# Supplementary Materials

Table S1: Antimicrobial susceptibility of the isolates LEV1449/17Ec and 39741

| | MIC mg/l | | | | | | | | | |
|---|---|---|---|---|---|---|---|---|---|---|
| | SAM | TZP | CAZ | ATM | MEM | GEN | AMK | CST | CIP | TGC |
| LEV1449/17Ec | 1 | 2 | 4 | 16 | 0.125 | 0.25 | 0.5 | 16 | 0.063 | 0.063 |
| 39741 | 1 | 2 | 4 | 16 | 0.125 | 0.25 | 0.5 | 16 | 0.063 | 0.063 |

SAM, ampicillin-sulbactam; TZP, piperacillin-tazobactam; CAZ, ceftazidime; ATM, aztreonam; MEM, meropenem; GEN, gentamicin; AMK, amikacin; CST, colistin; CIP, ciprofloxacin; TGC, tigecycline.

Table S2: Key genomic features of the two sequenced strains: LEV1449/17Ec and 39741

| **Strain ID** | **Position** | **Antibiotic Resistance genes** | **Virulence genes** | **Virulence factor** | **Virulence factor class** |
|---|---|---|---|---|---|
| **39741** | EH_chromosome | $bla_{\text{ADC-6}}$ | *ompA* | Outer membrane protein | Adherence |
| | | | *adeF-G* | Efflux pump | Biofilm formation |
| | | | *bap* | Biofil associated protein | |
| | | | *csuA-D* | Csu pili | |
| | | $bla_{\text{OXA-67}}$ | *lpxA/B/C/D/L/M* | LPS | Immune invasion |
| | | | *abaI, abaR* | Quorum sensing | Regulation |
| | | | *pbpG* | PbpG | Serum resistance |
| | pEH_mcr4.3 | *mcr-4.3* | | | |
| | pEH_gr3 | | | | |
| | pEH_gr13 | | | | |
| **LEV1449/17Ec** | EC_chromosome | $bla_{\text{ADC-6}}$ | *ompA* | Outer membrane protein | Adherence |
| | | | *adeF-G* | Efflux pump | Biofilm formation |
| | | | *bap* | Biofil associated protein | |
| | | | *csuA-D* | Csu pili | |
| | | $bla_{\text{OXA-67}}$ | *lpxA/B/C/D/L/M* | LPS | Immune invasion |
| | | | *abaI, abaR* | Quorum sensing | Regulation |
| | | | *pbpG* | PbpG | Serum resistance |
| | pEC_mcr4.3 | *mcr-4.3* | | | |
| | pEC_gr6 | | | | |
| | pEC_gr13 | | | | |

*Antibiotic resistance genes was detected using the ResFinder Databas and AMRFinder, while virulencegenes,factor,and class was detected using the VFDB database.

Table S3: Non-clustered SNPs between *A. baumannii* LEV1449/17Ec and 39741’s core genomes.

