Supplementary Information to

Pushing the envelope: LPS modifications and their consequences

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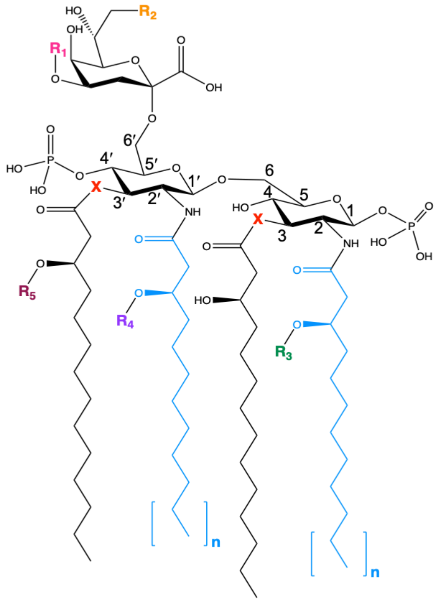
Supplementary Information S1. Variations to Kdo-lipid A introduced during the Raetz pathway. Tabular summary (left) and structural depiction (right) of sites that have variations between organisms or under different growth conditions within an organism.

Site of variation	Group in *E. coli* under standard lab conditions (enzyme)	Alternate group (enzyme, organism)		
X	-O- (GlcNAc synthesis)	-NH- (GnnA/B, *Campylobacter*/*Leigonella*/etc.)		
R1	Kdo	PO$_4$ (KdkA, *Vibrio*/*Haemophilus*/etc.)		
R2	-OH (Kdo synthesis)	NH$_2$ (KdnA/B, *Shewanella*)		
2 and 2′ primary acyl	3-OH, C14:0 (LpxD)	3-OH, C18:0 (LpxD1, *Francisella*)	3-OH, C16:0 (LpxD2, *Francisella*)	
	3-OH, C14:0 (LpxD)	3-OH, C16:0 (LpxD1, *Leptospira*)	3-OH, C12:0 (LpxD2, *Leptospira*)	
R3	-H (unmodified)	C12:0 (LpxM, *Acinetobacter*) (LpxL1, *Neisseria*)	2-OH, C12:0 (LpxL1, *Pseudomonas*)	
R4	C12:0 (LpxL, 37°C)	C16:1 (LpxP, *Salmonella*/*E.coli*/etc low temp)		
		C12:1 (LpxL1, *Klebsiella*)	C14:0 (LpxL2, *Klebsiella*)	
R5	C14:0 (LpxM)	-H (unmodified, *Francisella*/etc.)	C12:0 or C14:0 (LpxJ, *Helicobacter*/etc.)	3-OH, C12:0 (LpxN, *Vibrio*)



Supplementary Information S2. Enzymes that modify the Kdo-lipid A domain of LPS

Enzyme[a]	Protein localization	Active site topology	Pathogenic organisms[b]	Activity	Published structures (PDB ID)	Contributors to regulation	Effect of modification	References
AlmG	Inner membrane	Cytoplasmic	*Vibrio*	Glycine transfer to hydroxyl group of 3′ acyloxyacyl chain		VprAB (CarRS)	AMP resistance	1-3
ArnT (PmrK)	Inner membrane	Periplasmic	*Bordetella bronchiseptica*, *Burkholderia*, *Klebsiella*, *E. coli*, *P. mirabilis*, *Pseudomonas*, *Salmonella*, *Shigella*, *Yersinia*	Aminoarabinose addition, Glucosamine addition (Bordetella)	5EZM, 5F15	PmrAB, ParRS, CprRS	AMP resistance	4-9
EptA (PmrC, Mcr)	Inner membrane	Periplasmic	*Acinetobacter*, *Capnocytophaga*, *Cronobacter*, *E. coli*, *Haemophilus*, *Helicobacter*, *Klebsiella*, *Neisseria*, *Pseudomonas*, *Salmonella*, *Shigella*, *Vibrio*	Phosphoethanolamine addition	4KAV, 4KAY, 5FGN,	PmrAB, ColRS	AMP resistance	7,10-16
EptB	Inner membrane	Periplasmic	*E. coli*, *Salmonella*, *Yersinia*	Phosphoethanolamine transfer to Kdo		PhoPQ, sRNA MgrR	Modest AMP resistance	7,17
EptC	Inner membrane	Periplasmic	*Campylobacter*	Phosphoethanolamine transfer to lipid A, flagellar rod, and other substituents	4TN0	Present under normal laboratory conditions	TLR4 evasion, AMP resistance, motility	18,19
FlmF1	Inner membrane	Periplasmic	*Francisella*	Glucose, mannose addition to lipid A		Present under normal laboratory conditions	Possible role in AMP resistance	20
FlmF2	Inner membrane	Periplasmic	*Francisella*	Galactosamine addition to lipid A		Present under normal laboratory conditions	Possible role in AMP resistance	20,21
FlmK	Inner membrane	Periplasmic	*Francisella*	Glucose, mannose or galactosamine addition to lipid A		Present under normal laboratory conditions	Possible role in AMP resistance, TLR4 evasion	21
KdkA	Inner membrane	Cytoplasmic	*Actinobacillus*, *Bordetella*, *Haemophilus*, *Pasteurella*, *Shewanella*, *Vibrio*	Phosphorylation of Kdo		Present under normal laboratory conditions	Possible effect on toxin delivery	7,22
KdhA, KdhB (KdoH1, KdoH2)	Inner membrane	Cytoplasmic	*Francisella*, *Helicobacter*, *Legionella*	Removal of outer Kdo		Present under normal laboratory conditions	AMP Resistance	23-25
KdoO	Inner membrane	Cytoplasmic	*Burkholderia*, *Yersinia*	Hydroxylation of Kdo	5YKA, 5YVZ, 6A2E, FYW0	Present under normal laboratory conditions	Unknown	26

