

Table S1 - FastANI-based taxonomic refinement of clinical isolates initially identified as *Acinetobacter baumannii*.

Isolate	Best_ANI_species	Best_ANI_%	Best_hit_coverage_fraction	ANI_with_A_baumannii_%	ANI_with_A_nosocomialis_%	Coverage_with_A_baumannii	Coverage_with_A_nosocomialis	Taxonomic_interpretation
SEN0001	A. baumannii	97.97	0.94	97.97	92.165	0.94	0.89	Compatible with A. baumannii
SEN0006	A. nosocomialis	98.90	0.94	92.47	98.9063	0.87	0.94	Likely A. nosocomialis / non-baumannii ACB complex member
SEN0010	A. baumannii	99.84	0.93	99.84	92.1508	0.93	0.86	Compatible with A. baumannii
SEN0015	A. baumannii	97.99	0.92	97.99	92.0167	0.92	0.87	Compatible with A. baumannii
SEN0017	A. nosocomialis	98.62	0.93	92.21	98.6228	0.85	0.93	Likely A. nosocomialis / non-baumannii ACB complex member
RES014	A. baumannii	99.79	0.98	99.79	92.2149	0.98	0.84	Compatible with A. baumannii
RES047	A. baumannii	99.81	0.99	99.81	92.2823	0.99	0.86	Compatible with A. baumannii
RES079	A. baumannii	99.85	0.97	99.85	92.2258	0.97	0.85	Compatible with A. baumannii
RES087	A. baumannii	99.89	0.99	99.89	92.1646	0.99	0.83	Compatible with A. baumannii
RES168	A. baumannii	99.89	0.99	99.89	92.196	0.99	0.86	Compatible with A. baumannii
RES052	A. baumannii	99.84	0.96	99.84	92.1842	0.96	0.82	Compatible with A. baumannii
RES131	A. baumannii	99.81	0.96	99.81	92.1038	0.97	0.84	Compatible with A. baumannii
RES158	A. baumannii	99.90	0.97	99.90	92.2019	0.97	0.86	Compatible with A. baumannii
RES186	A. baumannii	99.91	0.98	99.91	92.2103	0.98	0.86	Compatible with A. baumannii

Average Nucleotide Identity (ANI)-based taxonomic assessment of the 14 genomes included in the main comparative analyses. Genome assemblies from clinical isolates initially identified as *Acinetobacter baumannii* by routine hospital microbiology were compared with reference genomes of *A. baumannii* and *A. nosocomialis* using FastANI. The table shows the best ANI species assignment, best-hit ANI value, best-hit coverage fraction, ANI values against *A. baumannii* and *A. nosocomialis*, corresponding coverage fractions, and final taxonomic interpretation. Most isolates showed ANI values compatible with *A. baumannii*. However, two susceptible isolates, SEN0006 and SEN0017, showed higher ANI values with *A. nosocomialis* than with *A. baumannii*, suggesting that they likely belong to *A. nosocomialis* or to a non-*baumannii* member of the *Acinetobacter calcoaceticus*–*baumannii* complex.

Table S2. Quinolone resistance-associated QRDR mutations detected by AMRFinderPlus.

Isolate	QRDR marker	Element_name	Class	%_identity _reference	Closest_reference _accession	Closest_reference_name	Phenotype
RES01 4	gyrA_S81 L	A. baumannii quinolone resistant GyrA	QUINOLON E	99.78	WP_000116450.1	DNA gyrase subunit A GyrA	MDR
RES04 7	gyrA_S81 L	A. baumannii quinolone resistant GyrA	QUINOLON E	99.78	WP_000116450.1	DNA gyrase subunit A GyrA	MDR
RES07 9	gyrA_S81 L	A. baumannii quinolone resistant GyrA	QUINOLON E	99.78	WP_000116450.1	DNA gyrase subunit A GyrA	MDR
RES08 7	gyrA_S81 L	A. baumannii quinolone resistant GyrA	QUINOLON E	99.78	WP_000116450.1	DNA gyrase subunit A GyrA	MDR
RES16 8	gyrA_S81 L	A. baumannii quinolone resistant GyrA	QUINOLON E	99.78	WP_000116450.1	DNA gyrase subunit A GyrA	MDR
RES16 8	parC_S84 L	A. baumannii quinolone resistant ParC	QUINOLON E	99.86	WP_000202259.1	DNA topoisomerase IV subunit A ParC	MDR
RES05 2	gyrA_S81 L	A. baumannii quinolone resistant GyrA	QUINOLON E	99.78	WP_000116450.1	DNA gyrase subunit A GyrA	XDR
RES13 1	gyrA_S81 L	A. baumannii quinolone resistant GyrA	QUINOLON E	99.78	WP_000116450.1	DNA gyrase subunit A GyrA	XDR
RES13 1	parC_S84 L	A. baumannii quinolone resistant ParC	QUINOLON E	99.59	WP_000202259.1	DNA topoisomerase IV subunit A ParC	XDR
RES15 8	gyrA_S81 L	A. baumannii quinolone resistant GyrA	QUINOLON E	99.78	WP_000116450.1	DNA gyrase subunit A GyrA	XDR
RES15 8	parC_S84 L	A. baumannii quinolone resistant ParC	QUINOLON E	99.86	WP_000202259.1	DNA topoisomerase IV subunit A ParC	XDR
RES18 6	gyrA_S81 L	A. baumannii quinolone resistant GyrA	QUINOLON E	99.78	WP_000116450.1	DNA gyrase subunit A GyrA	XDR
RES18 6	parC_S84 L	A. baumannii quinolone resistant ParC	QUINOLON E	99.86	WP_000202259.1	DNA topoisomerase IV subunit A ParC	XDR