| PROKKA name | LEV1449/17Ec number | SNP position | Gene product length (AA) | AA substitution |
|---|---|---|---|---|
| * | - | A40727T | - | - |
| L-carnitine/gamma-butyrobetaine antiporter | - | A41475T | 506 | T235T |
| hypothetical protein | - | A61927T | 292 | M177L |
| Aspartate/glutamate leucyltransferase | 2.3.2.29 | G63085C | 272 | G205R |
| hypothetical protein | - | T114607A | 311 | L49Q |
| Methionine synthase | 2.1.1.13 | A180632G | 1229 | D644G |
| hypothetical protein | - | T186284G | 516 | A487A |
| Sulfate adenylyltransferase subunit 2 | 2.7.7.4 | G216162C | 303 | D288H |
| hypothetical protein | - | C278147T | 383 | P132S |
| hypothetical protein | - | A294681T | 1149 | G954G |
| Chromosome partition protein Smc | - | T304306C | 187 | Y129H |
| putative HTH-type transcriptional regulator | - | G312338A | 297 | L234L |
| hypothetical protein | - | T351606A | 311 | L49Q |
| * | - | C358942T | - | - |
| 3-(3-hydroxy-phenyl)propionate transporter | - | G359174C | 411 | G77R |
| * | - | C413135T | - | - |
| Porin-like protein NicP | - | G433536C | 421 | E284Q |
| Porin-like protein NicP | - | G433542A | 421 | V282M |
| putative signaling protein | - | G491397A | 402 | D8N |
| hypothetical protein | - | T534668A | 311 | L49Q |
| 2-nitroimidazole transporter | - | G538792T | 258 | V207F |
| Bifunctional protein PaaZ | - | A561926G | 701 | K367E |
| Bifunctional protein PaaZ | - | T562321A | 701 | L235Q |
| Bifunctional protein PaaZ | - | A562330T | 701 | N232I |
| hypothetical protein | - | G635821A | 1161 | G1134G |
| HTH-type transcriptional regulator DmlR | - | T640228G | 314 | W268G |
| hypothetical protein | - | T665414A | 311 | L49Q |
| hypothetical protein | - | G675173T | 454 | R363L |
| * | - | A690123T | - | - |
| Acetyl-S-ACP:malonate ACP transferase | 2.3.1.187 | C708824T | 560 | T344M |
| Serine acetyltransferase | 2.3.1.30 | T752358C | 272 | C77R |
| tRNA (cytidine/uridine-2'-O-)-methyltransferase TrmJ | 2.1.1.200 | T753395C | 280 | A8A |
| DNA polymerase III subunit alpha | 2.7.7.7 | C755062A | 1188 | I645I |
| LL-diaminopimelate aminotransferase | 2.6.1.83 | A766687G | 409 | E166G |
| Bifunctional uridylyltransferase/uridylyl-removing enzyme | - | A768979T | 888 | A279A |
| Bifunctional uridylyltransferase/uridylyl-removing enzyme | - | T769326C | 888 | C164R |
| Ribosome-binding ATPase YchF | - | C775604T | 364 | A258V |
| Glutamate/aspartate import permease protein GltK | - | C787354T | 226 | I36I |
| * | - | A813563G | - | - |
| Transketolase 1 | 2.2.1.1 | A825809G | 663 | L384L |
| Sporulation initiation inhibitor protein Soj | 3.6.-.- | T860696C | 261 | F118F |
| Tetraacyldisaccharide 4'-kinase | 2.7.1.130 | C865327A | 337 | H155N |
| N(2)-citryl-N(6)-acetyl-N(6)-hydroxylysine synthase | 6.3.2.38 | C936464T | 595 | H562Y |
| Aerobactin synthase | 6.3.2.39 | C940834G | 614 | L458V |
| Putative 4-hydroxy-4-methyl-2-oxoglutarate aldolase | 4.1.3.17 | T944587C | 206 | N198N |
| Ferric aerobactin receptor | - | A946709G | 770 | G668G |
| DNA-binding transcriptional regulator NtrC | - | A1009011T | 424 | S152S |
| hypothetical protein | - | T1014723G | 306 | C90G |
| * | - | T1017149G | - | - |
| Chromate transport protein | - | A1018036T | 450 | L170L |
| Regulatory protein PchR | - | T1045249A | 329 | F316Y |
| Polyphosphate kinase | 2.7.4.1 | T1066831A | 503 | *503K |
| Outer membrane usher protein HtrE | - | T1086289C | 854 | G626G |
| NAD-dependent glycerol dehydrogenase | 1.1.1.6 | G1104521A | 255 | V185M |
| HTH-type transcriptional repressor Bm3R1 | - | C1106508T | 190 | A76V |

| | | | | |
|---|---|---|---|---|
| NADH oxidase | 1.-.-.- | C1113950T | 413 | A264V |
| Putative tartrate transporter | - | C1120152A | 435 | T252N |
| Flavin-dependent monooxygenase, oxygenase subunit HsaA | 1.14.14.12 | G1144378C | 389 | R271P |
| 3-oxoadipate enol-lactonase 2 | 3.1.1.24 | G1171636A | 262 | Q12Q |
| hypothetical protein | - | G1199192A | 507 | V1M |
| hypothetical protein | - | C1199672G | 507 | R161G |
| putative TonB-dependent receptor BfrD | - | T1212300A | 700 | V22E |
| * | - | A1224152G | - | - |
| * | - | A1233857G | - | - |
| Phosphoenolpyruvate-protein phosphotransferase | 2.7.3.9 | G1234612A | 953 | W199* |
| Sulfurtransferase TusE | 2.8.1.- | C1290488A | 104 | T15K |
| Nitrite reductase [NAD(P)H] | 1.7.1.4 | T1305586A | 849 | T825T |
| hypothetical protein | - | G1366811C | 145 | G59A |
| putative ABC transporter ATP-binding protein YheS | - | G1393082T | 528 | D229Y |
| DNA mismatch repair protein MutL | - | C1449583T | 651 | L189L |
| hypothetical protein | - | C1456879T | 143 | C8C |
| Inner membrane transport protein YdhP | - | C1457982T | 400 | G284G |
| Translocation and assembly module subunit TamB | - | A1467698C | 1502 | S118R |
| * | - | A1486416T | - | - |
| Bifunctional purine biosynthesis protein PurH | - | T1532225A | 525 | F211L |
| hypothetical protein | - | A1553974T | 185 | Q103L |
| * | - | A1575783T | - | - |
| HTH-type transcriptional regulator NorG | - | T1640184A | 487 | L276Q |
| Multidrug resistance protein MdtE | - | C1645553T | 407 | P391L |
| | | | | |
| NADP-dependent malic enzyme | 1.1.1.40 | G1687532T | 757 | G682V |
| * | - | C1787008T | - | - |
| * | - | C1797244G | - | - |
| Deoxyribodipyrimidine photo-lyase | 4.1.99.3 | T1840762C | 481 | S30P |
| hypothetical protein | - | A1846879T | 615 | H565L |
| Putative monooxygenase | 1.13.12.- | C1851661T | 349 | T106I |
| Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase | 2.4.2.43 | A1947527C | 549 | T194T |
| D-serine/D-alanine/glycine transporter | - | A1959553T | 493 | N13Y |
| Sulfur carrier protein FdhD | - | T1965603G | 121 | *121E |
| hypothetical protein | - | T1975755C | 169 | Y29H |
| Multidrug resistance protein MexB | - | T1992006C | 1032 | V400A |
| hypothetical protein | - | A2032807G | 7535 | I6861V |
| Transcriptional regulatory protein QseB | - | T2112744A | 225 | D181E |
| putative NTE family protein | - | T2119673A | 306 | R199R |
| hypothetical protein | - | C2150911T | 115 | S63F |
| Putative aminoacrylate hydrolase RutD | 3.5.1.- | C2191038A | 269 | A14D |
| putative thiol:disulfide interchange protein DsbC | - | C2199683T | 237 | S44L |
| Outer membrane protein Omp38 | - | G2217125A | 357 | K96K |
| hypothetical protein | - | A2250197T | 292 | H223L |
| hypothetical protein | - | A2259813C | 481 | K73Q |
| * | - | C2316998T | - | - |
| * | - | T2317000C | - | - |
| hypothetical protein | - | A2369343T | 224 | N43Y |
| 8-oxo-dGTP diphosphatase | 3.6.1.55 | G2427804A | 134 | V1V |
| HTH-type transcriptional regulator GltR | - | C2459431A | 289 | Q249K |
| 1-(5-phosphoribosyl)-5-[(5-phosphoribosylamino)methylideneamino] imidazole-4-carboxamide isomerase | 5.3.1.16 | G2612892A | 244 | A36T |
| hypothetical protein | - | A2621376G | 213 | N203S |
| * | - | G2636798C | - | - |
| hypothetical protein | - | A2645393G | 664 | T643A |
| hypothetical protein | - | A2645682G | 664 | K546K |
| hypothetical protein | - | G2645968A | 664 | G451D |

