Pseudomonas aeruginosa LptE is not directly involved in lipopolysaccharide transport but is crucial for LptD assembly, cell envelope integrity, antibiotic resistance and infectivity

Alessandra Lo Sciuto^{a*}, Alessandra M. Martorana^{b*}, Regina Fernández-Piñar^a, Carmine Mancone^c,

Alessandra Polissi^b, and Francesco Imperi^a#

Strain or plasmid	Genotype and/or relevant characteristics	Reference or source
P. aeruginosa		
PAO1 (ATCC15692)	Prototroph	American type culture collection
lptE	lptE conditional mutant of PAO1, deleted of the $lptE$ coding sequence and carrying <i>a</i> n arabinose-dependent copy of $lptE$	This work
lptH	<i>lptH</i> conditional mutant of PAO1, deleted of the <i>lptH coding</i> sequence and carrying an arabinose-dependent copy of <i>lptH</i>	Fernandez-Pinar et al., 2015
PAO1 lptD-6his	PAO1 carrying a 6his-tag sequence fused in frame to the 3' end of the <i>lptD</i> gene	This work
lptE lptD-6his	lptE conditional mutant carrying a 6his-tag sequence fused in frame to the 3' end of the $lptD$ gene	This work
E. coli		
S17.1λ <i>pir</i>	thi pro hsdRhsdM ⁺ recA RP4-2-Tc::Mu-Km::Tn7 λpir, Sm ^R	Simon et al., 1983
Plasmid		
pBluescript II KS+ (pBS)	Cloning vector; ColE1 replicon; Ap ^R	Stratagene
pDM4	Suicide vector; <i>sacB^R</i> , <i>oriR6K</i> ; Cm ^R	Milton et al., 1994
$pDM4\Delta lptE$	pDM4 derivative for <i>lptE</i> in-frame deletion	This work
mini-CTX1-araCP _{BAD} tolB	mini-CTX1 derivative carrying the $araCP_{BAD}tolB$, Tc ^R	Lo Sciuto et al., 2014
mini-CTX1-araCP _{BAD} lptE	$\begin{tabular}{lllllllllllllllllllllllllllllllllll$	
pME6032	IPTG inducible expression vector, Tc ^R	Heeb et al., 2002
pME <i>lptE</i>	pME6032-derivative carrying an IPTG-inducible copy of <i>lptE</i>	This work
pDM4 <i>lptD-6his</i>	pDM4 derivative for replacement of <i>lptD</i> with <i>lptD-6his</i> , encoding an LptD protein with a 6-His tag at the C-terminus	This work

Table S1. Bacterial strains and plasmids used in this study

References

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- Lo Sciuto A, Fernández-Piñar R, Bertuccini L, et al. The periplasmic protein TolB as a potential drug target in *Pseudomonas aeruginosa*. PLoS One. 2014;9:e103784.
- Milton DL, O'Toole R, Horstedt P, Wolf-Watz H. Flagellin A is essential for the virulence of *Vibrio anguillarum*. J Bacteriol. 1996;178:1310-1319.
- Simon R, Priefer U, Pühler A. A broad host range mobilization system for *in vivo* genetic engineering: transposon mutagenesis in Gram negative bacteria. Bio/Technology. 1983;1:784-790.

Primer name	Sequence (5'→3') ^b	Restriction	Application
		site	
<i>lptE_</i> FW	GGAGTGAGGG <u>AAGCTT</u> GATG	HindIII	Generation of mini-CTX1-
			$araCP_{BAD}lptE$
<i>lptE_</i> RV	cggaattcTCACGGGGTGGGGAACTC	EcoRI	Generation of mini-CTX1-
			$araCP_{BAD}lptE$
<i>lptE</i> mut_UP_FW	ccg <u>ctcgAG</u> GCCAGCCAGGATGTCG	XhoI	Generation of pDM4 $\Delta lptE$
<i>lptE</i> mut_UP_RV	cgggatcCGGCGCTGGTCAGGATAC	BamHI	Generation of pDM4 $\Delta lptE$
<i>lptE</i> mut_DOWN_FW	cgggatccTGAAGGTCACCAGCAACGC	BamHI	Generation of pDM4 $\Delta lptE$
<i>lptE</i> mut_DOWN_RV	gc <u>tctaga</u> TCACGGGGTGGGGAACTC	XbaI	Generation of pDM4 $\Delta lptE$
<i>lptE_</i> pME6032_FW	cg <u>gaattC</u> CGGGGGGCGCTGATCAAC	EcoRI	Generation of pME <i>lptE</i>
<i>lptE_</i> pME6032_RV	ccg <u>ctcgag</u> TCACGGGGGGGGGAACTC	XhoI	Generation of pME <i>lptE</i>
<i>lptD-6his_</i> UP_FW	gc <u>tctaGA</u> CTGGCGCATCAACTCCG	XbaI	Generation of pDM4lptD-6his
<i>lptD-6his_</i> UP_RV	cggaattcaatggtgatggtgatggtgCATAGCTTG	EcoRI	Generation of pDM4lptD-6his
	ATCTTCACGTTG		
<i>lptD-6his_</i> DOWN_FW	cggaattCAAGACGGAAATGTTCCTCG	EcoRI	Generation of pDM4lptD-6his
<i>lptD-6his_</i> DOWN_RV	ccg <u>ctcgAG</u> TTCTTCACCTCCTGCTCG	XhoI	Generation of pDM4lptD-6his
6his_check_FW	CACCATCACCATCACCATTGA		PCR screening of <i>lptD-6his</i>
			recombinant strains
M13FW	GTTTTCCCAGTCACGAC		Sequencing from pBS
M13RV	CAGGAAACAGCTATGAC		Sequencing from pBS
P _{BAD} FW	CATAAGATTAGCGGATCCTAC		Sequencing from mini-CTX1-
			araCP _{PAP} constructs

^a Preparative PCRs for cloning were performed using the genomic DNA of *P. aeruginosa* PAO1 as the template. ^b The restriction site used for cloning is underlined in the primer sequence.

