

Table S1 : Analysis of mutations in ACTi gene after comparison with ACT-77 (WP_060573544.1)

Mismatches and positions	Position	Accession number of similar proteins with similar mismatches
H-N	P35	WP_061099492.1
E-D	P115	WP_192986658.1 WP_061099492.1 WP_164461280.1 WP_059354427.1
R-K	P 203	WP_061099492.1
P-S	P 267	WP_193357670.1

Table S2 : Analysis of mutations in *qnr* gene in *E. bugandensis* 9i genome sequence

Mismatches and positions	Position	Accession number of similar proteins with similar mismatches
G—S	P7	WP_218307411.1
A-D	P94	NA
A-V	P99	(GJK31478.1)
		WP_039992288.1

Table S3: Primers of the target β -lactamase genes

β -lactamases	Primer sequence (5'-3')	Size (pb)	Reference
TEM	F :ATTCTTGAAGACGAAAGGGC R :ACGCTCAGTGGAACGAAAAC	1150 bp	[42]
SHV	F :CACTCAAGGATGTATTG TG R:TTAGCGTTGCCAGTGCTCG	885	
OXA-1	F :ACACAATACATATCAACTTCGC R :AGTG TGTTTAGAATGGTGATC	813	
CTX-M-1 group	F:GTTACAATGTGTGAGAAGCAG R:CCGTTTC CGCTATTACAAA	1041	
CTX-M-8 group	F:TGATGAGACATCGCGTTAAG R:TAACCGTCGGTG ACGATTTT	875	
CTX-M-9 group	F:GTG ACAAAGAGAGTGCAACGG R:ATGATTCTCGCCGCTGA AGCC	857	
CTX-M-10	F:CC GCGCTACACTTTGTGGC R:TTACAAACCGTTGGTGA CG	944	
CMY1,CMY-8 toCMY-11	F :GCTGCTCAAGGAGCACAGGAT R :CACATTGACATAGGTGTGGTGC	520	[43]
CMY-2 to CMY-7	F :TGGCCAGAACTGACAGGCAAA R :TTTCTCCTGAACGTGGCTGGC	462	
DHA-1, DHA-2	F :AACTTTCACAGGTGTGCTGGGT R :CCGTACGCATACTGGCTTTGC	405	
ACT-1	F:TCGGTAAAGCCGATGTTGCGG R:CTTCCACTGCGGCTGCCAGTT	302	
IMP	F : GGAATAGAGTGGCTTAAYTCTC R : GGTTTAAYAAAACAACCACC	232	[44]
SPM	F: AAAATCTGGGTACGCAAACG R : ACATTATCCGCTGGAACAGG	271	
VIM	F : GATGGTGTTTGGTCGCATA R : CGAATGCGCAGCACCAG	390	
OXA-48	F : GCGTGGTTAAGGATGAACAC	438	

	R : CATCAAGTTCAACCCAACCG		
GIM	F: TCGACACACCTTGGTCTGAA	477	
	R: AACTTCCAACCTTTGCCATGC		
SIM	F: TACAAGGGATTCTGGCATCG	570	
	R: TAATGGCCTGTCCCATGTG		
NDM	F : GGTTCGGCGATCTGGTTTTTC	621	
	R : CGGAATGGCTCATCACGATC		
KPC	F: CGTCTAGTTCTGCTGTCTTG	798	
	R: CTTGTCATCCTTGTTAGGCG		
IMI1-3 /NMC	F: TCGGGTCGATTGGAGATAAA	399	[45]
	R: CGATTCTTGAAGCTTCTGCG		
SME1-3	F: ACTTTGATGGGAGGATTGGC	551	
	R: ACGAATTCGAGCATCACCAG		
GES1-9	F: GCTTCATTACGCACTATT	323	
	R: CGATGCTAGAAACCGCTC		

Table S4: Primers of the target antimicrobial resistance genes.

