

Supplemental Material

Limited transmission of *Klebsiella pneumoniae* between humans, animals and the environment in a Caribbean island, Guadeloupe (French West Indies)

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Table S1. Risk factors for *K. pneumoniae* species complex rectal carriage in 185 household and shelter pets from Guadeloupe (French West Indies)

		<i>K. pneumoniae</i> species complex		Univariate analysis		Multivariate analysis
		No	Yes	p-value	OR Brut 95% CI	OR Brut 95% CI
Animal	Cat	40 (40.4)	20 (23.3)	0.013	Réf.	Réf.
	Dog	59 (59.6)	66 (76.7)		2.237 [1.178 - 4.249]	2.231 [1.171 - 4.252]
Sex	Male	44 (44.4)	36 (41.9)	0.723	Réf.	
	Female	55 (55.6)	50 (58.1)		1.111 [0.620 - 1.992]	
Shelter stay	No	90 (90.9)	80 (93.0)	0.599	Réf.	
	Yes	9 (9.1)	6 (7.0)		0.750 [0.256 - 2.200]	
Antibiotic administration \leq 3 months	No	88 (88.9)	70 (81.4)	0.150	Réf.	
	Yes	11 (11.1)	16 (18.6)		1.829 [0.798 - 4.191]	1.818 [0.782 - 4.225]
Chronic disease	No	93 (93.9)	80 (93.0)	0.801	Réf.	
	Yes	6 (6.1)	6 (7.0)		1.163 [0.361 - 3.747]	
Age \geq 20 months	No	50 (51.5)	42 (50.6)	0.899	Réf.	
	Yes	47 (48.5)	41 (49.4)		1.039 [0.578 - 1.866]	
Free wandering outdoor	No	93 (93.9)	79 (91.9)	0.581	Réf.	
	Yes	6 (6.1)	7 (8.1)		1.373 [0.443 - 4.255]	
Contact with other animals	No	97 (98.0)	85 (98.8)	1.000	Réf.	
	Yes	2 (2.0)	1 (1.2)		0.571 [0.051 - 6.404]	

Table S2. Resistance to specific antibiotics in 546 *K. pneumoniae* species complex isolates from Guadeloupe (French West Indies) according to the source

	Humans		Pets		Food-producing animals				Environment					Total n (%)
	Community	Nosocomial	Dog	Cat	Pig	Bovine	Chicken (litter)	Soil	River / Natural pond	Fruits	Vegetables	Condiments	Water catchment	
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	
N	56	223	74	20	30	39	11	14	7	10	42	5	15	546
AMC ^a	6 (10.7)	147 (65.9)	4 (5.4)	2 (10)	3 (10)	2 (5.1)	0 (0)	2 (14.3)	0 (0)	0 (0)	1 (2.4)	0 (0)	0 (0)	167 (30.6)
Cefoxitin	0 (0)	29 (13.0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	29 (5.3)
Cefotaxime	0 (0)	122 (54.7)	0 (0)	1 (5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	123 (22.5)
Ceftazidime	0 (0)	122 (54.7)	0 (0)	1 (5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	123 (22.5)
Cefepim	0 (0)	117 (52.5)	0 (0)	1 (5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	118 (21.6)
Ertapenem	0 (0)	10 (4.5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	10 (1.8)
Nalidixic acid	5 (8.9)	119 (53.4)	0 (0)	1 (5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	125 (22.9)
Ciprofloxacin	4 (7.1)	112 (50.2)	0 (0)	1 (5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	117 (21.4)
Amikacin	0 (0)	20 (9)	0 (0)	1 (5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	21 (3.8)
Gentamicin	0 (0)	95 (42.6)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	95 (17.4)
SXT ^b	5 (8.9)	111 (49.8)	1 (1.4)	1 (5)	3 (10)	0 (0)	2 (18.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	123 (22.5)
ESBL ^c	0 (0)	116 (52.0)	0 (0)	1 (5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	117 (21.4)
CoP ^d	0 (0)	12 (5.4)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	12 (2.2)
Carbapenemase	0 (0)	3 (1.3)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (0.5)
Wild-type phenotype	47 (82.1)	71 (31.8)	69 (93.2)	18 (90)	25 (83.3)	37 (94.9)	9 (81.8)	12 (85.7)	7 (100)	10 (100)	41 (97.6)	5 (100)	15 (100)	365 (66.8)
MDR ^e	0 (0)	112 (50.2)	0 (0)	1 (5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	113 (20.7)

