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# Characterization of *Pseudomonas aeruginosa* Enoyl-Acyl Carrier Protein Reductase (FabI): a Target for the Antimicrobial Triclosan and Its Role in Acylated Homoserine Lactone Synthesis

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**The *Pseudomonas aeruginosa fabI* structural gene, encoding enoyl-acyl carrier protein (ACP) reductase, was cloned and sequenced. Nucleotide sequence analysis revealed that *fabI* is probably the last gene in a transcriptional unit that includes a gene encoding an ATP-binding protein of an ABC transporter of unknown function. The FabI protein was similar in size and primary sequence to other bacterial enoyl-ACP reductases, and it contained signature motifs for the FAD-dependent pyridine nucleotide reductase and glucose/ribitol dehydrogenase families, respectively. The chromosomal *fabI* gene was disrupted, and the resulting mutant was viable but possessed only 62% of the total enoyl-ACP reductase activity found in wild-type cell extracts. The *fabI*-encoded enoyl-ACP reductase activity was NADH dependent and inhibited by triclosan; the residual activity in the *fabI* mutant was also NADH dependent but not inhibited by triclosan. An polyhistidine-tagged FabI protein was purified and characterized. Purified FabI (i) could use NADH but not NADPH as a cofactor; (ii) used both crotonyl-coenzyme A and crotonyl-ACP as substrates, although it was sixfold more active with crotonyl-ACP; and (iii) was efficiently inhibited by low concentrations of triclosan. A FabI $Gly^{95}$-to-Val active-site amino acid substitution was generated by site-directed mutagenesis, and the mutant protein was purified. The mutant FabI protein retained normal enoyl-ACP reductase activity but was highly triclosan resistant. When coupled to FabI, purified *P. aeruginosa* *N*-butyryl-L-homoserine lactone ($C_4$-HSL) synthase, RhlI, could synthesize $C_4$-HSL from crotonyl-ACP and *S*-adenosylmethionine. This reaction was NADH dependent and inhibited by triclosan. The levels of $C_4$-HSL and *N*-(3-oxo)-dodecanoyl-L-homoserine lactones were reduced 50% in a *fabI* mutant, corroborating the role of FabI in acylated homoserine lactone synthesis in vivo.**

The important opportunistic pathogen *Pseudomonas aeruginosa* contains a type II or dissociated fatty acid synthetase system, in which the individual reactions are catalyzed by separate proteins (22, 24). Although the overall organization of the *P. aeruginosa fab* genes is similar to that in *Escherichia coli* (for reviews see references 9 and 28), some potentially significant differences exist. First, the *P. aeruginosa fabA* and *fabB* genes, encoding β-hydroxyacyl-acyl carrier protein (ACP) dehydratase and β-ketoacyl-ACP synthase I, form an operon (22), whereas in *E. coli* these genes map to separate genetic loci. Second, unlike in *E. coli* and several other gram-negative bacteria, the *fabH* gene, encoding β-ketoacyl-synthase III, is absent from the *fabD-fabG-acpP-fabF* gene cluster, encoding malonyl-coenzyme A (CoA):ACP transacylase, β-ketoacyl-ACP reductase, ACP, and β-ketoacyl-ACP synthase II (25). Searches of the *P. aeruginosa* genome database revealed several potential *fabH* homologs located elsewhere on the genome.

Our current model for fatty acid biosynthesis in *P. aeruginosa* is shown in Fig. 1. Three β-ketoacyl-ACP synthases, KAS I (FabB), KAS II (FabF), and KAS III (FabH), play pivotal roles in fatty acid synthesis. Initiation requires malonyl-CoA and malonyl-ACP. Malonyl-CoA is synthesized from acetyl-CoA via the acetyl carboxylase reaction (5). Malonyl-ACP is derived from malonyl-CoA and ACP by malonyl-CoA:ACP transacylase (FabD) (24, 25). Although a *P. aeruginosa fabH* homolog has only tentatively been identified, the first cycle of elongation is probably initiated by KAS III (FabH), which condenses malonyl-ACP with acetyl-CoA. Subsequent cycles are then initiated by condensation of malonyl-ACP with acyl-ACP, catalyzed by KAS I (FabB) for saturated fatty acid substrates and KAS II (FabF) for unsaturated fatty acid substrates. In the second step, the resulting β-ketoester is reduced to a β-hydroxyacyl-ACP by a NADPH-dependent β-ketoacyl-ACP reductase (FabG). It has recently been shown that *P. aeruginosa* contains a FabG homolog, RhlG, which presumably functions as a NADPH-dependent β-ketoacyl-ACP reductase specific for rhamnolipid synthesis (6). The third step in the cycle is catalyzed by either the *fabA*- or *fabZ*-encoded β-hydroxyacyl-ACP dehydratase. The final step in each cycle involves conversion of *trans*-2-enoyl-ACP to acyl-ACP, a reaction catalyzed by NADH-dependent enoyl-ACP reductase (FabI). Physiologically, FabI is an important enzyme because (i) reduction of enoyl-ACP derivatives is thought to regulate the ratio of saturated to unsaturated fatty acids and to coordinate fatty acid and phospholipid syntheses (16, 23); and (ii) FabI plays a determinant role in completing cycles of fatty acid elongation (15). FabI belongs to the short-chain alcohol dehydrogenase family and in *E. coli* is the target of a group of antibacterial compounds, the diazoborines (44) and triclosan (19, 33). In *Mycobacterium tuberculosis*, the FabI homolog InhA is one of the targets for the clinically used antimycobac-

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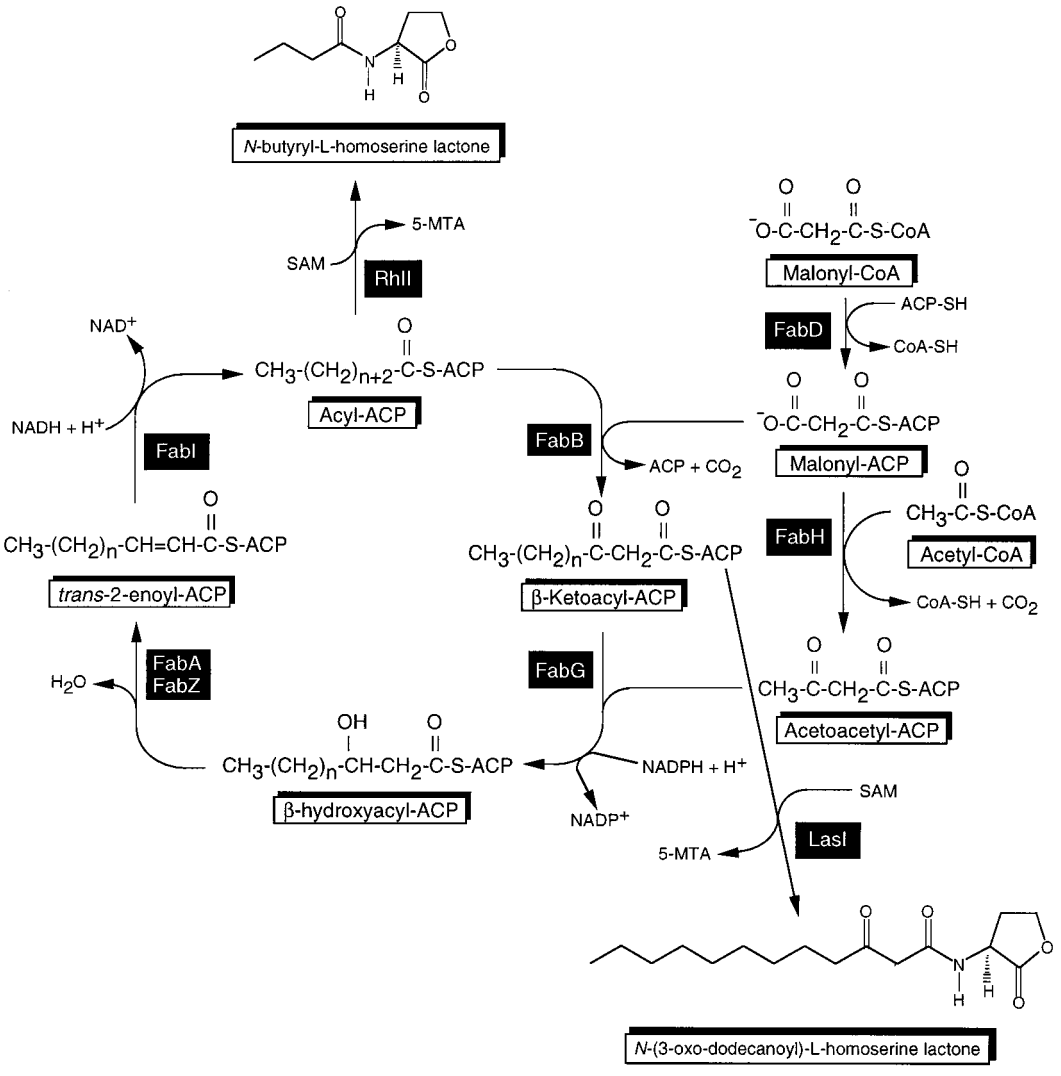


