

Table S1: Primer sequences of *wzi* capsular serotyping and MLST.

Gene	Sequence (5'-3')	Products /bp	annealing temperature /°C
wzi	F: GTGCCGCGAGCGCTTTCTATCTTGGTATTCC R: GAGAGCCACTGGTTCCAGAACTTGACCGC	580	60
rpoB	F: GGCGAAATGGCWGAGAAACCA R: GAGTCTTCGAAGTTGTAACC	1075	50
gapA	F: TGAAATATGACTCCACTCACGG R: CTTCAGAAGCGGCTTTGATGGCTT	662	60
mdh	F: CCCAACTCGCTTCAGGTTTCAG R: CCGTTTTTCCCCAGCAGCAG	756	50
pgi	F: GAGAAAAACCTGCCTGTACTGCTGGC R: CGCGCCACGCTTTATAGCGGTTAAT	566	50
phoE	F: ACCTACCGCAACACCGACTTCTTCGG R: TGATCAGAACTGGTAGGTGAT	602	50
infB	F: CTCGCTGCTGGACTATATTCG R: CGCTTTCAGCTCAAGAACTTC	462	50
tonB	F: CTTTATACCTCGGTACATCAGGTT R: ATTCGCCGGCTGRGCRGAGAG	539	45

Table S2: Primer sequences of virulence genes and resistance genes.

Gene	Sequence (5'-3')	Products /bp	annealing temperature/°C
fimH	F: GTCTACGTTAACCTGACCCCG R: ATTGATAGACAAAGGTGATGCCGAT	781	56
mrkD	F: AAGCTATCGCTGTACTTCCGGCA R: GCGTTGGCGCTCAGATAGG	340	60
uge	F: TCTTCACGCCTTCCTTCACT R: GATCATCCGGTCTCCCTGT	534	53
wabG	F: CTCTGGTGCGGCAGAAAGTAC R: TGGCCGTCGACGATAAACTC	931	52
rmpA	F: ACCCTTTACAGCCAAATTTTCTTGT R: CTGGGCTACCTCTGCTTCATAT	468	52
magA	F: TGATAAGTGGCGGAGATTCTGA R: TGATAAGTGGCGGAGATTCTGA	542	52
iroN	F: GAATGAAACTACCGCCCCCA R: TGTGGAGTGGAGGCGAGATA	1033	54
entB	F: ATTTCTCAACTTCTGGGGC R: AGCATCGGTGGCGGTGGTCA	371	60
iucA	F: GCTTATTTCTCCCCAACCC R: TCAGCCCTTTAGCGACAAG	583	59
kfu	F: GAAGTGACGCTGTTTCTGGC R: TTTCGTGTGGCCAGTGACTC	797	55
allS	F: CTTCAGCAGATAAATGACGGGGTAG R: GTGGGTAAACCGCCATATTTTCC	244	56
ureA	F: GCTGACTTAAGAGAACGTTATG R: GATCATGGCGCTACCT(C/T)A	337	55

blaCTX-M-2	F: AAATGTGCTGCTCCTTTTCGTGAGC R: AGGGTTCGTTGCAAGACAAGACTG	1122	55
blaSHV	F: ATGCGTTATATTCGCCTGTG R: TGCTTTGTTATTCGGGCCAA	747	55
blaTEM	F: TCGCCGCATACACTATTCTCAGAATGA R: ACGCTCACCGGCTCCAGATTTAT	445	55
blaIMP	F: GGAATAGAGTGGCTTAAYTCTC R: GGTTTAAAYAAAACAACCACC	232	55
blaVIM	F: GATGGTGTTTGGTCGCATA R: CGAATGCGCAGCACCAG	390	55
blaOXA-48	F: GCGTGGTTAAGGATGAACAC R: CATCAAGTTCAACCCAACCG	438	55
blaNDM	F: GGTTTGGCGATCTGGTTTTTC R: CGGAATGGCTCATCACGATC	621	55
blaKPC	F: CGTCTAGTTCTGCTGTCTTG R: CTTGTCATCCTTGTTAGGCG	798	55
blaDHA	F: GCCTGTTTGGTGCTCTGA R: GCACGGTTATACGGCTGA	460	55
blaFOX	F: AACATGGGGTATCAGGGAGATG R: CAAAGCGCGTAACCGGATTGG	190	55
oqxA	F: CTCGGCGCGATGATGCT R: CCACTCTTCACGGGAGACGA	392	55
aac(6')-Ib-cr	F: TTGCGATGCTCTATGAGTGGCTA R: CTCGAATGCCTGGCGTGTTT	482	55
qnrA	F: TCAGCAAGCGGATTTCTCA R: GGCAGCACTATTACTCCCA	608	55
gyrA	F: CGCGTACTATACGCCATGAACGTA R: ACCGTTGATCACTTCGGTCAGG	420	55
aadA1	F: TATCCAGCTAAGCGCGAAC R: ATTTGCCGACTACCTTGGT	447	55
aacC2	F: ATGCATACGCGGAAGGCAATAAC R: CTAACCGGAAGGCTCGCAAG	861	55
tetA	F: GTGAAACCCAACATACCCC R: GAAGGCAAGCAGGATGTAG	888	53
tetB	F: CCTCAGCTTCTCAACGCGTG R: GCACCTTGCTGATGACTCTT	634	55
sul1	F: GTGACGGTGTTTCGGCATTCT R: TCCGAGAAGGTGATTGCGCT	779	55
sul2	F: CGGCATCGTCAACATAACCT R: TGTGCGGATGAAGTCAGCTC	721	55
floR	F: TTTGGTCCGCTCTCAGAC R: CGAGAAGAAG(A\G)CGAAGAAG	496	53