^aAmoxicillin/clavulanic acid, ^bTrimethoprim/sulfamethoxazole, ^cExtended-spectrum β -lactamase, ^dPlasmid-mediated *ampC* gene, ^eMultidrug resistant

Table S3. Species and phylogroups distribution of 433 *K. pneumoniae* species complex isolates from Guadeloupe (French West Indies) according to the source by RT-PCR. Phylogroup typing was performed for all the isolates, except for those recovered in the hospital setting (around 50% were tested)

	Humans		Pets		Food-producing animals				Environment				Total	
	Community	Nosocomial	Dog	Cat	Pig	Bovine	Chicken (litter)	Soil	River / Natural pond	Fruits	Vegetables	Condiments		Water catchment
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)
N	56	110	74	20	30	39	11	14	7	10	42	5	15	433
Kp1	46 (82.1)	99 (90.0)	55 (74.3)	17 (85)	13 (43.3)	2 (5.1)	6 (54.5)	1 (7.1)	2 (28.6)	1 (10)	1 (2.4)	0 (0)	2 (13.3)	245 (56.6)
Kp2	1 (1.8)	2 (1.8)	5 (6.8)	1 (5)	11 (36.7)	13 (33.3)	3 (27.3)	2 (14.3)	1 (14.3)	3 (30)	18 (42.9)	1 (20)	1 (6.7)	62 (14.3)
Kp3/Kp5	2 (3.6)	6 (5.5)	5 (6.8)	1 (5)	4 (13.3)	16 (41)	2 (18.2)	4 (28.6)	4 (57.1)	4 (40)	19 (45.2)	3 (60)	11 (73.3)	81 (18.7)
Kp4	7 (12.5)	3 (2.7)	9 (12.2)	1 (5)	2 (6.7)	8 (20.5)	0 (0)	7 (50)	0 (0)	2 (20)	4 (9.5)	1 (20)	1 (6.7)	45 (10.4)
p	0.09		0.914		<0.001				0.016					

Table S5. Acquired antimicrobial resistance genes in 331 *K. pneumoniae* species complex isolates from Guadeloupe (French West Indies) according to the source