AMRFinderPlus analysis using the *Acinetobacter baumannii* organism-specific option identified quinolone resistance-associated point mutations in the quinolone resistance-determining regions (QRDRs) of *gyrA* and/or *parC*. The table summarizes the detected mutations, including *gyrA*_S81L and *parC*_S84L, their genomic location, reference coverage, identity, and corresponding isolate metadata. These mutations were detected predominantly among MDR and XDR isolates and provide genomic support for the ciprofloxacin-resistant phenotypes observed in the antimicrobial susceptibility testing. RES179 is reported for completeness but was excluded from the main comparative analyses due to anomalous genome size. Method POINTX and percentage of coverage reference all samples was 100%.

Table S3. Capsular polysaccharide and outer core locus typing of clinical isolates initially identified as *Acinetobacter baumannii*.

Isolate	Phenotype	KL_locus	KL_type	KL_identity_%	KL_coverage_%	OCL_locus	OCL_type	OCL_identity_%	OCL_coverage_%	Interpretation_note
SEN0001	SEN	KL194	unknown (KL194)	99.39	99.56	OCL2	unknown (OCL2)	98.73	100	Retained in main comparative analyses
SEN0006	SEN	KL24	unknown (KL24)	96.75	91.68	OCL1	OC1	94.04	98.03	FastANI suggested higher similarity to <i>A. nosocomialis</i>
SEN0010	SEN	KL47	K47	98.57	100	OCL7	unknown (OCL7)	98.6	99.48	Retained in main comparative analyses
SEN0015	SEN	KL194	unknown (KL194)	99.45	99.88	OCL2	unknown (OCL2)	98.73	100	Retained in main comparative analyses
SEN0017	SEN	KL96	unknown (KL96)	95.41	99.94	OCL4	unknown (OCL4)	92.73	76.23	FastANI suggested higher similarity to <i>A. nosocomialis</i>
RES014	MDR	KL22	K3	99.94	99.85	OCL10	unknown (OCL10)	99.91	98.77	Retained in main comparative analyses
RES047	MDR	KL22	K3	99.94	99.99	OCL10	unknown (OCL10)	99.91	99.97	Retained in main comparative analyses
RES079	MDR	KL22	K3	99.96	99.71	OCL10	unknown (OCL10)	99.94	99.91	Retained in main comparative analyses
RES087	MDR	KL49	K49	99.97	100	OCL10	unknown (OCL10)	99.94	99.94	Retained in main comparative analyses
RES168	MDR	KL81	K2	99.35	92.6	OCL7	unknown (OCL7)	99.19	100	Retained in main comparative analyses
RES052	XDR	KL9	K9	99.58	100	OCL10	unknown (OCL10)	99.94	99.99	Retained in main comparative analyses
RES131	XDR	KL1	K1	100	100	OCL1	OC1	100	100	Retained in main comparative analyses
RES158	XDR	KL81	K2	99.35	92.6	OCL7	unknown (OCL7)	99.19	100	Retained in main comparative analyses
RES186	XDR	KL81	K2	99.35	92.6	OCL7	unknown (OCL7)	99.19	100	Retained in main comparative analyses

In silico capsular polysaccharide locus (KL) and lipooligosaccharide outer core locus (OCL) typing was performed using Kaptive with *A. baumannii* reference databases. The table summarizes the best-match KL and OCL loci, predicted type, match confidence, identity, and coverage for each isolate. Results are reported according to the initial clinical identification and resistance phenotype used in the main comparative analyses. KL/OCL assignments for SEN0006 and SEN0017 should be interpreted with caution, as FastANI indicated higher genomic similarity to *A. nosocomialis* than to *A. baumannii*. RES179 was excluded from downstream comparative analyses due to anomalous genome size.