Target gene(s) or region	Primer sequence (5'-3')	Size (pb)	Reference
tetA	F:GTAATTCTGAGCACTGTCTGC R:CTGCCTGGACAACATTGCTT	937	[39]
tetB	F:CTCAGTATTCCAAGCCTTTG R:CTAAGCACTTGTCTCCTGTT	416	
sul1	F:TGGTGACGGTGTTCTGGCATTCT R:GCGAGGGTTTCCGAGAAGGTG	789	
sul2	F:CGGCATCGTCAACATAACC R:GTGTGCGGATGAAGTCAG	722	
sul3	F: CATTCTAGAAAACAGTCGTAGTTCTG R:CATCTGCAGCTAACCTAGGGCTTTGGA	990	
Int1	F:GGGTCAAGGATCTGGATTTCTG R: ACATGGGTGTAAATCATCGTC	483	
aac(3)-II	F:ACTGTGATGGGATACGCGTC	237	

	R:CTCCGTCAGCGTTTCAGCTA	
aac(3)-IV	F:CTTCAGGATGGCAAGTTGGT R:TCATCTCGTTCTCCGCTCAT	286
qnrA	F:AGAGGATTCTCACGCCAGG R:TGCCAGGCACAGATCTTGAC	580
qnrB	F:GATCGTGAAAGCCAGAAAGG R:ACGATGCCTGGTAGTTGTCC	469
qnrS	F:GCAAGTTCATTGAACAGGGT R:TCTAAACCGTCGAGTTCGGCG	550
qepA	F:GCAGGTCCAGCAGCGGGTAG R:GGACATCTACGGCTTCTTCG	617
aac(6')-Ib	F:TTGCGATGCTCTATGAGTGGCTA R:CTCGAATGCCTGGCGTGTTT	482

Table S5. ANI values of *E. bugandensis* 9i isolate with all genome sequences of *E. bugandensis* deposited in genbank (as of December 2022).

Genome assebmy	ANI(%)
GCF 001054435.1_ASM105443v1	95.23
GCF_023750845.1_ASM2375084v1	95.20
GCA_023750905.1_ASM2375090v1	95.16
GCF_023374275.1_ASM2337427v1	95.15
GCF 023154875.1_ASM2315487v1	95.15
GCA 023752545.1_ASM2375254v1	95.12
GCA 023152755.1_ASM2315275v1	95.10
GCA_023751035.1_ASM2375103v1	95.09
GCA 021287345.1_ASM2128734v1	95.08
GCA 023151965.1_ASM2315196v1	95.08
GCA_023153675.1_ASM2315367v1	95.08
GCA_023153675.1_ASM2315367v1	95.08
GCA 000515295.1_ASM51529v1	95.06
GCF 000515295.1_ASM51529v1	95.06
GCA 023151735.1_ASM2315173v1	95.06
GCA 021650125.1_ASM2165012v1	95.05
GCA 023151725.1_ASM2315172v1	95.05
GCA_023153975.1_ASM2315397v1	95.05
GCA_023153975.1_ASM2315397v1	95.05
GCF 903970915.1_ASM90397091v1	95.05
GCF 903970835.1_ASM90397083v1	95.05
GCA 018597305.1_ASM1859730v1	95.04