LmtA	Inner membrane	Cytoplasmic	*Leptospira interrogans*	Methylation of lipid A		Present under normal laboratory conditions	Unknown	27
LpxE	Inner membrane	Periplasmic	*Capnocytophaga*, *Francisella*, *Helicobacter*, *Porphyromonas*	1-phosphatase		Present under normal laboratory conditions	AMP resistance, TLR4 evasion	7,14
LpxF	Inner membrane	Periplasmic	*Capnocytophaga*, *Francisella*, *Helicobacter*, *Porphyromonas*	4'-phosphatase		Present under normal laboratory conditions	AMP resistance, TLR4 evasion	7,14
LpxO	Inner membrane	Cytoplasmic	*Bordetella*, *Klebsiella*, *Legionella*, *Pseudomonas*, *Salmonella*	Hydroxylation of lipid A acyl chains		Fnr and ArcA (oxygen sensing)	Stress response coordination	7,28
LpxR	Outer membrane	Extracellular	*E. coli 0157:H7*, *Helicobacter*, *Salmonella*, *Vibrio*, *Yersinia*	3'-*O*-deacylase	3FID	sRNA MicF, Lrp in *E. coli 0157:H7*, aminoarabinose lipid A modification	TLR4 evasion	7,29,30
LpxT	Inner membrane	Periplasmic	*E. coli*, *Pseudomonas*, *Salmonella*, *Yersinia*	Phosphorylation of lipid A, recycling of undecaprenyl pyrophosphate		PmrAB, small peptide PmrR	Unknown	7,13,31
PagL	Outer membrane	Extracellular	*Bordetella*, *Burkholderia*, *Pseudomonas*, *Salmonella*	3-*O*-deacylase	2ERV	PhoPQ, aminoarabinose lipid A modification	Lowered TLR4 activation	5,7
PagP	Outer membrane	Extracellular	*Bordetella*, *Erwinia*, *E.coli*, *Klebsiella*, *Legionella*, *Pseudomonas*, *Salmonella*, *Shigella*, *Yersinia*	Palmitate addition	1MM4, 1MM5, 1THQ, 3GP6	PhoPQ, membrane perturbation, RcsB (osmotic stress)	Selective AMP resistance, membrane integrity	7,32-35

[a] Alternative enzyme names in certain species are given in parentheses.

[b] Organisms containing homologs of these enzymes were excluded from the table if the respective modification has not been observed. This table is likely to expand as the lipid A-core is further characterized from a variety of species.

Supplementary Information S3. Regulatory mechanisms that affect LPS modifications

Two component systems

Response regulator/ Sensor kinase	Stimuli	Modification enzymes regulated	Organisms	References
PhoP/Q	low Mg^{2+}/Ca^{2+}, AMPs, acidic pH, osmotic shock	Direct: PagL, PagP Indirect: increased MgrR (see below) Indirect: increased PmrD which binds PO_4-PmrA	widespread	36-43
PmrA/B (BasR/S)	Fe^{3+}, Al^{3+}, acidic pH, vanadate	ArnT, EptA, LpxT	widespread	44-47
ArcA/B	Ubiquinone/Menaquinone redox states	LpxO	*Salmonella*	28
ParR/S	AMPs	ArnT	*Pseudomonas*	48
CprR/S	AMPs	ArnT	*Pseudomonas*	49
ColR/S	Zn^{2+}	EptA	*Pseudomonas*	13
CrrA/B	Unknown	Indirect: increased CrrC that regulates PmrAB	*Klebsiella*	50,51
VprA/B (CarR/S)	AMPs, bile, acidic pH	AlmG	*Vibrio*	1,3

Other transcriptional regulators

Regulator	Stimuli	Modification enzymes regulated	Organisms	References
Fnr	O_2	LpxO	*Salmonella*	28
Lrp	Butyrate	LpxR	EHEC	29
RcsB	Osmotic stress, independent of RcsC	PagP	*E. coli*	35

Small RNA regulators

Small RNA	Regulation of small RNA	Modification genes / mechanism of regulation	Organisms	References
MicA	Up regulated by σ^E	*phoP* / inhibit translation	widespread	52
MicF	Down regulated by Lrp stability by StpA and HU	*lpxR* / inhibit translation and decrease mRNA stability	widespread	53
MgrR	Up regulated by PhoP	*eptB* / inhibit transcription	widespread	39

Post-translational regulation

Post-translational effector	Mechanism of regulation	Modification enzyme regulated	Organisms	References
MgrB	Feed back, deactivation of PhoQ	Indirect: PagL, PagP, EptA, ArnT	widespread	54
PmrR (small peptide)	Inhibition of enzyme	LpxT	widespread	45
Disruption of OM asymmetry	Activation of enzyme	PagP	widespread	55
Aminoarabinose-lipid A	Prevents substrate recognition	PagL, LpxR	*Salmonella, Yersinia*	56,57

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