	Humans		Pets		Food-producing animals				Environment					Total
	Community	Nosocomial	Dog	Cat	Pig	Bovine	Chicken (litter)	Soil	River/Natural pond	Fruits	Vegetables	Flowering plants	Water catchment	
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	
N	56	97	45	11	20	31	9	12	7	1	28	8	6	331
<i>arr3</i>	2 (3.6)	8 (8.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	10 (3)
<i>aadA</i> -like	4 (7.1)	18 (18.6)	0 (0)	0 (0)	1 (5)	0 (0)	1 (11.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	24 (7.3)
<i>aac(3')-IId</i>	0 (0)	2 (2.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (0.6)
<i>aac(3)-IIa</i>	0 (0)	45 (46.4)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	45 (13.6)
<i>aac(6')-Ic</i>	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (14.3)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)
<i>aac(6')-Ib</i>	0 (0)	2 (2.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (0.6)
<i>aph(3')-Ia</i>	0 (0)	2 (2.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (0.6)
<i>catA</i> -like	1 (1.8)	7 (7.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	8 (2.4)
<i>catB</i> -like	1 (1.8)	20 (20.6)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	21 (6.3)
<i>cmlA5</i>	0 (0)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)
<i>dfrA</i> -like	6 (10.7)	61 (62.9)	0 (0)	1 (9.1)	1 (5)	0 (0)	1 (11.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	70 (21.1)
<i>mpHA</i>	0 (0)	4 (4.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	4 (1.2)
<i>mgrB</i>	0 (0)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)
Mutations QRDR ¹	4 (7.1)	42 (43.3)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	46 (13.9)
<i>qnrB</i>	2 (3.6)	47 (48.5)	0 (0)	1 (9.1)	0 (0)	0 (0)	1 (11.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	51 (15.4)
<i>strA</i>	2 (3.6)	40 (41.2)	1 (2.2)	1 (9.1)	6 (30)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	50 (15.1)
<i>strB</i>	2 (3.6)	41 (42.3)	1 (2.2)	1 (9.1)	6 (30)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	51 (15.4)
<i>sul1</i>	4 (7.1)	19 (19.6)	0 (0)	0 (0)	1 (5)	0 (0)	2 (22.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	26 (7.9)
<i>sul2</i>	1 (1.8)	42 (43.3)	0 (0)	1 (9.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (12.5)	0 (0)	45 (13.6)
<i>tetA</i>	0 (0)	38 (39.2)	0 (0)	1 (9.1)	1 (5)	0 (0)	2 (22.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	42 (12.7)
<i>tetB</i>	0 (0)	0 (0)	0 (0)	0 (0)	3 (15)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (0.9)

<i>tetC</i>	0 (0)	0 (0)	0 (0)	0 (0)	3 (15)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (0.9)
<i>tetD</i>	4 (7.1)	13 (13.4)	0 (0)	1 (9.1)	1 (5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	19 (5.7)
<i>bla_{OXA-1}</i>	1 (1.8)	47 (48.5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	48 (14.5)
<i>bla_{OXA-9}</i>	0 (0)	2 (2.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (0.6)
<i>bla_{DHA-1}</i>	0 (0)	3 (3.1)	0 (0)	0 (0)	0 (0)	0 (0)	1 (11.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	4 (1.2)
<i>bla_{KPC-2}</i>	0 (0)	2 (2.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (0.6)
<i>bla_{CTX-M-15}</i>	1 (1.8)	57 (58.8)	0 (0)	1 (9.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	59 (17.8)
<i>bla_{SHV12}</i>	0 (0)	3 (3.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (0.9)
No ESBL	0 (0)	56 (57.7)	0 (0)	1 (9.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	57 (17.2)
<i>bla_{TEM}</i>														

¹Quinolone resistance-determining regions in the *gyrA* and *parC* genes

Table S6. Plasmid incompatibility group from 331 *K. pneumoniae* species complex isolates from Guadeloupe (French West Indies) according to the source

