

Supplementary Legends

Supplementary Table 1. Primers used in this study.

Supplementary Figure Legends

Supplementary Figure 1. NaxD is conserved in numerous Gram-negative bacterial pathogens. (A) Protein BLAST analysis was used to determine the % identity and % similarity of NaxD homologs in the indicated species. (B) Amino acids surrounding YdjC superfamily putative active site residues are shown and numbers indicate their position in the sequence.

Conserved residues (*)

Supplementary Figure 2. Alignment of the 17 bp putative PmrA binding site in the promoter of *A. baumannii naxD*, with promoter regions of *A. baumannii pmrCAB*, *S. typhimurium pmrF* and *pmrCAB*. Consensus sequence of PmrA binding site are marked in bold and underlined. Y=C/T; K=G/T

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Primer Name	Sequence
qRT-PCR	
qRT 2623 F2	accgatcaatacccttcatt
qRT 2623 R2	gttgcgcataattggtcagt
16S rRNA 1	cagctcggtcgtagatgt
16S rRNA 2	cgttaaggccatgtgactt
<i>naxD</i> deletion	
A1S2623 f1	aatacttattggctactgcc
A1S2623 a1K R	ccggccatctccagcagccatctaaattccaccatagg
A1S2623 a1K F	ccctatggtaatttagatcggctgctggagatggcgg
A1S2623 Ka2 R	tggaaacaacgcaggataaaattagaaaaactcatcgagca
A1S2623 Ka2 F	tgctcgatgagtttctaatttatcctgcgttgttcca
A1S2623 r1	atagatgtcagaacaattgc
<i>naxD</i> complement	
pWH1266 2623comp F2	cgaccacacccgtcctgtggatccacttattataggctaataaagt
pWH1266 2623comp R2	gaaggctctcaagggcattggactcattgcattgccctagtctgg

A

Organism	% Identity	% Similarity
<i>Acinetobacter baumannii</i>	100	100
<i>Francisella tularensis</i>	50	32
<i>Legionella pneumophila</i>	37	53
<i>Brucella abortus</i>	36	48
<i>Coxiella burnetii</i>	34	52

B

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<i>A. baumannii</i>	4	VCYCADDFA	12	58	I	G	L	H	L	N
<i>F. tularensis</i>	5	IIICADDFG	13	60	V	G	I	H	L	N
<i>L. pneumophila</i>	7	IFLCADDFG	15	61	T	G	L	H	N	L
<i>B. abortus</i>	1	MMRIADDFG	9	56	V	G	L	H	N	T
<i>C. burnetii</i>	4	ITLCADDYG	12	58	I	G	L	H	F	N

PmrA consensus binding site
naxDA *A. baumannii*
pmrCAB *A. baumannii*
pmrFS *S. typhimurium*
pmrCAB *S. typhimurium*

Y T T A A K	N N N N N	Y T T A A K
C T T A A G	A A A A C	T T T A A G
T T T A A G	T C A T T	T T T A A G
C T T A A T	G T T A A	T T T A A T
C T T A A G	G T T C A	C T T A A T