Table S3. Analysis of *wzi* Allele Types for 62 *K. pneumoniae* isolates.

wzi allele types	Proportion (%)	No. of isolates from farm			
		Dairy	Chicken	Sheep	Pig
wzi46-KL61KL13-K46K61	8.06	5	0	0	0
wzi42-KL42-K42	6.45	4	0	0	0
wzi31-KL31-K31	6.45	2	2	0	0

wzi21-KL21-K21	4.84	3	0	0	0
wzi50-KL15KL17KL51KL52-K15K17K50K51K52	4.84	3	0	0	0
wzi130-KL58	4.84	3	0	0	0
wzi355-KL114	4.84	0	3	0	0
wzi33-KL64	4.84	2	0	0	1
wzi114-KL30KL2KL8KL111-K30	3.23	2	0	0	0
wzi385-KL22KL37	3.23	2	0	0	0
wzi592	3.23	2	0	0	0
wzi11-KL11-K11	1.61	1	0	0	0
wzi82-KL23KL18KL38-K23	1.61	1	0	0	0
wzi102-K31	1.61	1	0	0	0
wzi135-KL3-K3	1.61	1	0	0	0
wzi162-KL122-K35	1.61	1	0	0	0
wzi202-KL127KL155	1.61	1	0	0	0
wzi216-KL119	1.61	1	0	0	0
wzi274-KL30	1.61	1	0	0	0
wzi354-KL114	1.61	1	0	0	0
wzi447-KL124	1.61	1	0	0	0
wzi464	1.61	1	0	0	0
wzi472	1.61	1	0	0	0
wzi605	1.61	1	0	0	0
wzi645	1.61	1	0	0	0
wzi17-KL7-K7	1.61	0	0	1	0
wzi147-K79	1.61	0	0	1	0
wzi112-KL13KL39-K19	1.61	0	0	1	0
wzi43-KL43-K43	1.61	0	1	0	0
wzi19-KL19-K19	1.61	0	0	0	1
unknowns	14.52	1	5	2	1

Table S4. Analysis of MLST for 62 *K. pneumoniae* isolates.

ST	Proportion (%)	No. of isolates from farm			
		Dairy	Chicken	Sheep	Pig
791	6.45	4	0	0	0
5387	6.45	0	4	0	0
42	4.84	2	0	0	1
49	3.23	2	0	0	0
161	3.23	2	0	0	0
5121	3.23	2	0	0	0
5179	3.23	2	0	0	0
5490	3.23	2	0	0	0
6085	3.23	0	2	0	0
17	1.61	1	0	0	0
60	1.61	1	0	0	0
76	1.61	1	0	0	0
200	1.61	1	0	0	0
290	1.61	1	0	0	0