	Humans		Pets		Food-producing animals				Environment					Total n (%)
	Community	Nosocomial	Dog	Cat	Pig	Bovine	Chicken (litter)	Soil	River/Natural pond	Fruits	Vegetables	Flowering plants	Water catchment	
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	
N	56	97	45	11	20	31	9	12	7	1	28	8	6	331
ColRNAI	7 (12.5)	25 (25.8)	2 (4.4)	1 (9.1)	2 (10)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	37 (11.2)
ColpVC	0 (0)	2 (2.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (0.6)
IncFIA(HI1)	7 (12.5)	7 (7.2)	8 (17.8)	1 (9.1)	3 (15)	2 (6.5)	2 (22.2)	0 (0)	0 (0)	0 (0)	3 (10.7)	2 (25)	0 (0)	35 (10.6)
IncFIB(AP001918)	1 (1.8)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (0.6)
IncFIB(K)	44 (78.6)	65 (67)	27 (60)	8 (72.7)	15 (75)	4 (12.9)	1 (11.1)	5 (41.7)	1 (14.3)	0 (0)	10 (35.7)	2 (25)	0 (0)	182 (55.0)
IncFIB(Mar)	0 (0)	8 (8.2)	0 (0)	0 (0)	1 (5)	1 (3.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	10 (3.0)
IncFIB(pKPHS1)	4 (7.1)	3 (3.1)	1 (2.2)	0 (0)	3 (15)	2 (6.5)	0 (0)	2 (16.7)	1 (14.3)	0 (0)	0 (0)	2 (25)	1 (16.7)	19 (5.7)
Aph(3')-Ia	0 (0)	2 (2.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (0.6)
IncFIB(pQil)	1 (1.8)	3 (3.1)	1 (2.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	5 (1.5)
IncFII(29)	1 (1.8)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (0.6)
IncFII(p14)	0 (0)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)
IncFII(pCoo)	0 (0)	0 (0)	0 (0)	1 (9.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)
IncFII(pKPX1)	0 (0)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)
IncFII(pRSB107)	0 (0)	0 (0)	0 (0)	0 (0)	1 (5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)
IncFII	10 (17.9)	10 (10.3)	2 (4.4)	1 (9.1)	3 (15)	1 (3.2)	1 (11.1)	1 (8.3)	0 (0)	0 (0)	4 (14.3)	2 (25)	0 (0)	35 (10.6)
IncL/M(pMU407)	0 (0)	0 (0)	0 (0)	2 (18.2)	0 (0)	0 (0)	1 (11.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (0.9)
IncN	2 (3.6)	0 (0)	0 (0)	0 (0)	2 (10)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	4 (1.2)
IncR	12 (21.4)	29 (29.9)	5 (11.1)	2 (18.2)	3 (15)	0 (0)	1 (11.1)	0 (0)	0 (0)	0 (0)	0 (0)	1 (12.5)	0 (0)	53 (16.0)
IncX1	0 (0)	0 (0)	0 (0)	0 (0)	1 (5)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)
IncX3	0 (0)	2 (2.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	2 (0.6)
IncX4	0 (0)	0 (0)	0 (0)	1 (9.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)

Table S7. Virulence genes in 331 *K. pneumoniae* species complex isolates from Guadeloupe (French West Indies) according to the source

	Human		Pets		Food-producing animals				Environment				Total	
	Community	Nosocomial	Dog	Cat	Pig	Bovine	Chicken (litter)	Soil	River/Natural pond	Fruits	Vegetables	Flowering plants		Water catchment
	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)	n (%)		n (%)
N	56	97	45	11	20	31	9	12	7	1	28	8	6	331
Yersiniabactin (<i>ybt</i>)	26 (46.4)	41 (42.3)	7 (15.6)	3 (27.3)	2 (10)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (3.6)	0 (0)	0 (0)	80 (24.2)
<i>ybt</i> 1 ; ICEKp10	4 (7.1)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	5 (1.5)
<i>ybt</i> 12; ICEKp10	3 (5.4)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (0.9)
<i>ybt</i> 10; ICEKp4	7 (12.5)	32 (33)	1 (2.2)	1 (9.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	41 (12.4)
<i>ybt</i> 13; ICEKp2	0 (0)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)
<i>ybt</i> 14; ICEKp5	1 (1.8)	1 (1)	0 (0)	1 (9.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (0.9)
<i>ybt</i> 15; ICEKp11	1 (1.8)	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 (0.3)
<i>ybt</i> 16; ICEKp12	1 (1.8)	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 (0.3)
<i>ybt</i> 17; ICEKp10	4 (7.1)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	5 (1.5)
<i>ybt</i> 2; ICEKp1	0 (0)	0 (0)	3 (6.7)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (0.9)
<i>ybt</i> 4; plasmid	2 (3.6)	2 (2.1)	2 (4.4)	1 (9.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (3.6)	0 (0)	0 (0)	8 (2.4)
<i>ybt</i> 5; ICEKp6	0 (0)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)
<i>ybt</i> 6 ; ICEKp5	1 (1.8)	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 (0.3)
<i>ybt</i> 9; ICEKp3	1 (1.8)	2 (2.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (0.9)
<i>ybt</i> unknown	1 (1.8)	0 (0)	1 (2.2)	0 (0)	2 (10)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	4 (1.2)
colibactin (<i>clb</i>)	12 (21.4)	3 (3.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	15 (4.5)
<i>clb</i> 1	4 (7.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	4 (1.2)
<i>clb</i> 2	4 (7.1)	2 (2.1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	6 (1.8)
<i>clb</i> 3	4 (7.1)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	5 (1.5)
aerobactin (<i>iuc</i>)	12 (21.4)	3 (3.1)	2 (4.4)	0 (0)	3 (15)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	20 (6)
<i>Iuc</i> 1	7 (12.5)	2 (2.1)	1 (2.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	10 (3)
<i>Iuc</i> 2	5 (8.9)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	6 (1.8)