FIG. 1. Current model for fatty acid biosynthesis in *P. aeruginosa* and proposed role of butyryl-ACP as acyl donor in *N*-butyryl-L-homoserine lactone synthesis. The genes for all enzymes except one (*fabH*) have been identified and characterized; for *fabH*, only a tentative identification has been made among several paralogs. Abbreviations: ACP, acyl carrier protein; ACP-SH, ACP with 4′-phosphopantetheine co-factor; CoA-SH; coenzyme A; FabA (and FabZ), β-hydroxyacyl-ACP dehydratase; FabB, β-ketoacyl synthase I; FabD; malonyl-CoA:ACP transacylase; FabF, β-ketoacyl synthase II; FabG, β-ketoacyl-ACP reductase; FabH, β-ketoacyl synthase III; FabI; enoyl-ACP reductase; 5-MTA, 5-methylthioadenosine; SAM, *S*-adenosylmethionine; LasI, *N*-(3-oxo)-dodecanoyl homoserine lactone synthase; RhlI, *N*-butyryl homoserine lactone synthase.

terial isoniazid (2), and genetic evidence was obtained that *M. smegmatis* InhA is a triclosan target (32). More recently, it has been shown that *E. coli* mutants resistant to the antiseptic triclosan contain *fabI* mutations (33), and a subsequent study confirmed that triclosan and other related compounds indeed target FabI (19). Although *P. aeruginosa* PAO1 is resistant to triclosan due to constitutive expression of the *mexAB-oprM*-encoded efflux pump, Δ(*mexAB-oprM*) mutants are susceptible to triclosan (41). The *E. coli* FabI protein has been cocrystallized with NADH and thienodiazoborine (18), or $NAD^+$ (26), and these studies allowed definition of the enzyme active site and amino acid residues important in substrate and drug interactions.

Besides providing fatty acid intermediates for a multitude of cellular constituents (phospholipids [9], lipid A [37], etc.), the Fab pathway has been implicated in providing the acyl groups for the acylated homoserine lactones (HSLs) that are the signalling molecules in quorum sensing (14, 35, 39, 45). In *P. aeruginosa*, quorum sensing is a mechanism that regulates virulence factor gene expression (46), biofilm formation in vitro (10) and in natural settings (31), twitching motility (13), and other important cellular processes. According to the current model, quorum sensing in *P. aeruginosa* involves two separate systems, LasR-LasI and RhlR-RhlI. These proteins are encoded by two separate, tandemly arranged transcriptional units. In these two systems, the LasI and RhlI proteins are HSL synthases that direct the synthesis of *N*-(3-oxo)-dodecanoyl-L-homoserine lactone (3-oxo-$C_{12}$-HSL) and *N*-butyryl-L-homoserine lactone ($C_4$-HSL), respectively. According to the current model, the synthases react with acyl-ACPs and *S*-adenosylmethionine (SAM) to form the cognate HSLs, with concomitant release of 5-methylthioadenosine (35, 39). For $C_4$-HSL synthesis, the *rhlI*-encoded *P. aeruginosa* HSL synthase RhlI catalyzes the formation of $C_4$-HSL in a reaction

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

| Strain, plasmid, or primer | Description or sequence[a] | Reference or source |
|---|---|---|
| *E. coli* | | |
| DH5αF′ | [$F^+$ ϕ80*lacZ*ΔM15] Δ(*lacZYA-argF*)*U169 recA1 endA1 hsdR17* [$r_K^-$ $m_K^+$] *supE44 thi-1 gyrA relA1* | 27 |
| JP1111 | Hfr *galE45 fabI392*(Ts) *relA1 spoT1* | 44 |
| BL21(DE3) | *E. coli* B; $F^-$ *ompT* $r_B^-$ $m_B^-$ (λDE3) | 43 |
| *P. aeruginosa* | | |
| PAO1 | PAO1 | B. H. Holloway |
| PAO200 | PAO1 with Δ(*mexAB-oprM*) | 41 |
| PAO234 | PAO1 with *fabI*::$Gm^r$-*FRT* | This study |
| PAO235 | PAO1 with *fabI*::*FRT* | This study |
| Plasmids | | |
| pET-15b | $Ap^r$; hexahistidine fusion and expression vector | Novagen |
| pWSK29/30 | $Ap^r$; low-copy-number cloning and T7 expression vectors | 47 |
| pFLP2 | $Ap^r$; source of Flp recombinase | 21 |
| pPS856 | $Ap^r$ $Gm^r$; source of $Gm^r$-*FRT* cassette | 21 |
| pUCP21T | $Ap^r$; broad-host-range cloning vector | 42 |
| pEX18Tc | $Tc^r$; *sacB*-based gene replacement vector | 21 |
| pPS922 | $Ap^r$ *fabI*$^+$ (ligation of a 880-bp *Bam*HI-*Hin*dIII PCR fragment between the same sites of pWSK30; *fabI*-transcription driven by $P_{lac}$) | This study |
| pPS925 | $Ap^r$ *fabI*::$Gm^r$-*FRT* (ligation of a 1,053-bp blunt-ended *Sac*I fragment from pPS856 into the *Sma*I site of pPS922) | This study |
| pPS933 | $Ap^r$ *sacB*$^+$ *fabI*::$Gm^r$-*FRT* (ligation of a 1.95-kb *Bam*HI-*Hin*dIII fragment between the same sites of pEX18Tc) | This study |
| pPS935 | $Ap^r$; $H_6$-FabI expression vector (PCR-amplified 0.85-kb *Nde*I-*Bam*HI fragment cloned between same sites of pET-15b) | This study |
| pPS967 | $Ap^r$ *fabI*$^+$ (pUCP21T with *Bam*HI-*Hin*dIII fragment from pPS922; *fabI* transcription driven by $P_{lac}$) | This study |
| pPS1098 | $Ap^r$; $H_6$-FabI expression vector (PCR-amplified 0.85-kb *Nde*I-*Bam*HI fragment cloned between same sites of pET-15b); expresses $H_6$-FabI mutant protein | This study |
| Primers | | |
| FabIU | *Hin*dIII-GCAAGCttGCGGAAAACTGAGTAGCAGA | |
| FabID | *Bam*HI-ATGGatCCGCTTGAAGCGGCATTTTTC | |
| FabI-Nde | *Nde*I-GGcatATGGGATTTCTCACAGGAAAAC | |
| FabI G>V | CCACTCCGTCGtATTCGCTCCAG | |

[a] $P_{lac}$, *E. coli lac* operon promoter. Primer sequences are printed 5′ to 3′; lowercase letters indicate nonmatching oligonucleotides used to either form the indicated motif as underlined or introduce other nonmotif changes indicated in lowercase letters.

utilizing butyryl-ACP as the acyl donor and SAM as the nucleophile in a lactonization reaction (35, 39).

In this report, we describe the characterization of the *P. aeruginosa fabI* gene and its product, show evidence for the presence of at least one other enoyl-ACP reductase in this bacterium, provide biochemical evidence that FabI is a triclosan target, and demonstrate its role in $C_4$-HSL synthesis.

## MATERIALS AND METHODS

**Bacterial strains, plasmids, primers, and media.** The relevant strains, plasmids, and primers are described in Table 1. LB (Luria-Bertani) medium (34) was routinely used as the rich medium for all bacterial strains. For growth of the *fabI*(Ts) mutant JP1111, the NaCl concentration of LB medium was reduced to 0.05%. For some experiments, RB medium (20) was used instead of LB. The minimal medium used for growth of *P. aeruginosa* was VBMM (40). The antibiotics used in selection media were as follows: for *E. coli*, ampicillin (100 μg/ml) and gentamicin (15 μg/ml); for *P. aeruginosa*, carbenicillin (500 μg/ml) and gentamicin (200 μg/ml).

**General DNA procedures.** Routine DNA were performed as previously described (21). The details underlying construction of pPS921 were as follows. For PCR amplification of a fragment from chromosomal DNA, two mutagenic oligonucleotides were synthesized. The FabIU and FabID primers were designed to introduce a *Hin*dIII site upstream of *fabI* and a *Bam*HI site downstream of *fabI*, respectively (Table 1). These oligonucleotides were used to prime synthesis from PAO1 chromosomal DNA. PCRs were performed on a PTC-100 PCR system thermocycler (MJ Research, Watertown, Mass.) as previously described (21, 22). The ca. 870-bp PCR fragment was ligated to *Bam*HI-*Hin*dIII-digested pWSK30 (47) DNA to form pPS921. Nucleotide sequences were determined and analyzed as previously described (22). Motif searches were performed by using the on-line E-Motif program provided by Stanford University, Palo Alto, Calif.