322	1.61	1	0	0	0
774	1.61	1	0	0	0
776	1.61	1	0	0	0
1066	1.61	1	0	0	0
1337	1.61	1	0	0	0
1524	1.61	1	0	0	0
1540	1.61	1	0	0	0
1644	1.61	1	0	0	0
1832	1.61	1	0	0	0
2108	1.61	1	0	0	0
3030	1.61	1	0	0	0
3071	1.61	1	0	0	0
3839	1.61	1	0	0	0
4426	1.61	1	0	0	0
4568	1.61	1	0	0	0
5056	1.61	1	0	0	0
5154	1.61	1	0	0	0
967	1.61	0	0	0	1
2455	1.61	0	1	0	0
347	1.61	0	0	1	0
4844	1.61	0	0	1	0
unknowns	20.97	5	4	3	1

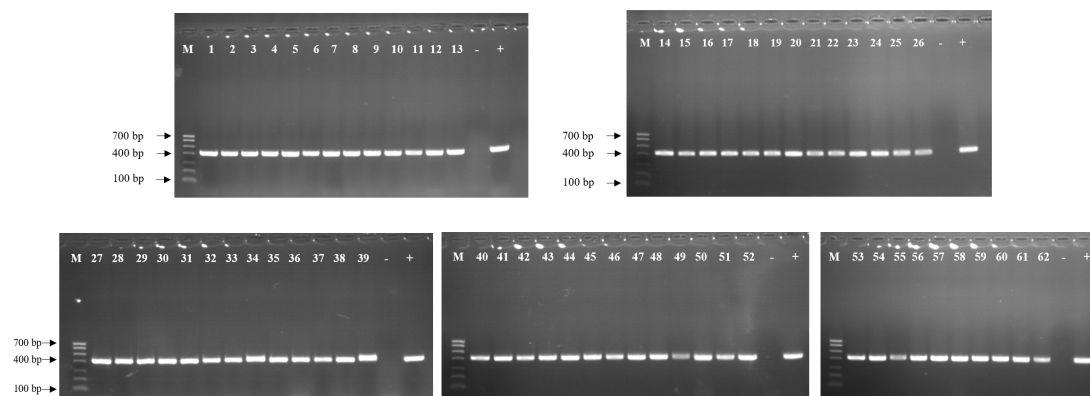


Figure S1: Electrophoresis of PCR products of *khe* gene of 62 isolates. M = molecular weight marker; - = negative control (water); + = positive control (*K. pneumoniae* CMCC 46117); 1-62 = PCR product of the *khe* gene of isolates.

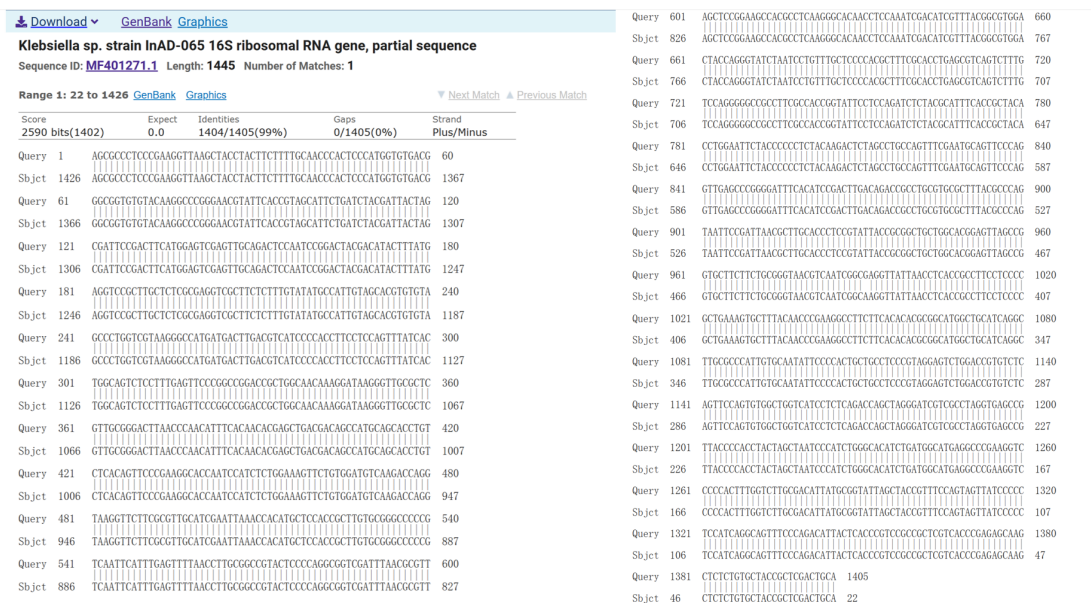


Figure S2. Blast of *K. pneumonia* in the NCBI database