

## Supporting information

Table S1: Results of the inhibition zone diameter of the isolates against the ten (10) antibiotics

S/N	Code / Isolate	TET	MER	STE	AZT	AXN	OFX	ETN	AZN	CHL	GEN
IZD (mm)											
1	U1	0.0±0.0	0.0 ± 0.0	0.0±0.0	12.0±0.29	0.0±0.0	23.7±0.33	1.0±0.29	0.0±0.0	17.0±0.58	14.0±0.58
2	U2	0.0±0.0	0.0 ± 0.0	0.0±0.0	9.0±0.1155	0.0±0.0	25.0±0.17	0.0±0.0	0.0±0.0	17.0±0.058	12.0±0.173
3	S1	0.0±0.0	5.0±0.12	0.0±0.0	8.0 ± 0.0	0.0±0.0	11.83±0.17	0.0±0.0	10.00±0.12	10.00±0.29	2.76±0.15
4	S2	0.0±0.0	4.33±0.09	0.0±0.0	7.43 ± 0.07	0.0±0.0	12.33±0.33	0.0±0.0	8.83±0.17	10.00±0.0	2.67±0.17
5	P1	0.0±0.0	0.0 ± 0.0	0.0±0.0	0.0 ± 0.0	0.0±0.0	0.0±0.0	0.0±0.0	1.0±0.12	0.0±0.0	2.0 ±0.12
6	P2	0.0±0.0	0.0 ± 0.0	0.0±0.0	0.0 ± 0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	0.0±0.0	2.0±0.17

NB: TET = Tetracycline (30 µg); MER = Meropenem (10 µg); STE = Sulphamethoxazole/Trimethoprim (25 µg); AZT = Azithromycin (15 µg); AXN = Amoxicillin (30 µg); OFX = Ofloxacin (5 µg); ETN = Erythromycin (15 µg); AZN = Aztreonam (30 µg); CHL = Chloramphenicol (30 µg); GEN = Gentamicin (10 µg).

Table S2: CLSI resistance classification of the isolates against the ten (10) antibiotics

Code	TET	MER	STE	AZT	AXN	OFX	ETN	AZN	CHL	GEN	MARI
U1	R	R	R	R	R	S	R	R	I	I	0.7
U2	R	R	R	R	R	S	R	R	S	R	0.8
S1	R	R	R	R	R	R	R	R	R	R	1
S2	R	R	R	R	R	R	R	R	R	R	1
P1	R	R	R	R	R	R	R	R	R	R	1
P2	R	R	R	R	R	R	R	R	R	R	1

NB: R = Resistance; I = Intermediate; TET = Tetracycline (30 µg); MER = Meropenem (10 µg); STE = Sulphamethoxazole/Trimethoprim (25 µg); AZT = Azithromycin (15 µg); AXN = Amoxicillin (30 µg); OFX = Ofloxacin (5 µg); ETN = Erythromycin (15 µg); AZN = Aztreonam (30 µg); CHL = Chloramphenicol (30 µg); GEN = Gentamicin (10 µg), MARI = multi-antibiotic-resistant index.

Table S3:

U1 has 89.17% pairwise similarity to *K. aerogenes* strain GB25 (NCBI accession MT664185). The isolated sequences are as follows:

GGAAAAAGCAAAGAGGTTTGTCTTGGTTGGGGAAGGGAAAGCTGGTTATCAAGGAGATGTGTGGCGGACGGGTGAGTAATGTC  
TGGGAAACTGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACCT  
CGGGCCTCTTGCCATCAGATGTGCCAGATGGGATTAGCTAGTAGGCGGGGTAACGGCCACCTAGGCGACGATCCCTAGCTGGTC  
TGAGAGGATGACCAGCCACACTGGAAGTGGAGACACGGCCAGACTCCTACGGGGAGGCAGCAGTGGGGGATTATTGCACAATGG  
GCGCAAGCCTGATGCGGCCATGCCGCGTGGGTTGAGGAAGGCTTTCGGGGTTGTAAAGCACTTTTCAGCGGGGGAGGAAGGGGGT  
ACGGTTAATAAACCGTGGCGGATTGGACGTTCCCCGCAGAAGAAGCACCGGTTAACTCCGTGCCAGCGGCCGGCGGTAATACGGA  
AGGGTGCAACCGTAAATCGGAAATTACTGGCCTAAACCCCCCGGGGGGTCTGTCAGGTTCGGATGTAAAATCCCCGGGTTCCACC  
CTGGGAACTGCTTTCGAAACTGGAGGCTGGAGTCTCGTAGAGGGGGGTAAATTTCCGGGTGGAGGCGGTGAAATGCGTGAGTTTT  
GGAGGGAATACCGGGGGGCAAAGGCCGCCTCCTGGAACAAAGACTGAGCCTCAGGTGCGAAGCTGGTGGGACCAACAGGATAGA  
ATCCCCTGGTAGTCACGCCCAGAACGATGTTCGATTTTGAAGTTGTGCCCTTGAGCGTGGCTTCCGGAGCTACGCGTTAAATCGACC  
CGCCTGGGGTACGGCGCAGGTTAAACTTAAATGAATTGACGGGGGCCCGCCAAAGCGTGGGACATGTGTTAAATTCGCTGCACGG  
GAGGAACCTTCCTTGTCTGATATCCCAGAACCTGACAAGATGCCGTGGTGCCTTCGGAAGTGTGAGAACAGGTGCTG