A two-step method was used for site-directed mutagenesis for *fabI*. First, PCRs were set up as described above but with pPS935 DNA as the template, and DNA synthesis was primed with the T7 terminator primer (Novagen, Madison, Wis.) and a mutagenic primer, FabI G>V (Table 1), that was designed to (i) introduce a single G-to-T change which leads to a $Gly^{95}$-to-Val amino acid change and (ii) yield a PCR product that would properly prime to pPS935 DNA in a second round of PCR even when T-tailed by *Taq* DNA polymerase. The single 1,046-bp PCR product was digested with *Bam*HI plus *Nde*I, and the resulting 840-bp *Bam*HI-*Nde*I fragment was gel purified and ligated to *Bam*HI-*Nde*I-digested pET-15b DNA. The presence of the single G-to-T change was verified by nucleotide sequence analysis.

**Disruption of the *fabI* gene.** The *fabI* strain PAO235 was isolated in several steps. A plasmid-borne *fabI* mutation was constructed by insertion of a blunt-ended 1,053-bp gentamicin resistance ($Gm^r$)-*FRT* cassette from pPS856 (21) into the *Sma*I site located within the *fabI* coding sequence. The resulting mutation was returned to the *P. aeruginosa* chromosome after subcloning into the *sacB*-based suicide vector pEX18Tc (21) to derive the *fabI*::$Gm^r$-*FRT* mutant PAO234. From PAO234, the unmarked *fabI*::*FRT* mutant PAO235 was then derived by in vivo excision of the $Gm^r$-*FRT* cassette with Flp recombinase (21). The mutants were confirmed by performing colony PCR (21) utilizing the FabIU and FabID primers.

**Purification of an polyhistidine-tagged FabI fusion protein.** A hexahistidine-FabI ($H_6$-FabI) expression vector was constructed by PCR amplifying the *fabI* coding sequence from PAO1 genomic DNA with primers FabI-Nde, creating a *Nde*I site at the *fabI* ATG initiation codon, and FabID, which creates a *Bam*HI site immediately downstream of *fabI*. The PCR fragment was digested with *Nde*I and *Bam*HI, and the resulting 840-bp *Bam*HI-*Nde*I fragment was ligated between the same restriction sites of pET-15b to form pPS935, which was then trans-

formed into *E. coli* BL21(DE3). Expression of $H_6$-FabI, cell lysis, and purification of the soluble fusion protein on a $Ni^{2+}$-agarose column (Qiagen) were performed as previously described (17) except that the cells were grown in LB medium containing ampicillin (LB-Ap medium). The same procedure was used for purification of a mutant FabI protein.

Protein concentrations were determined by using the Bradford dye binding assay (Bio-Rad Laboratories, Hercules, Calif.) and bovine serum albumin as the standard. Proteins were analyzed by electrophoresis on 0.1% sodium dodecyl sulfate–10% polyacrylamide gels (SDS-PAGE) as previously described (29). The proteins were visualized by quick staining with Coomassie brilliant blue R-250 (7).

**Enoyl-ACP reductase assays.** *P. aeruginosa* cell extracts were prepared from exponentially growing cells ($A_{540}$ of ~0.8 to 1.0). Cells grown in LB medium at 37°C were harvested by centrifugation and then suspended and washed in 0.1 M sodium phosphate buffer (pH 6.5). Cell lysates were prepared by passing the cell suspensions three times through a French pressure cell (19,000 lb/in$^2$). Cell debris was removed by ultracentrifugation for 1 h at 260,000 × *g*, and the supernatants were saved as cell extracts.

Enoyl-ACP reductase activity of purified $H_6$-FabI, as well as in cell extracts, was determined by using crotonyl-ACP as the substrate. This was done by measuring spectrophotometrically the decrease in absorbance at 340 nm at room temperature due to consumption of NADH (or NADPH) during reduction of crotonyl-ACP (3). In 500 μl, a typical assay mixture contained 0.1 M sodium phosphate (pH 7.5), 0.1 mM NADH, and 1 μg of purified $H_6$-FabI. The reactions were initiated by addition of 20 μM crotonyl-ACP. In some instances, 0.1 mM NADPH was used as the reductant. For some experiments, enzyme and substrate concentrations were varied as indicated in the figure legends. A stock solution of triclosan was prepared in 95% ethanol, and appropriate amounts of ethanol were added to control experiments to assess possible inhibitory effects of the solvent on enzyme activities.

Crotonyl-ACP was prepared by using a previously published procedure (48), with slight modifications. Briefly, 20 mg of purified *P. aeruginosa* ACP was precipitated as previously described (8) except that the hydroxylamine step was omitted. After precipitation of the protein with 10% trichloroacetic acid for 30 min on ice, the precipitate was pelleted in a microcentrifuge and then washed once with 0.2 M citrate buffer (pH 4.0) and once with water. The protein was resuspended in 0.1 M sodium phosphate buffer (pH 8.0) containing 2 μmol of dithiothreitol and reacted with a 10-fold molar excess of crotonic anhydride (Aldrich, Milwaukee, Wis.) for 30 min at 4°C with constant stirring. The reaction mixture was loaded on a PD10 column (Pharmacia Biotech, Uppsala, Sweden) that had been equilibrated with 0.1 M sodium phosphate buffer (pH 7.5), and the crotonyl-ACP was eluted with 3.5 ml of the same buffer. The crotonyl-ACP concentration was determined by measuring the difference in the number of free thiol groups of an untreated versus a hydroxylamine-treated sample by the Ellmann technique (12). The treatment of crotonyl-ACP (20 μl of the column eluate) was performed for 5 min at room temperature in a 1 M hydroxylamine solution in 0.1 M sodium phosphate buffer (pH 7.5). For thiol group determinations, hydroxylamine-treated or untreated crotonyl-ACP was reacted for 30 min at room temperature with 0.15 mM 5,5′-dithiobis (2-nitrobenzoic acid) (Aldrich) in a final volume of 0.8 ml of 0.1 M phosphate buffer (pH 7.5), and the absorption was measured at 400 nm. According to this determination, 80% of the ACP was acylated.

**Determination of acyl HSL concentrations in culture fluid.** Acyl HSLs were detected in culture fluids of LB-grown *P. aeruginosa* strains as previously described (36), using *E. coli* XL-1 Blue/pECP61.5 for detection of $C_4$-HSL and *E. coli* MG4/pKDT17 for detection of 3-oxo-$C_{12}$-HSL. Standard curves were prepared by using synthetic HSLs to ensure that bioassays were always performed in the linear range.

**$C_4$-HSL assays.** The in vitro $C_4$-HSL synthesis reactions contained (in 500 μl) Moré buffer (10 mM Tris-HCl [pH 7.4], 330 mM NaCl, 15% glycerol, 0.7 mM dithiothreitol, 2 mM EDTA, 25 mM $MgSO_4$, 0.1 mM $FeSO_4$) (35), 0.1 mM SAM, 0.2 mM NADH, 1 μg of purified $H_6$-RhlI (details to be published elsewhere), and various amounts of $H_6$-FabI. The reaction mixtures were incubated at 37°C for 1 h and then extracted three times with 250 μl of ethyl acetate. The ethyl acetate extracts were vacuum dried, and the residue was suspended in 20 μl of high-pressure liquid chromatography-grade acetonitrile (Fisher Scientific, Fair Lawn, N.J.). For detection of $C_4$-HSL, the *Chromobacterium violaceum* bioassay was used (30). Aliquots (5 μl) of the extracted reactions were spotted onto a Whatman (Clifton, N.J.) $C_{18}$ reverse-phase thin-layer chromatography (TLC) plate and allowed to air dry. The solvent used for chromatography was 60% methanol–40% water (vol/vol). For detection, 2.5 ml of an overnight culture of strain CV026 grown at room temperature in LB medium was diluted into 25 ml of 0.3% LB agar kept at 45°C, and the agar mixture was used to overlay the dried TLC plate. After solidification of the overlay, the TLC plate was incubated overnight at room temperature in a wet box. The presence of $C_4$-HSL in the extracted reactions was scored by appearance of a violet spot on the TLC plates.

**Nucleotide sequence accession number.** The DNA sequence of the *fabI* region has been deposited in GenBank under accession no. AF104262.