GCA 021650055.1 ASM2165005v1	95.03
GCA 021650105.1 ASM2165010v1	95.03
GCA_023154415.1_ASM2315441v1	95.02
GCA_023154415.1_ASM2315441v1	95.02
GCA_023750585.1_ASM2375058v1	95.02
GCF 900075815.1 12082 4 48	95.02
GCF 023752545.1 ASM2375254v1	95.02
GCF_023750585.1_ASM2375058v1	95.02
GCF 023154915.1 ASM2315491v1	95.02
GCA 015278715.1 ASM1527871v1	95.01
GCA 018597025.1 ASM1859702v1	95.01
GCF_023750405.1_ASM2375040v1	95.01
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GCF 015137655.1 ASM1513765v1	95.00
GCA 021650195.1 ASM2165019v1	95.00
GCA 023151635.1 ASM2315163v1	95.00
GCF 900324475.1 EB-247	95.00
GCA_023153995.1_ASM2315399v1	94.99
GCA_023153995.1_ASM2315399v1	94.99
GCF_023750245.1_ASM2375024v1_genomic.fna	94.99
GCA 019012175.1 ASM1901217v1	94.98
GCA 020042625.1 ASM2004262v1	94.98
GCA 018455145.1 PDT000712937.2	94.98
GCA 021650155.1 ASM2165015v1	94.98
GCA_023154055.1_ASM2315405v1	94.98
GCA_023154055.1_ASM2315405v1	94.98
GCF 900078165.1 11983 7 53	94.98
GCA 015704655.1 ASM1570465v1	94.97
GCA 023151665.1 ASM2315166v1	94.97
GCA_023153835.1_ASM2315383v1	94.97
GCA_023153835.1_ASM2315383v1	94.97
GCA_023752225.1_ASM2375222v1	94.97
GCA 017315445.1 ASM1731544v1	94.96
GCA 018455045.1 PDT000712935.2	94.96
GCA 023152215.1 ASM2315221v1	94.96
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GCA 023151655.1 ASM2315165v1	94.95
GCA 020099255.1 ASM2009925v1	94.94
GCA 023151825.1 ASM2315182v1	94.94

GCA_023153455.1_ASM2315345v1	94.94
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GCA_023153535.1_ASM2315353v1	94.94
GCA 019815185.1_ASM1981518v1	94.93
GCF 023155015.1_ASM2315501v1	94.93
GCA 019351665.1_ASM1935166v1	94.92
GCA 021286605.1_ASM2128660v1	94.92
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GCA 008641915.1_ASM864191v1	94.90
GCA 020097235.1_ASM2009723v1	94.90
GCA 023152155.1_ASM2315215v1	94.90
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GCA 008642035.1_ASM864203v1	94.89
GCF 023154985.1_ASM2315498v1_genomic.fna	94.89
GCA 019046905.1_ASM1904690v1	94.88
GCA 020099235.1_ASM2009923v1	94.87
GCA 018165775.1_PDT001012905.1	94.87
GCA 023151985.1_ASM2315198v1	94.87
GCA 015278695.1_ASM1527869v1	94.86
GCA 001054505.1_ASM105450v1	94.85
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GCA 013366475.1_ASM1336647v1	94.85
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GCA 009647485.1_ASM964748v1	94.84
GCA 013366535.1_ASM1336653v1	94.84
GCA 023152455.1_ASM2315245v1	94.84
GCA_023683925.1_PDT001324297.1	94.84
GCA 013366465.1_ASM1336646v1	94.83
GCA 015684375.1_PDT000538113.1	94.83
GCA_023688005.1_PDT001324324.1	94.83
GCA 013366435.1_ASM1336643v1	94.82
GCA 020673825.1_ASM2067382v1	94.82
GCA 023153335.1_ASM2315333v1	94.82
GCA 021416825.1_ASM2141682v1	94.82
GCA 021649885.1_ASM2164988v1	94.82
GCA_023153955.1_ASM2315395v1	94.82
GCA_023684465.1_PDT001323984.1	94.82
GCA 013403425.1_ASM1340342v1	94.81

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GCF 001022595.1 ASM102259v1	94.78
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GCF 023751985.1 ASM2375198v1	94.77
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GCA 023060615.1 ASM2306061v1	94.75
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GCA 008641635.1 ASM864163v1	94.74
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GCF 025536315.1 ASM2553631v1	94.49
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GCF 025535395.1 ASM2553539v1	94.42
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GCA 010597605.1 ASM1059760v1	92.43
GCA 003964645.1 ASM396464v1	91.04
GCA 001518395.1 ASM151839v1	90.96
GCF 003964255.1 ASM396425v1	90.40
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GCA 002848105.1 ASM284810v1	89.89
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GCF 002890755.1 ASM289075v1	85.65