence was observed to recover lipase activity of denatured LipA in the same way as Δ61LipB. Activity of the mutant LipBs relative to the wild-type is shown in Table 4-2. The recovery of lipase activity with all the mutants was lower than that with wild-type H6-Δ61LipB: this result was consistent with the features in tributyrin plate assay. Notably, Y99C, Y99H, S102R, and R115C expressed less than 1% activity of wild-type H6-Δ61LipB in 4-h reactivation of denatured LipA. Thus, amino acid residues of Tyr99, Ser102, and Arg115 play a significant role in reactivation activity of LipB. In contrast, D76G recovered lipase activity that is about one third of the recovery with wild-type H6-Δ61LipB. Initial rate of reactivation with D76G was observed to be 3% of that with wild-type H6-Δ61LipB.

Ability of the mutants to form a complex with denatured LipA was further examined by cross-linking with glutaraldehyde (Fig. 4-9). Wild-type H6-Δ61LipB was cross-linked with LipA after reactivation, and a 66-kDa band was detected by the SDS-PAGE. In contrast, Y99C, Y99H, S102R, and R115C, which almost lost reactivation activity, showed no detectable cross-linked product with LipA. Thus, these mutants altered to lose the ability to complex with LipA. In addition, D76G was slightly cross-linked with LipA.
4-4. Discussion

To find the functional amino acid residues of LipB, random mutagenesis was carried out on the gene of Δ61LipB, and mutant LipBs missing the activity were selected, of which an amino acid residue is substituted. The random mutation itself is readily introduced by error-prone PCR (Leung et al., 1989). Subsequently, two steps of screening methods were adopted to select the inactive LipBs from the given library: tributyrin plate assay in the first step and Western blotting to detect the molecular size of LipB in the second step. On the tributyrin plate, the secretion of lipase from bacterial colonies can be detected (Lawrence et al., 1967). It has been observed that the active LipA was secreted by an E. coli strain carrying pUL11, a plasmid containing lipB as well as lipA, so that the colonies formed clear zone due to the (Chihara-Siomii et al., 1992) hydrolysis of tributyrin. Furthermore, when the lipB gene was disrupted in the plasmid, the transformant did not secrete the active LipA, then the clear zone was not detected. By utilizing these features, the clones with inactive LipB were selected on tributyrin plate assay from the library of pUL32, a derivative of pUL11. However, a series of the clear zone-negative clones included the frameshift mutants and nonsense mutants (data not shown). It is reported that the error-prone PCR using MnCl₂ induces not only the base substitution but also the base deletion (Leung et al., 1989). The frameshift or nonsense mutants do not fit the present purpose, that is, determining the amino acid residues important to the activity of LipB. It is expected that such clones would produce a different molecular size of LipB from the wild-type one. Thus, the LipB production in each cell selected in the first screening was subsequently analyzed by Western blotting using anti-Δ61LipB to exclude those unnecessary mutants. The selected mutants with the normal molecular size were observed to be base-substituted proteins by DNA sequencing experiments. Consequently, these simple screening steps have allowed rapid discrimination of functional amino acid residues of LipB.

In Chapter 3, it is demonstrated that the N-terminal 61 residues of LipB is unnecessary for its reactivation activity. This feature indicates that all of the functional residues in the reactivation exist on the region of Δ61LipB. Therefore, for the purpose of the present study, it is sufficient that only the gene of Δ61LipB is served as a target DNA in the random mutagenesis. However, it was observed that the production of the full-length LipB (containing N-terminal 61 residues) is needed to detect the activity of LipB by the tributyrin plate assay. When the gene of the Δ61LipB instead of the full-length LipB gene was directly inserted at downstream of lipA in pUL11, clear zone was little detected around the colony of E. coli 1100 carrying this plasmid (data not shown). This result indicates that the secretion of LipA by E. coli cells seems to require the N-terminal region of the full-length LipB. Thus, it is relevant to employ the strategy that the gene library of Δ61LipB derived from the error-prone PCR was directly ligated to the DNA encoding the N-terminal 61 residues of pUL32. As a result, E. coli 1100 pUL32 produces the full-length LipB that is a mutant of K62M due to the plasmid construction. However, it was observed that this mutation does not affect the ability to form clear zone. After all, a reliable system of random mutagenesis was established that the gene of Δ61LipB is readily isolated from and ligated to the plasmids used in the present study at the common cloning sites of Neo I and Hind III (Fig.4-1).

