

Supplementary

Dataset S1. Genomes labelled *Klebsiella* in GenBank (accessed by 2021-01-01) and precise species identification.

Dataset S2. Genomes of the *K. oxytoca* complex in GenBank and genes encoding antimicrobial resistance and virulence.

Dataset S3. The 19 of genes unique to *K. oxytoca* complex could be assigned with an existing KEGG orthology (KO) number.

Dataset S4. SNP numbers between genomes belonging to STs seen in at least three countries.

Table S1. Type strains of *Klebsiella* and *Raoultella* species

Table S2. Precise species assignments of the 13,401 genomes labelled *Klebsiella* in NCBI (accessed by 2021-01-01).

Table S3. Genome characteristics of species of *Klebsiella oxytoca* complex, other *Klebsiella* species and *Raoultella* spp.

Table S4. Numbers of *K. oxytoca* complex genomes belonging to each ST.

References

Fig S1. The genetic context of *bla*_{OXY} in the *K. oxytoca* complex species, the corresponding region in *K. pneumoniae* and *K. indica*, and the region of the *K. oxytoca* species corresponding to that containing *bla*_{SHV} in *K. pneumoniae*. A, *bla*_{OXY} and surrounding genes in species of the *K. oxytoca* complex and the corresponding region in *K. pneumoniae* and *K. indica*. In the corresponding chromosomal location of *bla*_{OXY} in *K. oxytoca*, there is a gene encoding a myoinosose 2 dehydratase in *K. pneumoniae* and a gene encoding a transporter of the major facilitator superfamily (MFS). B, the region of the *K. oxytoca* species corresponding to that containing *bla*_{SHV} in *K. pneumoniae*. In *K. pneumoniae*, a 16.1-kb region containing *bla*_{SHV} is located between a gene encoding an AAA family ATPase and a gene encoding the peptidyl-dipeptidase Dcp and is absent from species of the *K. oxytoca* complex and *K. indica*. The corresponding regions species of the *K. oxytoca* complex and *K. indica* vary in genetic components and sizes and have no significant similarity with that of *K. pneumoniae*.