| | | | | |
|---|---|---|---|---|
| hypothetical protein | - | T2656968C | 177 | L158P |
| hypothetical protein | - | G2769257A | 447 | R13K |
| Multidrug export protein MepA | - | A2779493T | 456 | M30L |
| hypothetical protein | - | T2785944A | 399 | F63L |
| Carboxymethylenebutenolidase | 3.1.1.45 | T2841580A | 246 | A79A |
| UDP-glucose 4-epimerase | 5.1.3.2 | G3003840C | 339 | V205V |
| Quinone-dependent D-lactate dehydrogenase | 1.1.5.12 | T3010872C | 569 | I322T |
| HTH-type transcriptional repressor ComR | - | A3088378C | 214 | E78D |
| hypothetical protein | - | C3119153G | 156 | L76V |
| Elongation factor Tu | - | A3227707G | 397 | T178A |
| 50S ribosomal protein L1 | - | C3230162T | 232 | Y21Y |
| Transcription termination/antitermination protein NusA | - | C3284437T | 495 | R3R |
| Na()/H() antiporter subunit A | - | C3293523G | 946 | T597T |
| Ubiquinone/menaquinone biosynthesis C-methyltransferase UbiE | 2.1.1.163 | C3304064G | 316 | Q43E |
| Polyribonucleotide nucleotidyltransferase | 2.7.7.8 | A3320512T | 698 | P398P |
| hypothetical protein | - | G3424524A | 778 | D16N |
| * | - | T3466640C | - | - |
| hypothetical protein | - | A3598303C | 484 | T481P |
| S-formylglutathione hydrolase | 3.1.2.12 | A3598303C | 283 | K7N |
| NADH-quinone oxidoreductase subunit G | 1.6.5.11 | G3648919A | 895 | M365I |

* : SNP was located in an intergenic region

Table S4: AA substitutions in the PmrCAB and lpxA/lpxC/lpxD in *A. baumannii* LEV1449/17Ec and 39741strains when compared to ATCC 17978 (accession number: CP000521)

| | pmrB | pmrA | pmrC | lpxA | lpxC | lpxD |
|---|---|---|---|---|---|---|
| 39741 | A28T, K45Q, H54Y, F65L, K67R, I76L, H86N, L93F, E99Q, Q110E, I112V, I322V, E320D, **Y363F, H362N** | I18T, T44N, E133Q, T168S | V51I, L52F, I54L, L55I, V102F, I115V, **I212V, R332K** | **Y131H** | **C120R, N287D** | - |
| LEV1449/17Ec | A28T, K45Q, H54Y, F65L, K67R, I76L, H86N, L93F, E99Q, Q110E, I112V, I322V, E320D, **H362N, Y363F** | I18T, T44N, E133Q, T168S, **D181E** | V51I, L52F, I54L, L55I, V102F, I115V, **I212V, R332K**, **Q517K, A317V, V135A, V84I** | **Y131H** | **C120R, N287D** | - |

[a] Red indicates that these substitutions have been reported in both susceptible and resistant isolates elsewhere.

[b] Black color represents new substitutions that have not been reported before.

[c] Bold black represents shared substitutions between LEV1449/17Ec and 39741.