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Figure S1. Genomic region encompassing the 3' end of *lptD* and the 5' end of *surA* in (A) the wild type strain *P. aeruginosa* PAO1 (www.pseudomonas.com), and (B) the recombinant strains PAO1 *lptD-6his* and *lptE lptD-6his* (Table S1). The DNA region in panel B was verified by DNA sequencing for both PAO1 *lptD-6his* and *lptE lptD-6his*. The stop codon of *lptD* and the start codon of *surA* are highlighted in red and green, respectively. The annealing region of primers used for pDM4*lptD-6his* construction are highlighted in grey in panel A (from top to bottom: *lptD6his_UP_FW, lptD6his_DOWN_FW, lptD6his_UP_RV, lptD6his_DOWN_RV*; Table S2). The 6His-tag encoding sequence and the DNA region duplicated in the PAO1 *lptD-6his* and *lptE lptD-6his* and *lptE lptD-6his*.



Figure S2. Growth of *P. aeruginosa* PAO1 and the *lptE* conditional mutant in 96-well microtiter plates in MH broth supplemented with increasing concentrations of arabinose (ARA, 0-0.5%) at 37° C and vigorous shaking (200 rpm). Results are the mean (± SD) of three independent experiments performed in triplicate.



Figure S3. Intracellular levels of LptE and LptC in PAO1 and *lptE* cells grown for 14 h in MH supplemented or not with ARA, determined by western blot analysis of whole cell lysates (20 μ g of proteins) with antibodies against LptE or LptC, as indicated on the right of each blot. Filters were developed with ECL chemiluminescent reagents and visualized in a ChemiDoc XRS+ system.



Figure S4. Colony growth of *P. aeruginosa* PAO1, the *lptE* conditional mutant and the *lptH* conditional mutant (used as control) on LB (panel A) or M9 minimal medium supplemented with 20 mM succinate and 50 μ M FeCl₃ (panel B), in the presence or in the absence of 0.5% arabinose (ARA). Exponential phase cultures in LB or M9 with 0.5% ARA were normalized to OD₆₀₀ = 1 in saline, and 5 μ l of the 10⁻²-10⁻⁶ dilutions were spotted onto the plates and incubated for 20 h at 37°C. The images are representative of two independent experiments giving similar results.



Figure S5. Colony growth of the *P. aeruginosa lptE* conditional mutant cultured for up to 5 subsequent passages on MH agar plates. At each passage, several colonies from MH agar without arabinose (ARA) were resuspended in saline, normalized to $OD_{600} = 1$ in saline, and 5 µl of the 10^{-3} - 10^{-6} dilutions were spotted onto MH agar with or without 0.5% ARA. Pictures were taken after 20 h incubation at 37°C. The images are representative of two independent experiments giving comparable results.



Figure S6. Growth of the *lptH* conditional mutant at 37°C in MH at 200 rpm in flasks after two successive subcultures in the presence (filled symbols) or in the absence (open symbols) of 0.5% arabinose (ARA), in order to obtain cells depleted of LptH. Briefly, bacteria were cultured for 14 h in MH supplemented with 0.5% ARA (not shown in the figure) and then diluted 1:100 in fresh medium with or without ARA (time 0). After 3 h of growth, cultures were diluted again 1:10 in fresh medium and incubated at 37 °C. The graph is representative of several assays giving similar results.



Figure S7. Phase contrast and fluorescence microscopy images of *P. aeruginosa lptH* and *lptE* conditional mutant cells grown in the presence of 0.5% arabinose and stained with the membranebinding dye FMTM 5-95. Images are representative of several fields (≥ 10) showing comparable results. Scale bar: 3 µm.



Figure S8. Intracellular LptE levels in PAO1 pME6032, *lptE* pME6032 and *lptE* pME*lptE* cells grown for 14 h in MH supplemented or not with 0.5% ARA and 1 mM IPTG, determined by Western blot analysis of whole cell lysates (20 µg of proteins) using the anti-LptE antibody. The image is representative of three assays giving comparable results. Quantification of LptE levels is reported below each lane, expressed as percentage (mean±SD) of the amount present in the wild type carrying the empty plasmid.



Figure S9. Chemical structure and predicted molecular weight (MW) of the main lipid A forms identified in *P. aeruginosa* PAO1 and/or in the *lptE* conditional mutant. 3-OH-C10 and C16 (palmitoyl) acyl chains are shown in red and blue, respectively. The molecule highlighted in grey has not been observed in our MS spectra (Fig. 5), but represents the unmodified lipid A precursor synthesized by *P. aeruginosa* (King *et al.*, 2009). The enzymes responsible for lipid A modifications are shown, together with their subcellular localization (IM, inner membrane; OM, outer membrane). Chemical structures were drawn with the ACD/ChemSketch software, which also calculated their MW. The hydroxyl groups predicted to be attached by LpxO1 and/or LpxO2 are highlighted in yellow.