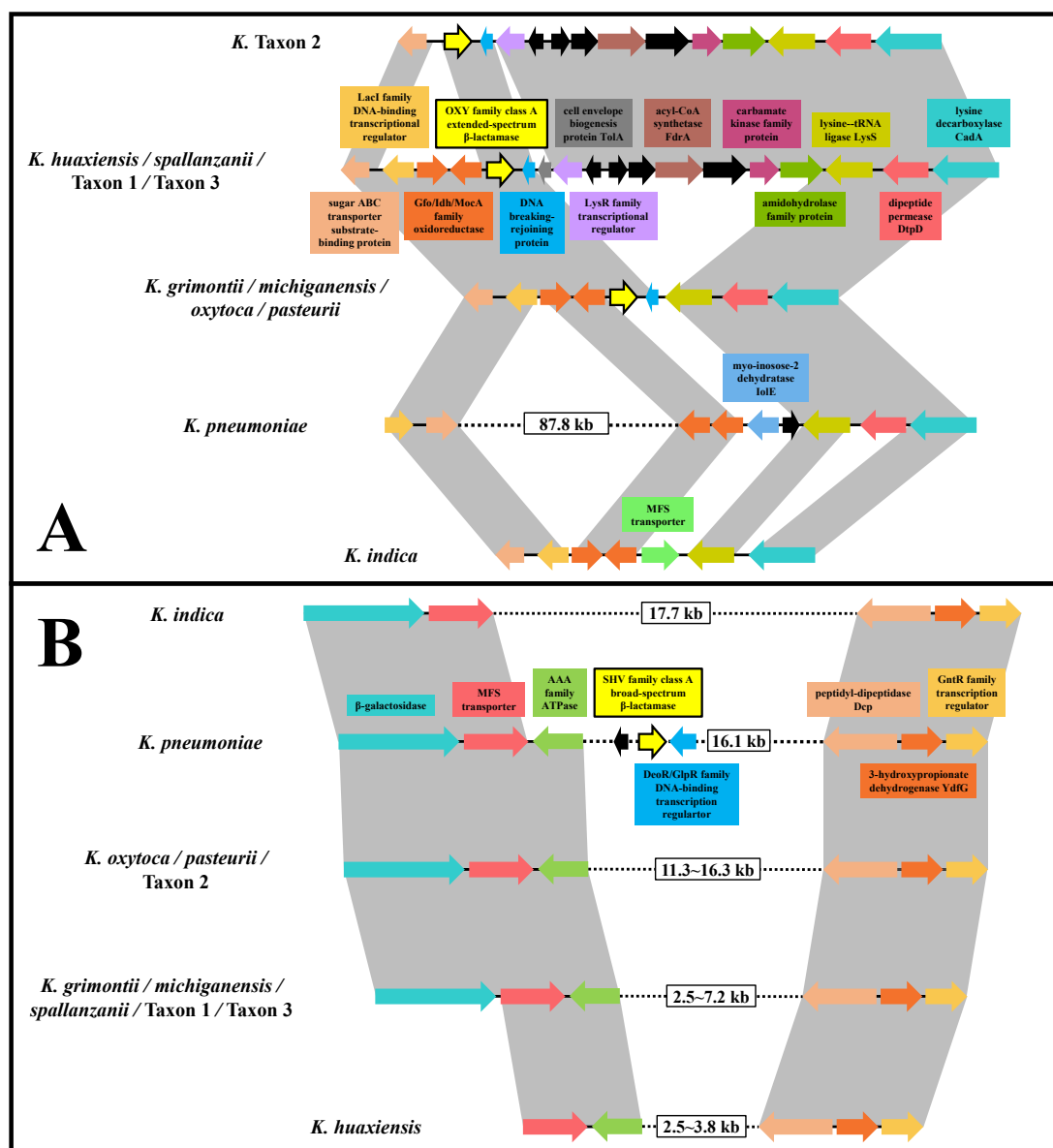


Table S1. Type strains of *Klebsiella* and *Raoultella* species

Species / Taxon	Type or reference strain	Assembly accession no.	Reference
<i>K. aerogenes</i>	KCTC 2190 ^T	GCA_000215745.1	(1)
<i>K. africana</i>	SB5857 ^T	GCA_900978845.1	(2)
<i>K. grimontii</i>	06D021 ^T	GCA_900200035.1	(3)
<i>K. huaxiensis</i>	WCHKI090001 ^T	GCA_003261575.2	(4)
<i>K. indica</i>	TOUT106 ^T	GCA_005860775.1	(5)
<i>K. michiganensis</i>	CCUG 66515 ^T	GCA_009173485.1	(6)
<i>K. oxytoca</i>	NCTC13727 ^T	GCA_900636985.1	(7)
<i>K. pasteurii</i>	SB6412 ^T	GCA_902158725.1	(8)
<i>K. pneumoniae</i>	FDAARGOS_775 ^T	GCA_006364295.1	(9)
<i>K. quasipneumoniae</i>	01A030 ^T	GCA_000751755.1	(10)
<i>K. quasivariicola</i>	KPN1705 ^T	GCA_002269255.1	(11)
<i>K. spallanzanii</i>	SB6411 ^T	GCA_902158555.1	(8)
<i>K. variicola</i>	DSM 15968 ^T	GCA_000828055.2	(12)
Taxon 1	67	GCA_003201885.1	(13)
Taxon 2	P620	GCA_009707385.1	(13)
Taxon 3	RHBSTW-00484	GCA_013705725.1	(13)
<i>R. electrica</i>	DSM 102253 ^T	GCA_006711645.1	(14)
<i>R. ornithinolytica</i>	NBRC 105727 ^T	GCA_001598295.1	(15)
<i>R. planticola</i>	ATCC 33531 ^T	GCA_000735435.1	(15)
<i>R. terrigena</i>	NBRC 14941 ^T	GCA_006539725.1	(15)

Table S2. Precise species assignments of the 13,401 genomes labelled *Klebsiella* in NCBI (accessed by 2021-01-01)

Species ^a	no. of strains
<i>Cedecea genomosp. B</i>	1
<i>Enterobacter cloacae</i>	1
<i>Escherichia coli</i>	1
<i>Klebsiella aerogenes</i>	268
<i>Klebsiella africana</i>	1
<i>Klebsiella grimontii</i>	128
<i>Klebsiella huaxiensis</i>	3
<i>Klebsiella indica</i>	2
<i>Klebsiella michiganensis</i>	233
<i>Klebsiella oxytoca</i>	183
<i>Klebsiella pasteurii</i>	31
<i>Klebsiella pneumoniae</i>	11,451
<i>Klebsiella quasipneumoniae</i>	535
<i>Klebsiella quasivariicola</i>	23
<i>Klebsiella spallanzanii</i>	4
<i>Klebsiella</i> Taxon 1	1
<i>Klebsiella</i> Taxon 2	1
<i>Klebsiella</i> Taxon 3	4
<i>Klebsiella</i> Taxon 4	16
<i>Klebsiella</i> Taxon 5	39
<i>Klebsiella variicola</i>	460
<i>Kluyvera ascorbata</i>	1
<i>Kluyvera genomosp. 2</i>	7
<i>Kosakonia cowanii</i>	1
<i>Raoultella ornithinolytica</i>	3
<i>Raoultella planticola</i>	1
<i>Serratia nevei</i>	1
<i>Superficieibacter electus</i>	1
Total	13,401

^aSpecies of *K. oxytoca* complex are highlighted in bold.