## RESULTS

**Cloning of the *fabI* gene of *P. aeruginosa*.** At the onset of this project, an examination of the incomplete *Pseudomonas* genome database release revealed two contigs which contained sequences that in BLAST searches showed extensive similarities to *E. coli fabI*. The amino and carboxy termini were located on two different contigs. The putative *fabI* coding sequence was successfully amplified from *P. aeruginosa* chromosomal DNA by using two oligonucleotide primers, FabIU and FabID (Table 1). These two primers were designed to introduce a unique *Hin*dIII site upstream of *fabI* and its putative ribosome binding site and to introduce a unique *Bam*HI site downstream of *fabI*. PCR amplification was very specific and yielded a 880-bp product that was digested with *Bam*HI plus *Hin*dIII and ligated to similarly digested pWSK30 DNA to form pPS922. This procedure placed *fabI* under transcriptional control of the *lac* promoter ($P_{lac}$) since the cloned *fabI* gene presumably lacks its own promoter. The low-copy-number (five to eight copies per cell) cloning vector pWSK30 (47) was used to avoid potential toxicity problems that we had observed during the cloning of other *fab* genes (25). The *fabI*(Ts) *E. coli* strain JP1111 does not grow at 42°C and has a low-salt tolerance at the nonpermissive temperature; e.g., it does not grow on regular LB medium containing 0.5% NaCl. This strain was transformed with pPS922 DNA, and $Ap^r$ transformants were selected at 30°C on LB-Ap medium. The transformants were then transferred to LB-Ap medium with and without 1 mM isopropyl-β-D-thiogalactopyranoside (IPTG) and incubated at 42°C. Within 24 h, only the colonies plated on LB-Ap medium with IPTG grew under these conditions, indicating that the cloned *fabI* (i) complemented the temperature-sensitive (Ts) and low-salt-tolerance phenotype of the *E. coli fabI*(Ts) mutant and (ii) does not contain its own promoter since transcription from $P_{lac}$ requires IPTG induction in the *lac* repressor producing strain JP1111. When JP1111 was transformed with pPS967, a multicopy plasmid expressing *fabI* from $P_{lac}$ (Table 1), complementation was observed in the absence of IPTG since the amounts of chromosomally encoded *lac* repressor were insufficient to fully repress *fabI* transcription.

**Sequence analysis of the *fabI* gene.** Since the *fabI* gene sequence in the incomplete genome database was contained on two separate contigs, we sequenced the cloned 874-bp *Hin*dIII-*Bam*HI fragment which contained a single open reading frame (ORF), and BLAST searches revealed significant identity of the protein to other FabI proteins. Alignments showed the greatest similarities with FabI proteins from *E. coli* and *Salmonella typhimurium* (69% identity; 81% similarity) and *Haemophilus influenzae* (63% identity; 76% similarity). This similarity also extended to FabIs from gram-positive bacteria, including *Bacillus subtilis* (49% identity; 66% similarity).

Analysis of the deduced FabI amino acid sequence using the E-Motif program revealed a glucose/ribitol dehydrogenase family signature motif (P..[KR].....[DE][FILVY].....[FWY].[AST]), as well as a signature motif for the FAD-dependent pyridine nucleotide reductase family (D..[FILMV]..[IV]G..P...L]. The latter sequence includes $Gly^{95}$, which is equivalent to a glycine found in position 93 of *E. coli* FabI. In *E. coli*, $Gly^{93}$-to-Ser and $Gly^{93}$-to-Ala changes, which lead to resistance to diazoborine (4) and triclosan (33), respectively, map close to the nucleotide binding site.

Examination of the latest *P. aeruginosa* genome database revealed a complete *fabI* gene sequence. Our sequence was identical to the database sequence with the exception of an additional G residue. This discrepancy arose from a mistake in the previous contig sequence after which our primer FabID

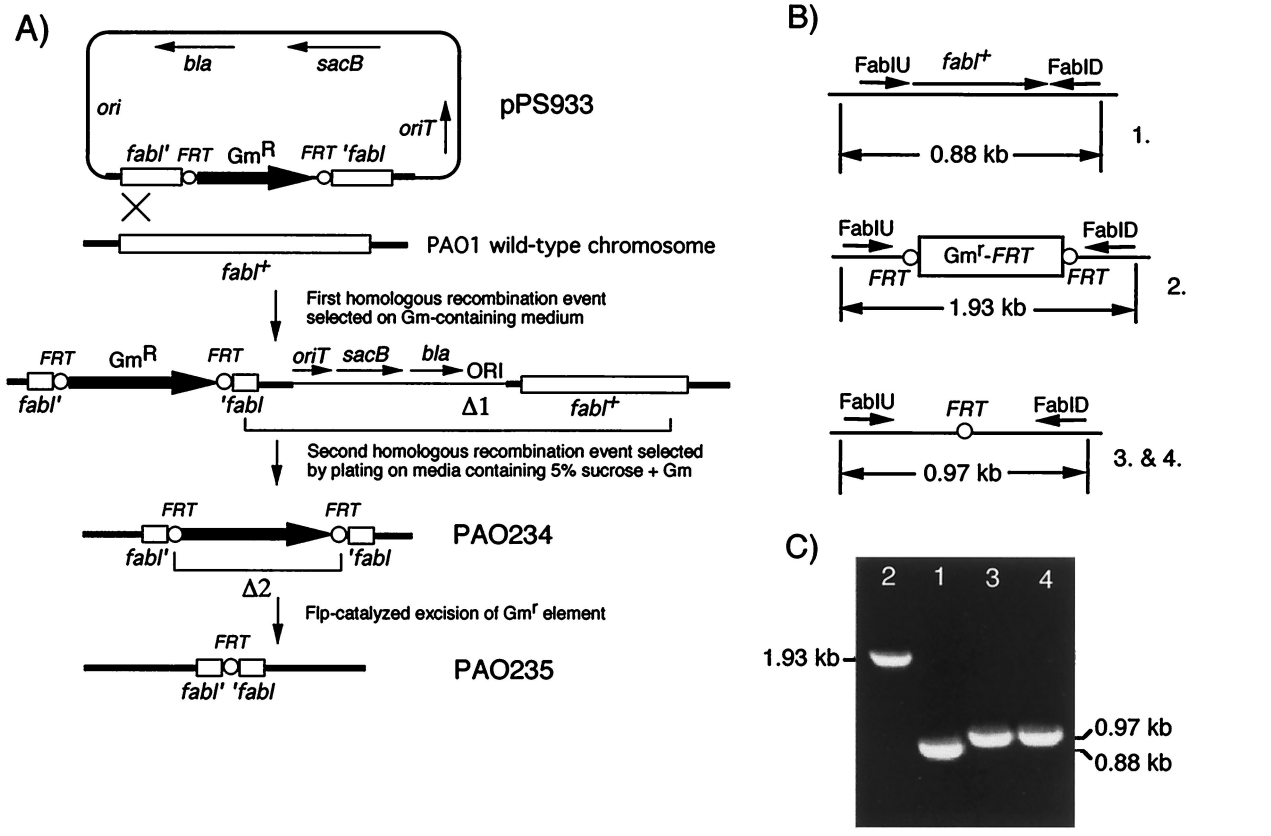


FIG. 2. (A) Strategy for isolation of an unmarked chromosomal *fabI* mutation via *sacB*-counterselected gene replacement (Δ1) and Flp-mediated excision of the Gm$^r$ marker (Δ2). (B) Genetic organization of the *fabI* region in wild-type PAO1 (1.), the *fabI*::Gm$^r$-*FRT* insertion mutant (2.), and the unmarked *fabI* mutant after Flp-mediated excision of the Gm$^r$ marker (3. and 4.). (C) PCR analysis of genomic DNA from the strains depicted in panel B. The PCRs were primed with the primers FabIU and FabID (B). Abbreviations: *bla*, β-lactamase-encoding gene; *FRT*, Flp recombinase target sites; Gm, Gm$^r$ marker; *ori*, pMB1 origin of replication; *oriT*, origin of transfer; *sacB*, levansucrase-encoding gene.

was modeled. The *fabI* gene is followed by a sequence that could assume a stem-loop structure ($\Delta G = -48.2$ kcal/mol) indicative of Rho-independent transcriptional terminators (38). Analysis of the *fabI* upstream sequence did not reveal any obvious promoter/regulatory sequences. Instead, the *fabI* gene is separated by 21 nucleotides from another ORF whose gene product exhibits significant similarity to many bacterial ATP-binding proteins that are components of ABC transporters; this ORF is 58% identical and 74% similar to the hypothetical *E. coli* ABC transporter ATP-binding protein YejF (GenBank accession no. U00008).

**Disruption of the chromosomal *fabI* gene.** A defined pPS933-borne *fabI*::Gm$^r$ insertion was constructed as described in Table 1, and the deletion was returned to the *P. aeruginosa* chromosome as illustrated in Fig. 2A. After conjugal transfer of the nonreplicative pPS933 from *E. coli* SM10 into PAO1, merodiploids were obtained by selecting for Gm$^r$. From these, colonies having undergone Δ1 were selected as sucrose resistant, Gm$^r$, and carbenicillin resistant. The unmarked *fabI*::*FRT* mutant PAO235 was then derived from PAO234 by Flp-catalyzed excision of the Gm$^r$ marker. During its expression in the recipient, Flp recombinase acted at the *FRT* sites to catalyze excision of the Gm$^r$ element (labeled Δ2 in Fig. 2A), leaving behind a short *FRT*-containing sequence.

