

Supplementary Material

Technical Appendix

Acinetobacter baumannii-specific gene encoding for Type VI secretion system OmpA/MotB (accession number CP019034.1, GenBank) was chosen *in silico* for the experimental design. Sequence similarity searching is provided by the BLAST (<http://www.ncbi.nlm.nih.gov/>) and all sequences ($\geq 85\%$ identity score with reference sequence): *A. baumannii* (CP026943.1, LT594095.1, CP022283.1, CP020598.1, CP006768.1, CP015121.1, CP027183.1, CP021345.1, CP026711.1, CP026761.1, CP009256.1, CP026125.1, CP018332.1), *A. calcoaceticus* (LT605059, APQJ01000008, CP020000), *A. nosocomialis* (CP010368, CP020588, CP014019) were downloaded from the Taxonomy server of GenBank (Benson et al., 2000) and aligned using the Bioedit 7.0.5 software ([www.http://bioedit.software.informer.com](http://www.bioedit.com)). Based on comprehensive analysis and alignment of each gene type, primers and probes (Supplementary Table 2) were designed and verified again *in silico* by conducting a BLAST search in GenBank.

The specificity of the system was determined *in vitro* using a panel of DNA extracted from the following organisms available in our institute (<https://www.mediterranee-infection.com/diagnostic/les-centres-nationaux-de-reference-cnr/cnr-rickettsioses/collection-de-souches/>): 14 *A. baumannii* strains, 12 *Acinetobacter spp.* strains different from *A. baumannii*; 30 organisms others than *Acinetobacter spp.* (Supplementary Table 3 and Supplementary Figure 1). The specificity of *A. baumannii* qPCR was 100% among the species tested: 14/14 *A. baumannii* strains were positive; meanwhile 42/42 organisms different from *A. baumannii* (including genetically related *A. nosocomialis* and *A. calcoaceticus*) tested negative. In order to test the sensitivity of the method, a serial 8-fold dilutions for each of the 14 *A. baumannii* strains were performed; the result was confirmed as shown, for example, in Supplementary Figure 2.

References

Benson, D.A., Karsch-Mizrachi, I., Lipman, D.J., Ostell, J., Rapp, B.A., and Wheeler, D.L. (2000). GenBank. *Nucleic. Acids. Res.* 28, 15-18.

Collection de souches. Méditerranée Infection. (<https://www.mediterranee-infection.com/diagnostic/les-centres-nationaux-de-reference-cnr/cnr-rickettsioses/collection-de-souches/>)

Supplementary table 1. Lice-sampling strategy

Number of lice collected from homeless subjects (N, min-max per individual)	Theoretical percentage of lice tested among lice collected	Lice tested/Lice collected (N)
1-10	100%	24/24
11-50	50%	39/80
51-100	30%	86/293
101-250	15%	24/160
251-500	7.50%	0
501-1000	3.75%	46/1223
Total		219/1780

Supplementary table 2. List of organisms used in this study

<i>Genomic species</i>	<i>No. clinical isolates</i>	<i>STRAIN</i>	<i>GenBank access numbers</i>	<i>Origin</i>	<i>Type of sample</i>
A. The genus <i>Acinetobacter</i> spp.					
<i>Acinetobacter baumannii</i>	CSURP1574			Human	Feces
<i>Acinetobacter baumannii</i>	CSURP1875			Human	Unknown
<i>Acinetobacter baumannii</i>	CSURP1887			Human	Unknown
<i>Acinetobacter baumannii</i>	CSURP1888			Human	Unknown
<i>Acinetobacter baumannii</i>	CSURP1889			Human	Unknown
<i>Acinetobacter baumannii</i>	CSURP1891			Human	Unknown
<i>Acinetobacter baumannii</i>	CSURP24	AYE	CU459141.1	Human	Blood
<i>Acinetobacter baumannii</i>	CSURP25	SDF	CU468230.2	Animal	<i>Pediculus humanus</i>
<i>Acinetobacter baumannii</i>	CSURP266			Human	ND
<i>Acinetobacter baumannii</i>	CSURP270	<i>ABIsac-ColiR</i>	NZ_CAKB00000000.1	Human	
<i>Acinetobacter baumannii</i>	CSURP271	<i>ABIsac-ColiS</i>	NZ_CAKA00000000.1	Human	
<i>Acinetobacter baumannii</i>	CSURP2941			Environment	Permafrost
<i>Acinetobacter baumannii</i>	CSURP414			Human	Pus
<i>Acinetobacter baumannii</i>	CSURP981			Human	Sputum
<i>Acinetobacter calcoaceticus</i>	CSURP4654			Human	Unknown
<i>Acinetobacter bereziniae</i>	CSURP2349			Human	Skin
<i>Acinetobacter genospecies</i>	CSURP367			Human	Blood
<i>Acinetobacter johnsonii</i>	CSURP3183			Human	Blood
<i>Acinetobacter Iwoffii</i>	CSURP308			Human	Feces
<i>Acinetobacter Iwoffii</i>	CSURP3143			Human	Urine
<i>Acinetobacter Iwoffii</i>	CSURP786			Human	Feces
<i>Acinetobacter nosocomialis</i>	CSURP2568			Human	ND
<i>Acinetobacter pittii</i>	CSURP610			Human	Feces
<i>Acinetobacter schindleri</i>	CSURP1134			Human	Feces
<i>Acinetobacter ursingii</i>	CSURP3381			Environment	Permafrost
<i>Acinetobacter variabilis</i>	CSURP2356			Human	Skin
B. Other bacteria					
<i>Anaplasma phagocytophilum</i>				Animal	Tick
<i>Bartonella quintana</i>	CSURB177			Animal	<i>Pediculus</i>