	Human		Pets		Food-producing animals				Environment				Total	
	Community	Nosocomial	Dog	Cat	Pig	Bovine	Chicken (litter)	Soil	River/Natural pond	Fruits	Vegetables	Flowering plants		Water catchment
<i>Iuc 3</i>	0 (0)	0 (0)	1 (2.2)	0 (0)	3 (15)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	4 (1.2)
salmochelinsalmochelin (<i>iro</i>)	12 (21.4)	3 (3.1)	4 (8.9)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	19 (5.7)
<i>iro 1</i>	7 (12.5)	2 (2.1)	1 (2.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	10 (3)
<i>iro 2</i>	5 (8.9)	1 (1)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	6 (1.8)
<i>iro 3</i>	0 (0)	0 (0)	3 (6.7)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	3 (0.9)
<i>rmpA</i>	5 (8.9)	2 (2.1)	2 (4.4)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	9 (2.7)
<i>rmpA2</i>	0 (0)	0 (0)	1 (2.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (0.3)
Allantoinase	4 (7.1)	4 (4.1)	1 (2.2)	0 (0)	0 (0)	2 (6.5)	0 (0)	3 (25)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	14 (4.2)
K1	3 (5.4)	2 (2.1)	1 (2.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	1 (3.6)	0 (0)	0 (0)	7 (2.1)
K2	8 (14.3)	2 (2.1)	1 (2.2)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	0 (0)	11 (3.3)

Supplementary Materials and Methods 1

Detection of individual *Klebsiella pneumoniae* phylogroups by real-time PCR

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In silico identification of candidate genes for phylogroup identification

A collection of 66 reference genomes (Table 1) from Institut Pasteur (n=52) and public databases (n=14), including representatives of Kp1 to Kp6 phylogroups, was used to construct a pangenome with Roary v3.11 (1) using a blastP identity cut-off of 80%, and with core genes being defined as those present in more than 90% of the isolates. From the pangenome, we have selected genes exclusive of each phylogroup (i.e. unique genes for Kp1, Kp2, etc), with a total of 96 candidate target genes being obtained (n=8 for Kp1; n=5 for Kp2, n=32 for Kp3 and Kp5, n=9 for Kp4, n=42 for Kp6). No exclusive genes were found to Kp3, so we selected genes targeting Kp3 and Kp5 simultaneously. Note that Kp7 (*K. africana*) was not discovered at the time of these analyses. The specificity of each candidate was checked using BLAST with customized parameters against: (i) all available *Klebsiella* spp. genomes; and (ii) all available genomes excluding *Klebsiella* spp (NCBI GenBank; last accessed: February 2018). After filtering based on G+C content (retention criteria: between 50% and 60%), 19 candidate target genes were selected.