Successful execution of the steps labeled Δ1 and Δ2 in Fig. 2A was monitored by colony PCR analysis using the FabIU and FabID primers. As expected, the primers amplified a 880-bp *fabI*-containing fragment from wild-type PAO1 DNA (Fig. 2C, lane 1). In PAO234 (lane 2), this fragment was increased to 1.93 kb by insertion of the 1,053-bp Gm$^r$-*FRT* cassette. After Flp-mediated excision of the Gm$^r$ marker, the PCR fragment was reduced to ~970 bp (880 bp and one 86-bp *FRT*-containing sequence from pPS856) (lanes 3 and 4). These events were further verified by genomic Southern analyses utilizing Gm$^r$ and *fabI*-specific DNA segments as the probes (data not shown).

***fabI* mutants contain reduced levels of enoyl-ACP reductase activity.** The growth rates of wild-type PAO1 and the *fabI* mutant PAO235 were superimposable when grown in RB medium and other media (data not shown). Since PAO235 contains only a 86-bp nonpolar insertion at a *Sma*I site that is located late in the *fabI* gene, we considered the possibility that this strain could still express a functional FabI protein. To rule out this possibility, we PCR amplified the *fabI* region from PAO235 by using the primers FabIU and FabID and subcloned the resulting *Bam*HI-*Hin*dIII fragment into pWSK30. Under inducing conditions, this DNA segment no longer complemented the Ts and low-salt-tolerance phenotypes of *E. coli fabI*(Ts) strain JP1111.

Determination of enzyme activities in cell extracts of wild-type and mutant PAO235 confirmed the existence of residual NADH-dependent activity in the mutant that amounted to 62% of the total activity observed in PAO1 extracts (Fig. 3). Whereas total NADH-dependent enoyl-ACP reductase in

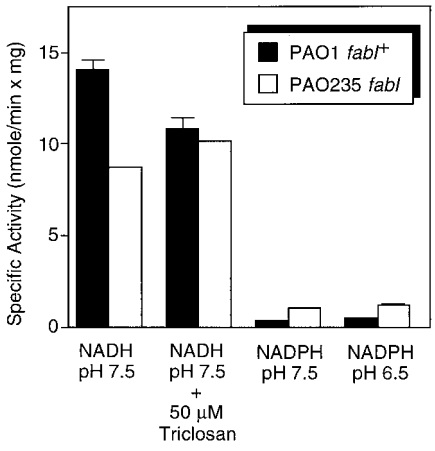


FIG. 3. Enoyl-ACP reductase activities in cell extracts of wild-type PAO1 and the *fabI* mutant PAO235. The 500-μl reactions contained in phosphate buffer with the indicated pH, 0.1 mM NADH or NADPH, and 50 to 100 μg of PAO1 extract or 300 μg of PAO235 extract for determination of NADH- or NADPH-dependent enoyl-ACP reductase activities, respectively. The reactions were initiated by addition of 13 μM crotonyl-ACP, and the decrease in absorbance at 340 nm was recorded. The results shown represent the means plus standard deviations of three experiments.

PAO1 was inhibited by the addition of 50 μM triclosan, this inhibitor had no effect on the residual activity found in PAO235, even when its concentration was increased to 100 μM (data not shown). Cell extracts from both strains showed very little NADPH-dependent enoyl-ACP reductase activity when assayed at pH 7.5 or 6.5.

**Purification and properties of purified FabI.** An expression vector was constructed, and FabI was purified as an $H_6$-FabI protein. When transformed into *E. coli* JP1111, the expression vector could complement the *fabI*(Ts) mutation of this strain, indicating expression of a functional $H_6$-FabI protein. The purified FabI protein (Fig. 4A) could utilize crotonyl-CoA and crotonyl-ACP as substrates (Fig. 4B), although it was 5.9-fold more active with crotonyl-ACP as the substrate. The enzyme was unable to utilize NADPH as cofactor (not shown), which may be a consequence of its purification at alkaline pH, conditions that may inactivate its NADPH-dependent activity, as has been observed with the *E. coli* enzyme (3).

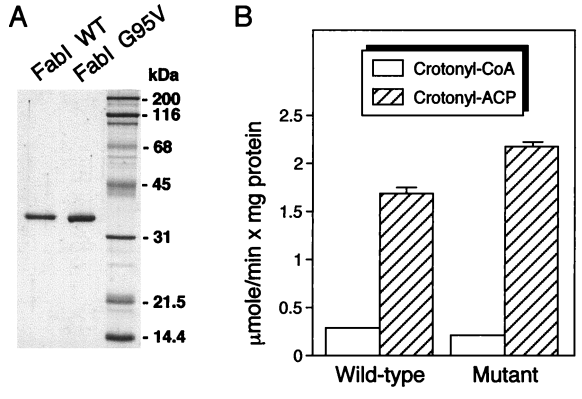


FIG. 4. (A) SDS-PAGE of purified wild-type (WT) FabI and FabI G95V mutant proteins; (B) substrate preference and specific activities of wild-type and mutant FabI proteins. (A) The proteins were expressed as $H_6$-tagged proteins and purified by $Ni^{2+}$ affinity chromatography. One microgram of each protein was analyzed by SDS-PAGE, and proteins were detected by Coomassie blue staining. The protein standards (Bio-Rad Laboratories) in the rightmost lane were (top to bottom) myosin, β-galactosidase, bovine serum albumin, ovalbumin, carbonic anhydrase, trypsin inhibitor, and lysozyme; molecular masses are shown on the right. (B) Enoyl-ACP reductase activities were measured with 20 μM crotonyl-CoA or 13 μM crotonyl-ACP as substrate and 0.1 mM NADH as cofactor. The reaction mixture contained either 1 μg of wild-type FabI or 1 μg of mutant FabI protein. The results shown represent the means plus standard deviations of three experiments.

The enoyl-ACP reductase activity was inhibited by very low concentrations of triclosan (Fig. 5). Triclosan-resistant *E. coli* strains contain changes in amino acid residues that are thought to line the enzyme active site (1, 33), and the most resistant strains contained $Gly^{93}$-to-Val substitutions (33). We therefore changed the corresponding $Gly^{95}$ in the *P. aeruginosa* enzyme to a Val and purified the resulting $H_6$-tagged mutant protein. The mutant protein (Fig. 4A) was slightly less active than wild-type FabI with crotonyl-CoA as the substrate and slightly more active with crotonyl-ACP as the substrate (Fig. 4B). The mutant enzyme was significantly more resistant to triclosan (Fig. 5).

**Role of FabI in HSL synthesis in vitro and in vivo.** Reduction of crotonyl-ACP by FabI to form butyryl-ACP is the last step in the first cycle of fatty acid elongation following condensation of malonyl-ACP with acetyl-CoA (Fig. 1). Theoretically, butyryl-ACP generated by FabI could serve as a substrate for transacylation of RhlI, followed by a lactonization reaction utilizing SAM as the substrate to form $C_4$-HSL, and inhibition of FabI or mutational inactivation should therefore lead to reduced levels of HSL production.

To test this hypothesis, we first set up an in vitro $C_4$-HSL synthesis system with purified $H_6$-FabI and $H_6$-RhlI. In this system, RhlI synthesized $C_4$-HSL from crotonyl-ACP in the presence of FabI, NADH, and SAM (Fig. 6, lane g). Under the same conditions, $C_4$-HSL synthesis was completely inhibited by 25 μM triclosan (lane b), and this inhibition was partially relieved by increasing concentrations of FabI (lane c to f). Inhibition of $C_4$-HSL synthesis by triclosan could not be relieved by increasing the RhlI concentration sevenfold (lane h).

To confirm the in vivo role of *fabI* in HSL synthesis, HSL levels were measured in culture fluids of wild-type PAO1 and *fabI* mutant PAO235. The *fabI* mutant produced only 50% of the 3-oxo-$C_{12}$-HSL and $C_4$-HSL levels of wild-type PAO1 (Fig. 7), paralleling the reduction of FabI enoyl-ACP reductase activity observed in this mutant (Fig. 3).

## DISCUSSION

**The *fabI* gene encodes an enoyl-ACP reductase.** We have cloned and characterized a gene from *P. aeruginosa*, encoding an enoyl-ACP reductase, by PCR amplification from genomic DNA and complementation of a defined *E. coli fabI*(Ts) mutant. Sequence analysis revealed that this gene may be transcriptionally linked to an upstream ORF encoding an ATP-binding protein of an ABC transporter of unknown function, and the presence of strong downstream Rho-independent transcriptional terminator indicated that it is probably the last gene in a transcriptional unit.