U2 has 89.75% pairwise similarity to *C. freundii* strain R2A5 (NCBI accession MT103108). The isolated sequence is as follows:

GGGGCCAAAATGGAGAGGTGTGATTTTGGGCTAGGAAAAGGCGAAAAAGGGATAACAATGGGGTTTGGGTGGCGGAGGGTGAGT  
ATGTATGGGACACTACAGGATTTAGCGGGATACTACTGGAAACGGAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGACC  
TTCGGGCCTCTTGATCGGATTTGCCAGATGGGATTAGCTAGGGGTGGGGTAAGGCTCACCTAGGCGACGATCCCTAGCTGGTCT  
GAGAGGATGACCAGCCACCTGGGAACTGAGACACGGTCCAGACTCCTACGGGAAGCAGCAGTGGGGAAATATTGCACAAGGGGC  
GCAAGCCTGATGCAGCCATGCCGCGTGTGTTGAAGAAGGCCTTCGAGTTGAAAAGTACTTTTCGGCGAGGGAGGAAGGCGTGGTGGT  
TAAAAAACCCGCGACGATTGAGGTTACTCGGAAAAAAAAGCACCGGCTTAAATTCGTCGCAAGCGGCCCGGG

S1 has 74.91% pairwise similarity to *S. enterica* strain ZD2 (NCBI accession number ON661792). The isolated sequence is as follows:

GGGTAAACTCTTAGATTTGATCTGGCTCAGGGGCGCTTGAACCCCCCTTAAATTTTTTTCCTGGCCCCAATGCGGTTTTATACCC  
CCTTTTAAATTTTTACAGGGGGAGAAAAACAGTGAAGGACCCTAATACCATATAGTCTCACAAGCCCAATGAGGGAGATTCTC  
GGCCCTCGTGCCCTCAGATGTGCCATATGAGATTATCTAATGTGTGGGATAGCCTCACATCTAGGACACTATCTATATGTGCTGAG  
AGAAGATGCCCCACACTGTGGCAGTGACACGCGGTCCACACTTCCAGGAGAGGGCGGTGTGGAAAATATTGCACTGTGGGCACA  
CCCAGACGCCCCGTTGGCGCGTGTGAGAAAAACCTTCTCGTTGTGAAAACTTTTCGCGGAGGAAAAGGTTATAATTTTAATC  
CTCTTGCA

S2 has 78.93% pairwise similarity with *S. enterica* subsp. *enterica* serovar Brandenburg strain FSIS1607501 (NCBI accession number CP082464). The isolated sequence is as follows:

GGGGCCCTCATTAGGTTGACAGGGTTCAGGGGCGCTGGAAACCCCCCTTAAAGTTTAAACCGGCTCCAGGGGGGTGTGATCACCC  
CCTTAAATTTTTCCACCGGGCCAAGGGGCTGAAATAACAATCCATATCCTTATAGCGTCCCAGACAAAAGGGGGGGCCTTGGGCG

TCTCTTGCTATCAGATGTGCCAGATGGGATTATAGAGTTGGTGGGATAGCGGCACCCATAGGACAAGATCCATATGTGGTCTGAG  
AGTAAGACCACACACAGTGGAAAGTGACACACGGTCCAGACTTCTAGGGGAGGCAGAAGTGGAAATATAGTGAATATGGGAACACG  
TCAGAAGCCCCCATGGCGCGTGTAAAGAAGAACGTTCTCGGGGTAAAAGCTTTTTTCGGGGGGAAGAAGGGATAAACTTAATACCTT  
TGCTT

P1 has 95.82% pairwise similarity to the *E. coli* strain Rizhao\_490\_1 (NCBI accession number MN314233). The isolated sequence is as follows:

