

Supplementary Material

Surface-related features and virulence among *Acinetobacter baumannii* clinical isolates belonging to international clone I and II

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Supplementary Table S2. Oligonucleotides, plasmids and strains used in this study.

Primers	Sequence (5' to 3')	Product size (bp)	Purpose	Source
Eps1	CATTAATAAGCGCAATATTGAC			
Eps2	GTTATATAAAGCGCTTGAGAAACCCTTGTGTATTATCT	1024	wza upstream region amplification	This study
Eps3	TCTCAAGCGCTTATATAAC			
Eps4	GTCGAGGCATTCTGTCCTAGAACGACACCTTGCTGTC	684	wza downstream region amplification	This study
Fjgms	AGGACAGAAATGCCTCGAC			
Rjgms	ATCTCGGCTGAACGAATT	854	aac(3)-I amplification	This study
EpgR	TGTATTCAGTTTATATTCACTAC		Conformation for wza deletion	This study
P-Ab-ITSF	CATTATCACGGTAATTAGTG			
P-Ab-ITSB	AGAGCACTGTGCACTTAAG	208	A. baumannii species detection	Chiang <i>et al.</i> , 2011

gnaaF	CNTAYTAYYTACNCATAAAGC		K locus amplification and sequencing	
galuR	GTCAACNACBGTDACCATTTC	various		This study
wzy11F	AACGTTGGACTATAGCAACAAAT			
wzy11R	CCTGTTGATGGGTGGTCT	841	<i>wzy11</i> detection/ KL2 identification	This study
KL27F	GGAGACTGGCTGCAACCTTAT			
KL27R	AGAGCTGTGCACCCAAACAG	333	KL27 identification	This study
KL6F	CCACTTGGGGAGTGTGATT			
KL6R	AACTTTCCGCCCAACTTA	236	KL6 identification	This study
KL1F	ACGAAAACAACAGTTATGGCGA			
KL1R	ATGGGGGAGGTGTTACAGGT	193	KL1 identification	This study
KL40F	GGAAGTTAACGTACTCTGCATTAT			
KL40R	ACACACCTGTAAGCTTGCCT	648	KL40 identification	This study
KL4F	AACGCGGCAAACTTACTGGA			
KL4R	CGCCGATAAACCCACCTAAG	654	KL4 identification	This study
KL20F	GAACGCGGCAAACTTACAGG			
KL20R	CAGGAGAGGGACCTGCAATC	934	KL20 identification	This study
RH1704	CCCTACAAGGTCTTGCCAAT			
RH1705	CCTCAGCCGTACTTACAAC	2116	OCL1 identification	Kenyon <i>et al.</i> , 2014, c
Citrat F1	AATTACAGTGGCACATTAGGTCCC			
Citrat R12	GCAGAGATACCAGCAGAGATACACG	722	<i>gltA</i> amplification and sequencing	https://pubmlst.org

gyrB_F	TGAAGGCGGCTTATCTGAGT	594	gyrB amplification and sequencing	https://pubmlst.org
gyrB_R	GCTGGGTCTTTTCCTGACA			
RA1	CCTGAATCTTCYGGTAAAAC	425	recA amplification and sequencing	https://pubmlst.org
RA2	GTTTCTGGGCTGCCAACATTAC			
gpi_F	GAAATTCCGGAGCTCACAA	456	gpi amplification and sequencing	https://pubmlst.org
gpi_R	TCAGGAGCAATACCCCACTC			
GDHB1F	GCT ACT TTT ATG CAA CAG AGC C	774	gdhB amplification and sequencing	https://pubmlst.org
GDHB775R	GTTGAGTTGGCGTATGTTGTGC			
cpn60_F	GGTGCTCAACTGTTCGTGA	640	cpn60 amplification and sequencing	https://pubmlst.org
cpn60_R	CACCGAAACCAGGAGCTTA			
rpoD-F	ACCCGTGAAGGTGAAATCAG	672	rpoD amplification and sequencing	https://pubmlst.org
rpoD-R	TTCAGCTGGAGCTTAGCAAT			

Plasmids	Relevant characteristics	Source
pUC19_sacB	pUC19 derivative with <i>sacB</i> gene from <i>Bacillus sp.</i>	Laboratory collection
pUC19_sacB_UDwzaGm	pUC19_sacB derivative with upstream and downstream regions of <i>A. baumannii</i> <i>wza</i> gene and <i>aac(3)-I</i> gentamicin aminoglycoside cassette from clinical <i>A. baumannii</i> strain	This study

Strains	Relevant characteristics	Source
<i>Escherichia coli</i> OP50	Wild type, bacterial food source for <i>C. elegans</i>	Brenner, 1974
<i>Acinetobacter baylyi</i> ADP1	Wild type	ATCC 33305*

Brenner, S. (1974). The genetics of *Caenorhabditis elegans*. *Genetic* 77, 71–94;

Chiang, M.C., Kuo, S.C., Chen, Y.C., Lee, Y.T., Chen, T.L., and Fung, C.P. (2011). Polymerase chain reaction assay for the detection of *Acinetobacter baumannii* in endotracheal aspirates from patients in the intensive care unit. *J Microbiol Immunol Infect.* 44(2), 106-10. doi: 10.1016/j.jmii.2010.04.003;

Kenyon, J.J., Nigro, S.J., and Hall, R.M. (2014). Variation in the OC Locus of *Acinetobacter baumannii* Genomes Predicts Extensive Structural Diversity in the Lipooligosaccharide. *PLoS ONE* 9(9):e107833. doi: 10.1371/journal.pone.0107833;

This publication made use of the *Acinetobacter baumannii* MLST website (<https://pubmlst.org/abaumannii/>) sited at the University of Oxford (Jolley & Maiden 2010, BMC Bioinformatics, 11:595). The development of this site has been funded by the Wellcome Trust.