Although our experiments showed that *P. aeruginosa* contains several enoyl-ACP reductases, several lines of evidence strongly support the notion that the cloned gene is *fabI*. First, the deduced FabI sequence is 69% identical to FabI sequences from *E. coli* and *S. typhimurium* and contains the signature motif (D..[FILMV]..[IV]G..P...L]) for the FAD-dependent pyridine nucleotide reductase family. Second, this motif contains the amino acid residues forming the enzyme active site that when mutationally altered confer resistance to specific inhibitors of FabI enoyl-ACP reductase activity. This included $Gly^{95}$, which is equivalent to $Gly^{93}$ found in *E. coli* FabI. In *E.*

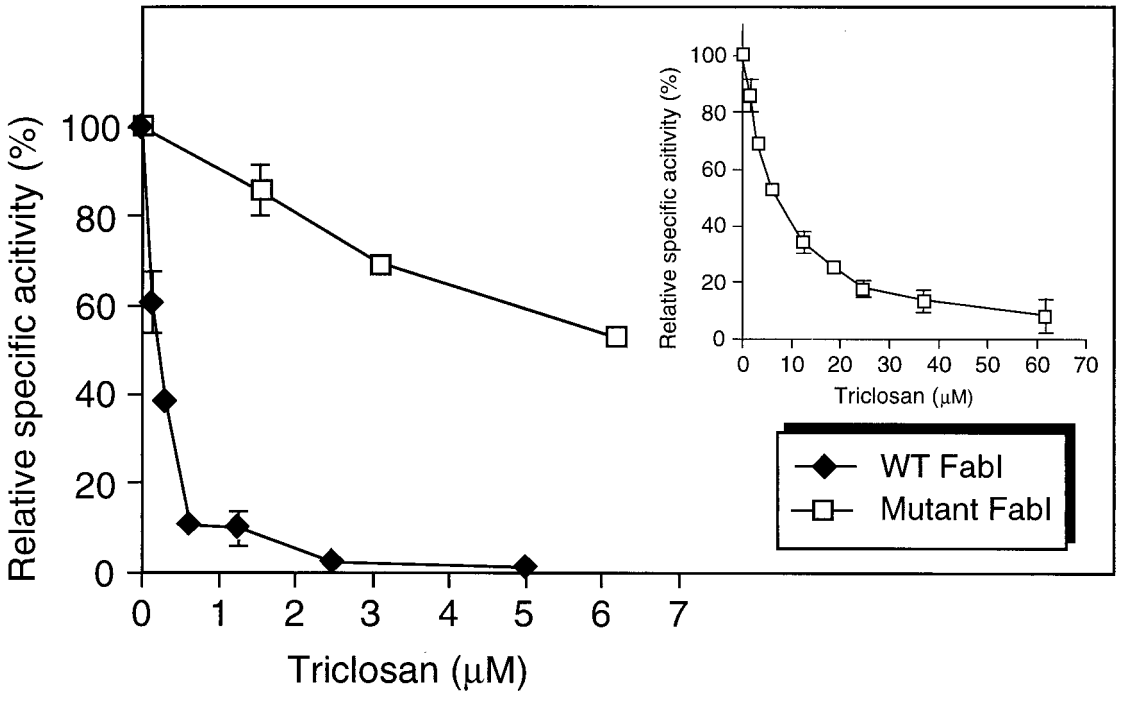


FIG. 5. Inhibition of FabI activity by triclosan. The reaction mixtures (500 μl) in phosphate buffer (pH 7.5) contained either 1 μg of purified wild-type (WT) FabI or 1 μg of mutant FabI protein, 0.1 mM NADH, 13 μM crotonyl-ACP, and increasing concentrations of triclosan. The insert shows the inhibition curve for the mutant FabI protein over a wider triclosan range; the first four values are identical to the ones plotted in the larger graph. Each value shown represents the mean plus standard deviation of three independent enzymatic reactions.

*coli*, $Gly^{93}$-to-Ser and $Gly^{93}$-to-Ala changes led to resistance to diazoborine (4) and triclosan (33), respectively. In *M. tuberculosis*, a $Ser^{94}$-to-Ala mutation, which leads to isoniazid resistance, lies in the same region of the mycobacterial FabI homolog, InhA (11).

In *E. coli*, *fabI* is an essential gene and *fabI* knockout mutants are not viable. Mutants containing single-amino-acid substitutions can be isolated, but they grow at reduced rates (33) or contain Ts alleles (4) that grow only at the permissive temperature. We were able to disrupt the chromosomal *fabI* gene and showed that the disrupted gene no longer complemented an *E. coli fabI*(Ts) allele. This was expected since the insertion at a *Sma*I site disrupted amino acid residues that form an integral part of the enzyme active site (18, 26). Since we could isolate a *fabI* insertion mutant and since this mutant was not altered in its growth rate, we concluded that unlike *E. coli*, *P. aeruginosa* must contain more than one enoyl-ACP reductase activity. This was corroborated by the presence of significant levels of NADH-dependent enoyl-ACP reductase activities in cell extracts of the *fabI* mutant PAO235 (Fig. 3). Since the activity found in the mutant amounted to 62% of the total activity found in the wild type, we concluded that FabI contributes a substantial part of the total enoyl-ACP reductase activity found in *P. aeruginosa*. This was corroborated by triclosan inhibition studies which indicated that ~23% of the total enoyl-ACP reductase activity in the wild type was inhibited by this drug, whereas the residual activity in PAO235 was

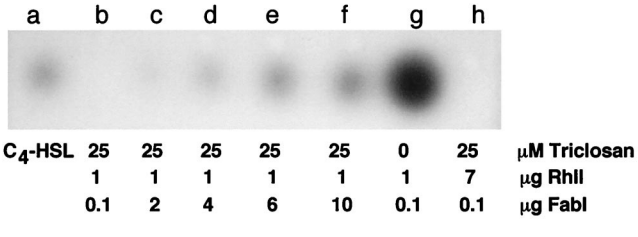


FIG. 6. In vitro synthesis of $C_4$-HSL and inhibition by triclosan. In vitro synthesis reaction mixtures containing the indicated components plus 20 μM crotonyl-ACP, 0.1 mM SAM, and 0.2 mM NADH were extracted with ethyl acetate, and portions of the concentrated residues were separated by TLC. $C_4$-HSL in the samples was detected by overlaying the TLC plate with the *C. violaceum* indicator strain CV026. Lane a contained 50 pmol of synthetic $C_4$-HSL.

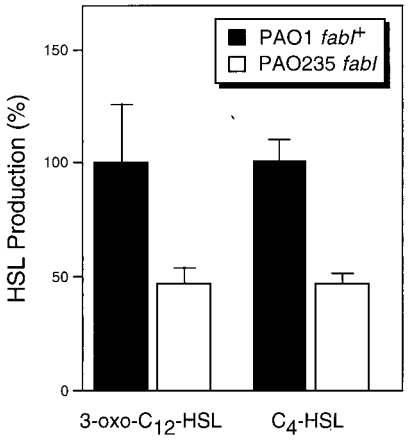


FIG. 7. HSL levels in wild-type and a *fabI P. aeruginosa* mutant. HSLs were extracted from overnight culture supernatants, and relative levels were determined by using *E. coli*-based $C_4$-HSL and 3-oxo-$C_{12}$-HSL bioassays. Values were determined in triplicate, and the values shown represent the means plus standard deviations.

triclosan insensitive. Searches of the *P. aeruginosa* genome database revealed at least 18 possible paralogs exhibiting on average 25% identity and 40% similarity to FabI, but none of them contained the signature motifs found in FabI proteins.

In cell extracts prepared at pH 6.5, *E. coli* FabI accepted both NADH and NADPH as cofactors, but when cell extracts were prepared at 7.5, only the NADH-dependent enoyl-ACP reductase activity remained (3). However, the NADPH-dependent FabI activity amounted to only 14 to 22% of the NADH-dependent enzyme. Although we isolated our cell extracts at pH 6.5, the NADPH-dependent FabI activity in wild-type or mutant cell extracts was very low, even at pH 6.5, and required three to six times more enzyme for detection (Fig. 3). Under these conditions, the NADPH-dependent activities were 3.5 or 10% of the NADH-dependent activities observed with wild-type and mutant extracts, respectively. We do not yet know what proportion, if any, of this activity is attributable to FabI, since our purified FabI protein does not exhibit NADPH-dependent enoyl-ACP reductase activity (see below).