Distribution of the selected target genes in the *K. pneumoniae* species complex

The phylogenetic distribution of candidate target genes was assessed using a previous genomic collection of 1,001 genomes from NCBI GenBank (February 2018) and Institut Pasteur's internal collection, and which included *Klebsiella* spp. and closely related species (*Raoultella* spp.). The full description of this final collection is described elsewhere (2) Nucleotide BLAST (BLASTN) was used to detect the presence of the target sequences in the 1,001 genomes collection, using 80% nucleotide identity and 80% length coverage as cutoffs. A phylogenetic tree was constructed (3)

and the output visualized using iTOL (4). After visual inspection of the distribution of gene presence across the phylogenetic tree leaves, five candidate genes were selected (Fig. 1).

Table 1. Reference genomes used to obtain the pangenome and to search for specific target genes for each *K. pneumoniae* phylogroup.

Taxonomic Designation (PhG)	Strain Name	Strain bank (SB) ID ^a	Isolation Year	Origin	Source	Country	ST	Accession no.
<i>K. pneumoniae</i> (Kp1)	04A025	SB20	1997	Human	Blood	Paris	15	ERS2786696
	MGH 78578	SB107	1994	Human	Blood	n.a.	38	GCF_000016315.1
	5-2	SB617	2000	Water	Natuurgebied canal	The Netherlands	55	ERS2786695
	-	SB615	2000	Water	n.a.	The Netherlands	62	GCF_020525945.1
	SB4-2	SB1067	2002	Human	Feces	The Netherlands	17	ERS2786693
	-	SB1139	2002	Human	Feces	The Netherlands	37	ERS2786694
	-	SB1170	2002	Human	Feces	The Netherlands	45	GCF_020525645.1
	cur15505	SB2390	2002	Human	Urinary tract	n.a.	14	GCF_000689275.1
	03-9138	SB3332	2003	Human	Anal abscess	Martinique	65	n.a.
	Kp 52.145	SB3341	1935	Human	n.a.	Indonesia	66	GCF_000968155.1
	NTUH-K2044	SB3928	1996	Human	Blood	Taiwan	23	GCF_000009885.1
	CG43	SB4454	n.a.	Human	Liver abscess	Taiwan	86	GCF_000474015.1
	BJ1-GA	SB4496	2011	Human	Liver abscess	France	380	ERS2786698
	T69	SB4536	2010	Human	Liver abscess	France	375	GCF_020525865.1
	Kp13	SB4938	2009	Human	Blood	Brazil	442	GCF_000512165.1
NJST258_1	SB4975	2010	Human	Urinary tract	USA	258	GCF_000598005.1	
<i>K. quasipneumoniae</i> subsp <i>quasipneumoniae</i> (Kp2)	01A030T	SB11	1997	Human	Blood	Austria	1528	GCF_000751755
	18A069	SB59	1997	Human	Blood	Spain	1118	ERS2786701
	Kleb Ali 0320584	SB98	n.a.	n.a.	n.a.	n.a.	622	ERS2786702
	-	SB1124	2002	Water	n.a.	The Netherlands	2274	ERS2786699
	U41	SB2110	1990	Environment	n.a.	Germany	526	ERS2786700
	1214	SB5487	2016	Human	Feces	Madagascar	2507	ERS3557014
	1281	SB5543	2016	Human	Feces	Madagascar	526	ERS3557044