Table S3. Genome characteristics of species of *Klebsiella oxytoca* complex, other *Klebsiella* species, and *Raoultella* spp.^a

	No. of CDS ^a	No. of tRNA ^a	Genome size, bp ^a	GC content, % ^a
<i>Klebsiella oxytoca</i> complex	5,757 [4,542 - 6,902]	75 [24 - 92]	6,190,463 [4,959,239 - 7,227,285]	55 [52.90 - 56.65]
<i>Klebsiella pneumoniae</i> complex	5,242 [4,219 - 6,433]	77 [20 - 115]	5,601,000 [4,571,695 - 6,719,317]	57 [54.73 - 58.63]
<i>Klebsiella aerogenes</i> complex	4,889 [4,519 - 5,591]	72 [24 - 116]	5,281,915 [4,934,573 - 5,833,521]	55 [54.22 - 55.43]
<i>Klebsiella indica</i>	4,688 [4,677 - 4,698]	82 [77 - 86]	5,230,046 [5,215,453 - 5,244,638]	54 [53.51 - 53.53]
<i>Raoultella</i> spp.	5,380 [4,664 - 6,236]	78 [26 - 116]	5,800,232 [5,105,583 - 6,722,439]	56 [54.13 - 58.04]

^aValues are mean [range].

Table S4. Numbers of *K. oxytoca* complex genomes belonging to each ST^a.

ST	No.	ST	No.	ST	No.	ST	No.	ST	No.	ST	No.
1	1	108	5	236	1	375	4	N40	1	N80	6
2	25	109	2	237	2	N1	3	N41	3	N81	1
11	6	127	2	239	2	N2	1	N42	1	N82	1
13	1	135	2	240	1	N3	1	N43	1	N83	2
18	1	138	3	246	3	N4	1	N44	2	N84	1
19	4	141	1	253	1	N5	1	N45	1	N85	1
20	1	143	4	257	1	N6	1	N46	1	N86	2
27	8	144	1	258	4	N7	1	N47	1	N87	1
28	1	145	7	262	1	N8	3	N48	1	N88	1
29	11	146	1	263	8	N9	1	N49	1	N89	1
30	2	151	3	266	1	N10	1	N50	1	N90	1
31	1	153	1	278	4	N11	2	N51	1	N91	1
32	4	157	4	279	1	N12	1	N52	1	N92	2
34	1	168	4	282	1	N13	1	N53	1	N93	1
36	8	170	1	285	1	N14	1	N54	2	N94	2
37	5	172	2	287	1	N15	1	N55	1	N95	1
40	6	176	12	291	1	N16	1	N56	1	N96	1
41	2	177	2	294	1	N17	2	N57	1	N97	1
43	7	179	1	300	1	N18	1	N58	2	N98	1
44	2	180	2	302	1	N19	1	N59	1	N99	1
47	2	181	1	303	1	N20	2	N60	2	N100	1
48	2	182	1	311	3	N21	1	N61	1	N101	1
50	10	183	2	315	1	N22	1	N62	1	N102	1
52	4	184	3	316	1	N23	1	N63	1	N103	3
53	3	185	1	317	2	N24	1	N64	1	N104	1
58	9	186	8	319	1	N25	1	N65	1	N105	1
59	1	193	1	320	1	N26	7	N66	1	N106	1
82	1	199	36	321	1	N27	1	N67	1	N107	1
83	1	200	1	322	1	N28	1	N68	1	N108	1
84	7	202	7	323	1	N29	1	N69	1	N109	4
85	16	205	1	324	4	N30	1	N70	4	N110	1
86	1	213	2	327	1	N31	1	N71	1	N111	1
88	10	215	10	330	1	N32	1	N72	1	N112	1
92	3	216	8	341	1	N33	1	N73	1	N113	1
93	1	221	1	350	2	N34	14	N74	4	N114	1
95	4	222	2	351	5	N35	1	N75	1	N115	1
98	2	223	3	360	1	N36	4	N76	1	N116	1
101	1	225	2	361	5	N37	2	N77	1		
103	1	226	1	364	2	N38	6	N78	2		
104	4	227	1	366	1	N39	1	N79	2		

^aST, the ST number; N1 to N116 are new STs whose numbers have been assigned in the multi-locus sequence typing database (<https://pubmlst.org/organisms/klebsiella-oxytoca>). No., the numbers of genomes for each ST.

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