GCGGTGCTCCTGAGTATCTTGGTGGACAGGTAGGGGGGCTGGAAACCCCCTTTAAAGTTGAACCCGGCCCCATGGGGGAGTAAT  
GTATGGGAAATGCCTGATGGAGGGGGATAACTACTGGAAACGGTAGCTAATACCGCATAACGTCGCAAGACCAAAGAGGGGGAC  
CTTCGGGCCTCTTGCCATCGGATGTGCCAGATGGGATTAGCTTGTGGTGGGGTAACGGCTCACCTAGGCGACGATCCCTAGCTG  
GTCTGAGAGGATGACCAGCCACACTGGAAGTGAACACGGTCCAGACTCCTACGGGAGGCAGCAGTGGGGGAATATTGCACAATGG  
GCGCAAGCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCAGCGGGGAGGAAGGGAGTAAAG  
TTAATACCTTTGCTCATTGACGTTACCCGCAAAAAAAGCACCCGGCTAACTCCGTGGCAGCAGCCGCGGTAATACGGAGGGTGCAA  
GCGGTAATCGGAATTACTGGGCGTAAAGCGCACGCAGGGCCTTTGTAAACTCAGATGTGAAATCCTGGGGCTCAACCCGGGAAACT  
GCTTCTAATATTGGCCAAGCTTGACTCTCCACAGGGGGGGTTAAATTTCCCGGGTGTAAACCCCGAAAAGGCCTTAAAAATCGGG  
GAAAAAATCCCGGGGCAAAATCCGGCCCCCGGGGAAAAAACCAGGTTTCCAGATCCCAATTTTTCGCCCCACACATTTTAA  
TTAAAAAACCCCTTGTTTTTTTCCCCCCCCGGGGACCCCTCTCCCCCTTGAAAGTTTTCCCCCTTAAACCCCTTGCTTTCCGAACCT  
AACCCCGTTGAAATTTCCCCCCCCCTGGGAAAAAACCCCGGTTGGGTAAAAAATAAAAAATGATTTTCCCGGGGGGCCCCCCCC  
GGTTTTTTTACCATTTTGTTTTTTAAATTTCCCGCCGGGGGGGATAAACACCCCGGGTTTTTTTACATAATCACGGGGGTCTCTCC  
CCAAAATATAAAACCCGCGCTTCTCAAAAAAAGAAGAATACGGGGGGGTGTCTTGTGGGGGGGACTCACATCTATATAAAAA  
GAAAATCTTATTTTTATTTTTTCTTTGCTTTCCCGGGAGGGAAAAAAGAAATCAAACGCAATTCAACACGAGCTGACCGGGACGG  
TCGTC

P2 has 90.27% pairwise similarity to the *E. coli* strain AF1 (NCBI accession number ON653022). The isolated sequence is as follows:

GGGTAATTCATAAAGTGGTCTGGCTCAGGGGGGCTGGAAACCCCCTTTTAATTTTTTCTGGCCCCATGCGCCTTAATGTCCCCCT  
TTATGCCCGATGGCGGGGGATAACTACTGGAACAGTGGCTAATACCGCATAACCCCTACGGACCAAAGGGGGGATCTTCGGAC  
CTCTTGCTATCGGATGGGCCATATGGGATTAGCTAGTTGGTGGGGTAACGGCTCACCAAGGCGACGATCCCTAGCTGGTCTGAGA  
GGATGACCAGCCACACTGGGACTGAGACACGGCCAGACTCCTACGGGAGGCAGCAGTGGGGAAATTTTGGACAATGGGGCGAAA  
GCCTGATGCAGCCATGCCGCGTGTATGAAGAAGGCCTTCGGGTTGTAAAGTACTTTCGGCGGAGAAGAAAAGGAATCCCGTTAAT  
ACCTTAGCCTGCTGACGTTACCCGCGAGAATAAGCACCCGGCTAACTCCGTGCCAGCAGCCGCGGTAATACGGAGGGGTGCAAGCGT  
TAATCGGAATTACTGGGCGTAAAGCGCGCGCAGGCGGTTTTGGAAAGACAGATGTGAAATCCCGGGCTCAACCTTGGAAGTGCAT  
TTTAAACTGGCCAGCTTGAGTCTCGCAGAGGGGGGTAGAATTCCACGTTTAGCGGTGAAATGCTAGATATCGGGAAGAATACCGG  
TGGCGAAGGCGCCCCCTGGGCAAAACTGACGCTCAGGTGCGAAATCTGGGGAGCAAACAAGATTAGATACCCCTGTAGTCCAGC  
CTAAACGATGTCAACATGAAGTTTGGCCCTTGAGCTTAGCTTCCAGT