To assess the substrate specificity of FabI, we expressed and purified FabI as an $H_6$-tagged protein. As its *E. coli* counterpart, the purified FabI protein could use both crotonyl-CoA and crotonyl-ACP as substrates, although it was much more active with crotonyl-ACP (Fig. 4B). The purified enzyme could not use NADPH as cofactor (data not shown). We do not yet know whether this reflects an intrinsic property of the *P. aeruginosa* FabI enzyme or whether the NADPH-dependent activity was lost during the purification steps that involve buffers with alkaline pH. We were unable to differentiate between these two possibilities since $H_6$ fusion proteins cannot be purified at pH 6.5.

**FabI is a triclosan target.** It has recently been shown that in *E. coli* triclosan targets lipid synthesis, and since triclosan-resistant mutants harbor mutations in *fabI*, it was concluded that the most likely target is enoyl-ACP reductase (33); this was subsequently confirmed in assays using purified FabI (19). To examine whether *P. aeruginosa* FabI is a triclosan target, we used the purified $H_6$-FabI in triclosan inhibition studies (Fig. 5). The purified protein was efficiently inhibited by very low concentrations of triclosan, showing 50% inhibition (50% inhibitory concentration [$IC_{50}$]) with 0.2 μM triclosan. McMurry et al. (33) and Heath et al. (18, 19) showed that their most triclosan-resistant mutants contained $Gly^{93}$-to-Val substitutions. To assess whether changing a glycine residue at the equivalent position 95 in *P. aeruginosa* FabI would lead to synthesis of a triclosan-resistant FabI enzyme, we introduced a $Gly^{95}$-to-Val change by site-directed mutagenesis and then expressed and purified the mutant $H_6$-FabI protein. Although the mutant protein exhibited a slightly increased enoyl-ACP reductase activity (Fig. 4B), it showed an $IC_{50}$ of 7 μM for triclosan and was not yet completely inhibited by the highest concentration (62 μM) tested in our experiments (Fig. 5, insert). While our studies neared completion, Heath et al. (18, 19) arrived at similar results after comparing the purified *E. coli* FabI with $Gly^{93}$-to-Ser and $Gly^{93}$-to-Val mutant enzymes; the triclosan $IC_{50}$s were 2 μM for FabI, 8 μM for the $Gly^{93}$-to-Ser mutant enzyme (19), and 10 μM for the $Gly^{93}$-to-Val mutant enzyme (18). Although both proteins were purified by using the same expression vector and same $NH_2$-terminal $H_6$ extension, *P. aeruginosa* FabI was ~10-fold more sensitive than the *E. coli* enzyme to triclosan. Although we do not know the reason(s) for this observation, the differences may be partially due to the different enoyl-ACP reductase assays used for the inhibition studies. We used the natural substrate crotonyl-ACP, whereas Heath et al. (18, 19) used the synthetic substrate *trans*-2-octadecenoyl-*N*-cysteamine, and the latter assay required substantially more FabI (12 μg, versus 1 μg in our assays). The recent determination of the X-ray structure of the *E. coli* FabI-$NAD^+$-triclosan complex confirmed that triclosan interacts with both the $NAD^+$ and the protein via hydrogen and hydrophobic bonds, forming a stable ternary complex (18, 26). Mutations in the FabI active site interfere with the formation of a stable FabI-$NAD^+$-triclosan ternary complex and thus confer resistance to the drug.

We have previously shown that *P. aeruginosa* PAO1 is resistant to triclosan due to efflux by the tripartite MexAB-OprM multidrug efflux system, but Δ(*mexAB-oprM*) mutants are susceptible to triclosan (41). The same efflux system seems also partially responsible for diazoborine resistance. Both wild-type PAO1 and *fabI* mutant PAO235 showed high levels of resistance to diazoborine (the MIC in both strains was >160 μg/ml), and the MIC for diazoborine was significantly lower (80 μg/ml) in the Δ(*mexAB-opM*) mutant PAO200.

**FabI participates in homoserine lactone synthesis.** According to the current model, butyryl-ACP serves as the most likely acyl donor in $C_4$-HSL synthesis. To confirm that FabI can indeed provide butyryl-ACP for $C_4$-HSL synthesis by RhlI, we set up an in vitro synthesis system containing purified FabI, RhlI, the cofactor NADH, and the substrates crotonyl-ACP and SAM. This reconstituted system allowed synthesis of biologically active $C_4$-HSL that comigrated with synthetic $C_4$-HSL (Fig. 6). Synthesis of $C_4$-HSL was efficiently inhibited by triclosan. This inhibition was relieved by increasing concentrations of FabI but not RhlI, indicating that FabI and not RhlI is the triclosan target. Corroborating evidence that FabI plays a central role in HSL synthesis in vivo was provided by the observation that a *fabI* mutant produced only 50% of the HSLs found in wild-type cells. This is the first documented evidence that an enzyme of the fatty acid biosynthetic pathway plays a crucial role in HSL synthesis, and the establishment of an in vitro HSL synthesis system will facilitate the search for novel antimicrobials aimed at interfering with the pathways involved in HSL biosynthesis. The design and development of new FabI inhibitors will form an integral part of such strategies.

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## REFERENCES

1. **Baldock, C., J. B. Rafferty, S. E. Sedelnikova, P. J. Baker, A. R. Stuitje, A. R. Slabas, T. R. Hawkes, and D. W. Rice.** 1996. A mechanism of drug action revealed by structural studies of enoyl reductase. Science **274:**2107–2110.
2. **Banerjee, A., E. Dubnau, A. Quemard, V. Balasubramanian, K. S. Um, T. Wilson, D. Collins, G. de Lisle, and W. R. Jacobs.** 1994. *inhA*, a gene encoding a target for isoniazid and ethionamide in *Mycobacterium tuberculosis*. Science **263:**227–230.
3. **Bergler, H., S. Fuchsbichler, G. Hoegenauer, and F. Turnowsky.** 1996. The enoyl-[acyl-carrier-protein] reductase (FabI) of *Escherichia coli*, which catalyzes a key regulatory step in fatty acid biosynthesis, accepts NADH and NADPH as cofactors and is inhibited by palmitoyl-CoA. Eur. J. Biochem. **242:**689–694.
4. **Bergler, H., G. Hoegenauer, and F. Turnowski.** 1992. Sequences of the *envM* gene and of two mutated alleles in *Escherichia coli*. J. Gen. Microbiol. **138:**2093–2100.
5. **Best, E., and V. C. Knauf.** 1993. Organization and nucleotide sequence of the