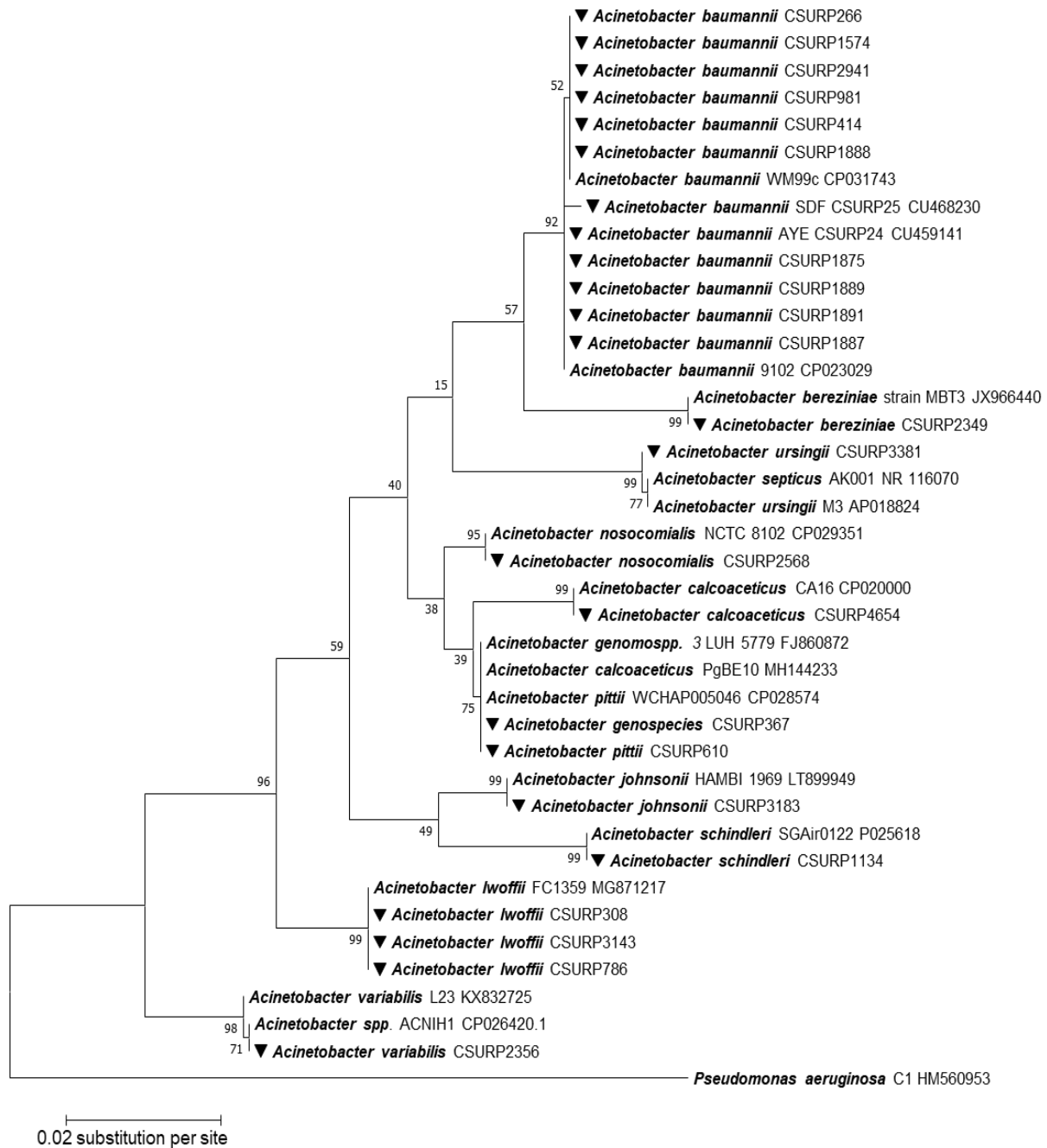
				<i>humanus</i>
<i>Borrelia recurrentis</i>	CSURP2		Animal	<i>humanus</i> <i>Pediculus</i>
				<i>humanus</i>
				<i>humanus</i>
<i>Coxiella burnetii</i>	CSURC1		Human	ND
<i>Enterobacter aerogenes</i>	CSURP210		Human	Blood
<i>Enterococcus faecium</i>	CSURP306		Human	Blood
<i>Gardnerella vaginalis</i>	CSURP3048			
<i>Haemophilus influenzae</i>	CSURP750		Human	Blood
<i>Lactobacillus gasseri</i>				
<i>Rickettsia conorii</i>	CSURR118		Human	Skin
<i>Rickettsia felis</i>	CSURR21	NR_074483	Animal	Flea
<i>Rickettsia massiliae</i>	CSURR131		Animal	Tick
<i>Rickettsia typhi</i>	CSURR162		Animal	Flea
<i>Rickettsia raoultii</i>	CSURR3		Animal	Tick
<i>Salmonella spp.</i>	CSURP404		Human	Blood
<i>Staphylococcus aureus</i>	CSURP566		Human	Blood
<i>Staphylococcus haemolyticus</i>	CSURP295		Human	Blood
<i>Stenotrophomonas maltophilia</i>	CSURP1214		Human	Blood
<i>Staphylococcus hominis</i>	CSURP2339		Human	Blood
<i>Streptococcus agalactiae</i>	CSURP679		Human	Blood
<i>Streptococcus pyogenes</i>	CSURP739		Human	Blood
<i>Streptococcus pneumoniae</i>	CSURP1177		Human	Blood
<i>Yersinia pestis</i>	CSURP100		Rodent	ND
<i>Ehrlichia spp.</i>				
<i>Wolbachia spp.</i>				
C. Parasites				
<i>Ctenocephalides felis</i>				
<i>Babesia canis</i>				
D. Mammal animals				
<i>Canis lupus familiaris</i>			Dog	Blood
<i>Equus ferus caballus</i>			Horse	Blood
<i>Homo sapiens</i>			Human	Blood