The random mutagenesis suggests that four residues of LipB, Asp76, Tyr99, Ser102, and Arg115 are likely to participate in its reactivation activity. The single-residue substituted mutants, Y99C, Y99H, S102R, and R115C were observed to decrease the activity of reactivated LipA, and to form no detectable complex with LipA. Notably, it is proposed that Tyr99 and Arg115 are the residues on the surface of the LipB molecule, because the single cysteine residue of Y99C and R115C formed the intermolecular disulfide bond. Thus, Tyr99 and Arg115 could directly interact with LipA. Regarding above four residues of LipB, only Tyr99 is completely conserved among the lipase activator proteins (Fig. 1-3). In the case of the activator proteins form P. cepacia group (Iizumi et al., 1991, Jørgensen et al., 1991, Nakanishi et al., 1991), residues corresponding to Ser102 and Arg115 are threonine and alanine, respectively. In Chapter 2, it is demonstrated that LipB of P. aeruginosa TE3285 reactivated LipA from the same origin and Pseudomonas sp. 109 lipase that has 98% identical sequence with LipA, but not from the other Pseudomonas species. This feature suggests that several amino acid residues of LipB would be attributed to the strict substrate specificity. In this respect, such residues important to specific recognition of LipA would not be necessarily conserved among the lipase activator proteins. Therefore, Ser102 and Arg115 of LipB may be responsible for the specificity of LipB.
CHAPTER 5

Conclusions

LipB, lipase activator protein of *Pseudomonas aeruginosa* TE3285, is a folding factor for producing active extracellular lipase (LipA) in the cell. In this study, roles of LipB in the reactivation process of LipA were analyzed at the molecular level by means of protein engineering techniques.

LipB was overproduced in *Escherichia coli*, and purified 4.9-fold over the crude extract in the presence of SDS. The purified LipB reactivated LipA that is denatured with guanidine hydrochloride, and this reactivation did not involve multiple turnover. In this reactivation, a 1:1 complex between LipA and LipB was detected in a cross-linking experiment, suggesting that LipB still binds to LipA after the reactivation. Calcium ion was essential for the complex formation and the reactivation, and addition of EDTA caused inactivation of the reactivated LipA bound to LipB more rapidly than the native LipA. These findings suggest that LipB could affect the calcium binding to LipA in the reactivation process. LipB was unable to reactivate lipases from other sources except *Pseudomonas* sp. 109; this lipase has an amino acid sequence which is 98% identical to that of LipA. Thus, it may be concluded that LipB specifically recognizes a unique structural element of LipA.

Two mutant forms, which had truncated N-terminals, of LipB were prepared, and their molecular properties and activity were compared with those of the full-length form. A truncated LipB lacking its hydrophobic N-terminal 21 residues was dispersed homogeneously in solution, and could reactivate the stoichiometric amount of denatured LipA. In contrast, full-length LipB formed soluble aggregates, and reactivated less than an equimolar amount of LipA even under the most suitable conditions. These findings suggest that some or all of the N-terminal 21 residues caused aggregation of the protein molecules, and prevented LipB from fully stoichiometric reactivation. A truncated LipB lacking the N-terminal 61 residues also re-
activated denatured LipA, suggesting that the N-terminal 61-residue region of LipB is not involved in reactivation.

To find important amino acid residues of LipB in reactivation of LipA, random mutagenesis using error-prone PCR was performed on a gene encoding Δ61LipB. The given DNA library was introduced into the lipase expression system using E. coli, and LipBs losing its activity was selected by two screening procedures. First, on agar plates containing tributyrin for substrate of LipA, single colonies without active LipA secretion were selected as clones missing active LipB. Second, to exclude nonsense mutants and frameshift ones, molecular size of LipB in the given clones was confirmed by Western blotting. From the selected mutants, of which multiple residues are replaced, five single-residue substituted mutants were newly prepared. Consequently, Y99C, Y99H, S102R, and R115C mutants formed no detectable complex with LipA and lost the in vitro reactivation activity. In the case of Y99C and R115C, their single cysteine residue formed the intermolecular disulfide bridge. Thus, Tyr99 and Arg115 are likely to exist on the molecular surface of LipB, and directly interact with the denatured LipA in the reactivation process.

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REFERENCES


LIST OF PUBLICATIONS

Chapter 2

Chapter 3

Chapter 4