genes encoding the biotin carboxyl carrier protein and biotin carboxylase protein of *Pseudomonas aeruginosa* acetyl coenzyme A carboxylase. J. Bacteriol. **175:**6881–6889.
6. **Campos-Garcia, J., A. D. Caro, R. Najera, R. M. Miller-Maier, R. A. Al-Tahhan, and G. Soberon-Chavez.** 1998. The *Pseudomonas aeruginosa rhlG gene* encodes an NADPH-dependent β-ketoacyl reductase which is specifically involved in rhamnolipid synthesis. J. Bacteriol. **180:**4442–4451.
7. **Chen, H., H. Cheng, and M. Bjerkness.** 1993. One-step Coomassie Brilliant Blue R-250 staining of proteins in polycarylamide gel. Anal. Biochem. **212:** 295–296.
8. **Cronan, J. E., and A. L. Klages.** 1981. Chemical synthesis of acyl thioesters of acyl carrier protein with native structure. Proc. Natl. Acad. Sci. USA **78:**5440–5444.
9. **Cronan, J. E., and C. O. Rock.** 1996. Biosynthesis of membrane lipids, p. 612–636. *In* F. C. Neidhardt, R. Curtiss III, J. L. Ingraham, E. C. C. Lin, K. B. Low, B. Magasanik, W. S. Reznikoff, M. Riley, M. Schaechter, and H. E. Umbarger (ed.), *Escherichia coli* and *Salmonella*: cellular and molecular biology, 2nd ed. American Society for Microbiology, Washington, D.C.
10. **Davies, D. G., M. R. Parsek, J. P. Pearson, B. H. Iglewski, J. W. Costerton, and E. P. Greenberg.** 1998. The involvement of cell-to-cell signals in the development of a bacterial biofilm. Science **280:**295–298.
11. **Dessen, A., A. Quemard, J. S. Blanchard, W. R. Jacobs, and J. C. Sacchettini.** 1995. Crystal structure and function of the isoniazid target of *Mycobacterium tuberculosis*. Science **267:**1638–1641.
12. **Ellmann, G. L.** 1959. Tissue sulfhydryl groups. Anal. Biochem. **82:**70–77.
13. **Glessner, A., R. S. Smith, B. H. Iglewski, and J. B. Robinson.** 1999. Roles of *Pseudomonas aeruginosa las* and *rhl* quorum-sensing systems in control of twitching motility. J. Bacteriol. **181:**1623–1629.
14. **Greenberg, E. P.** 1997. Quorum sensing in Gram-negative bacteria. ASM News **63:**371–377.
15. **Heath, R. J., and C. O. Rock.** 1995. Enoyl-acyl carrier protein reductase (*fabI*) plays a determinant role in completing cycles of fatty acid elongation in *Escherichia coli*. J. Biol. Chem. **270:**26538–26542.
16. **Heath, R. J., and C. O. Rock.** 1996. Regulation of fatty acid elongation and initiation by acyl-acyl carrier protein in *Escherichia coli*. J. Biol. Chem. **271:**1833–1836.
17. **Heath, R. J., and C. O. Rock.** 1996. Roles of the FabA and FabZ β-hydroxyacyl-acyl carrier protein dehydratase in *Escherichia coli* fatty acid biosynthesis. J. Biol. Chem. **271:**27795–27801.
18. **Heath, R. J., J. R. Rubin, D. R. Holland, E. Zhang, M. E. Snow, and C. O. Rock.** 1999. Mechanism of triclosan inhibition of bacterial fatty acid synthesis. J. Biol. Chem. **274:**11110–11114.
19. **Heath, R. J., Y.-T. Yu, M. A. Shapiro, E. Olson, and C. O. Rock.** 1998. Broad spectrum antimicrobial biocides target the FabI component of fatty acid biosynthesis. J. Biol. Chem. **273:**30316–30320.
20. **Henry, M. F., and J. E. Cronan.** 1992. A new mechanism of transcriptional regulation: release of an activator triggered by small molecule binding. Cell **70:**671–679.
21. **Hoang, T. T., R. R. Karkhoff-Schweizer, A. J. Kutchma, and H. P. Schweizer.** 1998. A broad-host-range Flp-*FRT* recombination system for site-specific excision of chromosomally-located DNA sequences: application for isolation of unmarked *Pseudomonas aeruginosa* mutants. Gene **212:**77–86.
22. **Hoang, T. T., and H. P. Schweizer.** 1997. Fatty acid biosynthesis in *Pseudomonas aeruginosa*: cloning and characterization of the *fabAB* operon encoding β-hydroxyacyl-acyl carrier protein dehydratase (*fabA*) and β-ketoacyl-acyl carrier protein synthase I (*fabB*). J. Bacteriol. **179:**5326–5332.
23. **Kater, M. M., G. M. Konigstein, H. J. J. Nijkamp, and A. R. Stuitje.** 1994. The use of a hybrid genetic system to study the functional relationship between prokaryotic and plant multi-enzyme fatty acid synthase complexes. Plant Mol. Biol. **25:**771–790.
24. **Kutchma, A. J.** 1997. Characterization of a gene cluster containing the *Pseudomonas aeruginosa fabD*, *fabG*, *acpP* and *fabF* genes involved in fatty acid biosynthesis. M.S. thesis. Colorado State University, Fort Collins, Colo.
25. **Kutchma, A. J., T. T. Hoang, and H. P. Schweizer.** 1999. Characterization of a *Pseudomonas aeruginosa* fatty acid biosynthetic gene cluster: purification of acyl carrier protein (ACP) and malonyl-coenzyme A:ACP transacylase (FabD). J. Bacteriol. **181:**5498–5504.
26. **Levy, C. W., A. Roujeinikova, S. Sedelnikova, P. J. Baker, A. R. Stuitje, A. R. Slabas, D. W. Rice, and J. B. Rafferty.** 1999. Molecular basis of triclosan activity. Nature **398:**383–384.
27. **Liss, L.** 1987. New M13 host: DH5αF′ competent cells. Focus **9:**13.
28. **Magnuson, K., S. Jackowski, C. O. Rock, and J. E. Cronan.** 1993. Regulation of fatty acid biosynthesis in *Escherichia coli*. Microbiol. Rev. **57:**522–542.
29. **Makowski, G. S., and M. L. Ramsby.** 1993. pH modification to enhance the molecular sieving properties of sodium dodecyl sulfate-10% polyacrylamide gel. Anal. Biochem. **212:**283–285.
30. **McClean, K. H., M. K. Winson, L. Fish, A. Taylor, S. R. Chhabra, M. Camara, M. Daykin, J. H. Lamb, S. Swift, B. W. Bycroft, G. S. A. B. Stewart, and P. Williams.** 1998. Quorum sensing and *Chromobacterium violaceum*: exploitation of violacein production for the detection of *N*-acylhomoserine lactones. Microbiology **143:**3703–3711.
31. **McLean, R. J. C., M. Whiteley, D. J. Stickler, and W. C. Fuqua.** 1997. Evidence of autoinducer activity in naturally occurring biofilms. FEMS Microbiol. Lett. **154:**259–263.
32. **McMurry, L. M., P. F. McDermott, and S. B. Levy.** 1999. Genetic evidence that InhA of *Mycobacterium smegmatis* is a target for triclosan. Antimicrob. Agents Chemother. **43:**711–713.
33. **McMurry, L. M., M. Oethinger, and S. B. Levy.** 1998. Triclosan targets lipid synthesis. Nature **394:**531–532.
34. **Miller, J. H.** 1992. A short course in bacterial genetics. Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y.
35. **Moré, M. I., D. Finger, J. L. Stryker, C. Fuqua, A. Eberhard, and S. C. Winans.** 1996. Enzymatic synthesis of a quorum-sensing autoinducer through use of defined substrates. Science **272:**1655–1658.
36. **Parsek, M. R., A. L. Schaefer, and E. P. Greenberg.** 1997. Analysis of random and site-directed mutations in *rhlI*, a *Pseudomonas aeruginosa* gene encoding an acylhomoserine lactone synthase. Mol. Microbiol. **26:**301–310.
37. **Raetz, C. H. R.** 1996. Bacterial lipopolysaccharides: a remarkable family of bioactive macroamphiphiles, p. 1035–1063. *In* F. C. Neidhardt, R. Curtiss III, J. L. Ingraham, E. C. C. Lin, K. B. Low, B. Magasanik, W. S. Reznikoff, M. Riley, M. Schaechter, and H. E. Umbarger (ed.), *Escherichia coli* and *Salmonella*: cellular and molecular biology, 2nd ed. American Society for Microbiology, Washington, D.C.
38. **Rosenberg, M. C., and D. Court.** 1979. Regulatory sequences involved in the promotion and termination of RNA transcription. Annu. Rev. Genet. **13:** 319–353.
39. **Schaefer, A. L., D. L. Val, B. L. Hanzelka, J. E. Cronan, and E. P. Greenberg.** 1996. Generation of cell-to-cell signals in quorum sensing: acyl homoserine lactone synthase activity of a purified *Vibrio fischeri* LuxI protein. Proc. Natl. Acad. Sci. USA **93:**9505–9509.
40. **Schweizer, H. P.** 1991. The *agmR* gene, an environmentally responsive gene, complements defective *glpR*, which encodes the putative activator for glycerol metabolism in *Pseudomonas aeruginosa*. J. Bacteriol. **173:**6798–6806.
41. **Schweizer, H. P.** 1998. Intrinsic resistance to inhibitors of fatty acid biosynthesis in *Pseudomonas aeruginosa* is due to efflux: application of a novel technique for generation of unmarked chromosomal mutations for the study of efflux systems. Antimicrob. Agents Chemother. **42:**394–398.
42. **Schweizer, H. P., T. R. Klassen, and T. Hoang.** 1996. Improved methods for gene analysis and expression in *Pseudomonas*, p. 229–237. *In* T. Nakazawa, K. Furukawa, D. Haas, and S. Silver (ed.), Molecular biology of pseudomonads. American Society for Microbiology, Washington, D.C.
43. **Studier, F. W., A. H. Rosenberg, J. J. Dunn, and J. W. Dubendorff.** 1990. Use of T7 RNA polymerase to direct expression of cloned genes. Methods Enzymol. **185:**60–89.
44. **Turnowsky, F., K. Fuchs, C. Jeschek, and G. Hoegenauer.** 1989. *envM* genes of *Salmonella typhimurium* and *Escherichia coli*. J. Bacteriol. **171:**6555–6565.
45. **Val, D. L., and J. E. Cronan.** 1998. In vivo evidence that *S*-adenosylmethionine and fatty acid intermediates are the substrates for the LuxI family of autoinducer synthases. J. Bacteriol. **180:**2644–2651.
46. **Van Delden, C., and B. H. Iglewski.** 1998. Cell-to-cell signaling and *Pseudomonas aeruginosa* infections. Emerg. Infect. Dis. **4:**551–560.
47. **Wang, R. F., and S. R. Kushner.** 1991. Construction of versatile low-copy-number vectors for cloning, sequencing and gene expression in *Escherichia coli*. Gene **100:**195–199.
48. **Weeks, G., and S. J. Wakil.** 1968. Studies on the mechanisms of fatty acid synthesis. J. Biol. Chem. **243:**1180–1189.