Supplementary table 3. Sequences of primers and probes used for real-time PCR in this study

Target		Name	Primers (5'-3') and probes	Amplicon size
<i>Acinetobacter baumannii</i>	Forward		TCAACATCACAATCTTTAGTAGCTGA	215 pb
	Reward	ompA/motB	CGCTCTTGCCAGCATAAAGA	
	Probe		6FAM-AAGTCGCCAAGAAACCTTGA-TAMRA	

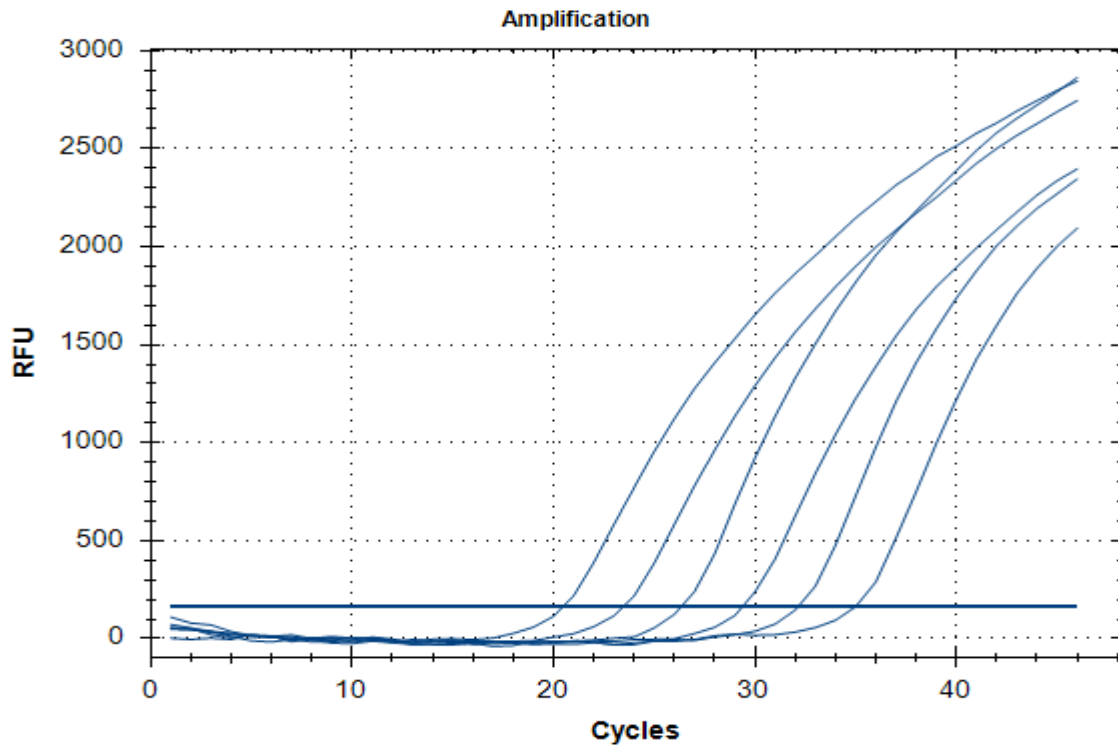
Supplementary table 4. Detail of distribution of the number of lice collected, number of lice analysed, number of crushed lice positive to *A. baumannii* DNA and *A. baumannii* DNA skin-carriage from sheltered homeless persons of Marseille

Year of study	ID code homeless persons	Number of lice collected	Number of lice analysed	Number of lice-washing liquid of lice positive for <i>A. baumannii</i> N (%)	Number of crushed lice positive for <i>A. baumannii</i> N (%)	<i>A. baumannii</i> on the skin
2 013	N°1	560	21	4 (19)	6 (28.6)	Yes
2 013	N°2	90	25	0 (0)	0 (0)	No
2 013	N°3	663	25	13 (52)	14 (56)	No
2 013	N°4	6	6	1 (16.7)	1 (16.7)	No
2 013	N°5	17	8	5 (62.5)	6 (75)	No
2 013	N°6	70	21	0 (0)	0 (0)	No
2 013	N°7	2	2	0 (0)	0 (0)	No
2 013	N°8	10	10	0 (0)	0 (0)	No
2 013	N°9	80	24	0 (0)	0 (0)	No
2 013	N°10	12	6	0 (0)	0 (0)	Yes
2 013	N°11	19	9	3 (33.3)	6 (66.7)	No
2 014	N°12	6	6	0 (0)	1 (16.7)	No
2 014	N°13	32	16	1 (6.25)	3 (18.8)	Yes
2 014	N°14	53	16	7 (43.8)	10 (62.5)	Yes
2 014	N°15	160	24	6 (25)	12 (50)	Yes
Total	15 individuals	1780	219	40 (18.3)	59 (26.9)	



Supplementary Figure 1. Maximum-likelihood phylogenetic tree highlighting the position of the *Acinetobacter spp.* strains used for test sensitivity and specificity of the new system in the present study compared to another *Acinetobacter* available in the GenBank database and based on partial 16S rRNA gene sequences (data not shown), with *Pseudomonas aeruginosa* C1 (HM560953) used as outgroups. Identification of 16S rRNA gene sequences of each strain was carried out as previously described (1).

(1) Drancourt M, Berger P, Raoult D. Systematic 16S rRNA Gene Sequencing of Atypical Clinical Isolates Identified 27 New Bacterial Species Associated with Humans. *J Clin Microbiol* **2004**; 42:2197–2202.



Supplementary Figure 2. The sensitivity of the real-time PCR assay tested on 8-fold serial dilutions of *A. baumannii* DNA strain SDF