	1284	SB5545	2016	Human	Feces	Madagascar	2604	ERS3557045
	1385	SB5617	2016	Human	Feces	Madagascar	526	ERS3557081
	1392	SB5621	2016	Human	Feces	Madagascar	526	ERS3556845
<i>K. quasipneumoniae</i>	07A044T	SB30	1997	Human	Blood	Germany	1215	GCF_000613225.1
subsp	09A323	SB164	1997	Human	Blood	Greece	414	ERS2786705
<i>similiipneumoniae</i>	12A476	SB203	1998	Human	Blood	Netherlands	384	ERS2786706
(Kp4)	CIP110288	SB4697	n.a.	Environment	Farmland soil	China	2275	ERS2786707
	857	SB5420	2016	Human	Feces	Madagascar	841	ERS3556979
	1196	SB5477	2015	Human	Feces	Madagascar	2503	ERS3556801
	1268	SB5533	2016	Human	Feces	Madagascar	2562	ERS3556843
	1367	SB5607	2016	Human	Feces	Madagascar	1584	ERS3557075
	ATCC 700603	-	1994	Human	n.a.	USA	489	GCF_003181175.1
	HKUOPA4	-	2013	Giant panda	Feces	China	3870	GCF_002240295.1
<i>K. variicola</i> subsp.	01A065	SB1	1997	Human	Blood	Austria	2273	ERS2786703
<i>variicola</i> (Kp3)	F2R9T	SB48	n.a.	Food	Banana	Mexico	2263	ERS2786704
	Kp342	SB579	n.a.	Plant	Maize endophytic diazotroph	USA	146	GCF_000019565.1
	At22	SB4767	n.a.	Environment	Atta cephalotes fungus garden	n.a.	1220	GCF_000025465.1
	806	SB5379	2015	Human	Feces	Madagascar	906	ERS3556874
	869	SB5430	2016	Human	Feces	Madagascar	919	ERS3556984
	1232	SB5505	2016	Human	Feces	Madagascar	2553	ERS3557026
	1355	SB5600	2016	Human	Feces	Madagascar	2594	ERS3557069
	DX120E	-	2008	Environment	Sugarcane root	China	3926	GCF_000812205.2
	Gj1	-	2014	Water	River	South Korea	363	GCF_001989495.1
<i>K. variicola</i> subsp.	CDC 4241-71	SB94	n.a.	Environment	n.a.	n.a.	1216	ERS2786710
<i>tropica</i> (Kp5)	814	SB5387	2015	Human	Feces	Madagascar	2466	ERS2787526

	885	SB5439	2016	Human	Feces	Madagascar	2486	ERS2787527
	1266T	SB5531	2016	Human	Feces	Madagascar	2561	ERS2787528
	1283	SB5544	2016	Human	Feces	Madagascar	2605	ERS2787529
	1375	SB5610	2016	Human	Feces	Madagascar	2600	ERS2787530
	01-436MBV	-	2014	Human	Vaginal swab	Madagascar	3306	n.a.
	02-174MBV	-	2013	Human	Vaginal swab	Madagascar	3316	n.a.
	02-182MBV	-	2013	Human	Vaginal swab	Madagascar	3316	n.a.
	02-846MBV	-	2015	Human	Vaginal swab	Madagascar	3323	n.a.
'K. quasivariicola'	08A119	SB33	1997	Human	Blood	Germany	1214	ERS2786709
(Kp6)	10982	SB6071	2005	Human	Peri-rectal	USA	1155	GCA_000523395.1
	01-467-2ECBU	SB6094	2015	Human	Urinary tract	Madagascar	2830	n.a.
	KPN1705T	SB6096	2014	Human	Wound	USA	209	GCA_002269255.1
	01-467-1ECBU	-	2014	Human	Urinary tract	Madagascar	2830	n.a.
	PO552	-	2009	Human	Blood	Nigeria	3897	GCA_002186515.2
	VRCO0126	-	2014	Environment	Wastewater	United Kingdom	4706	ERR972056
	VRCO0168	-	2015	Environment	n.a.	United Kingdom	4708	ERR1796023
	SAMEA2053849	-	n.a.	n.a.	n.a.	n.a.	2830	ERR319537
	SAMEA2053913	-	n.a.	n.a.	n.a.	n.a.	2830	ERR319550

PhG, phylogroup; ST, sequence-type; n.a., information not available; T, reference strain.

^a Internal strain collection number of the Biodiversity and Epidemiology of Bacterial Pathogens unit, Institut Pasteur.

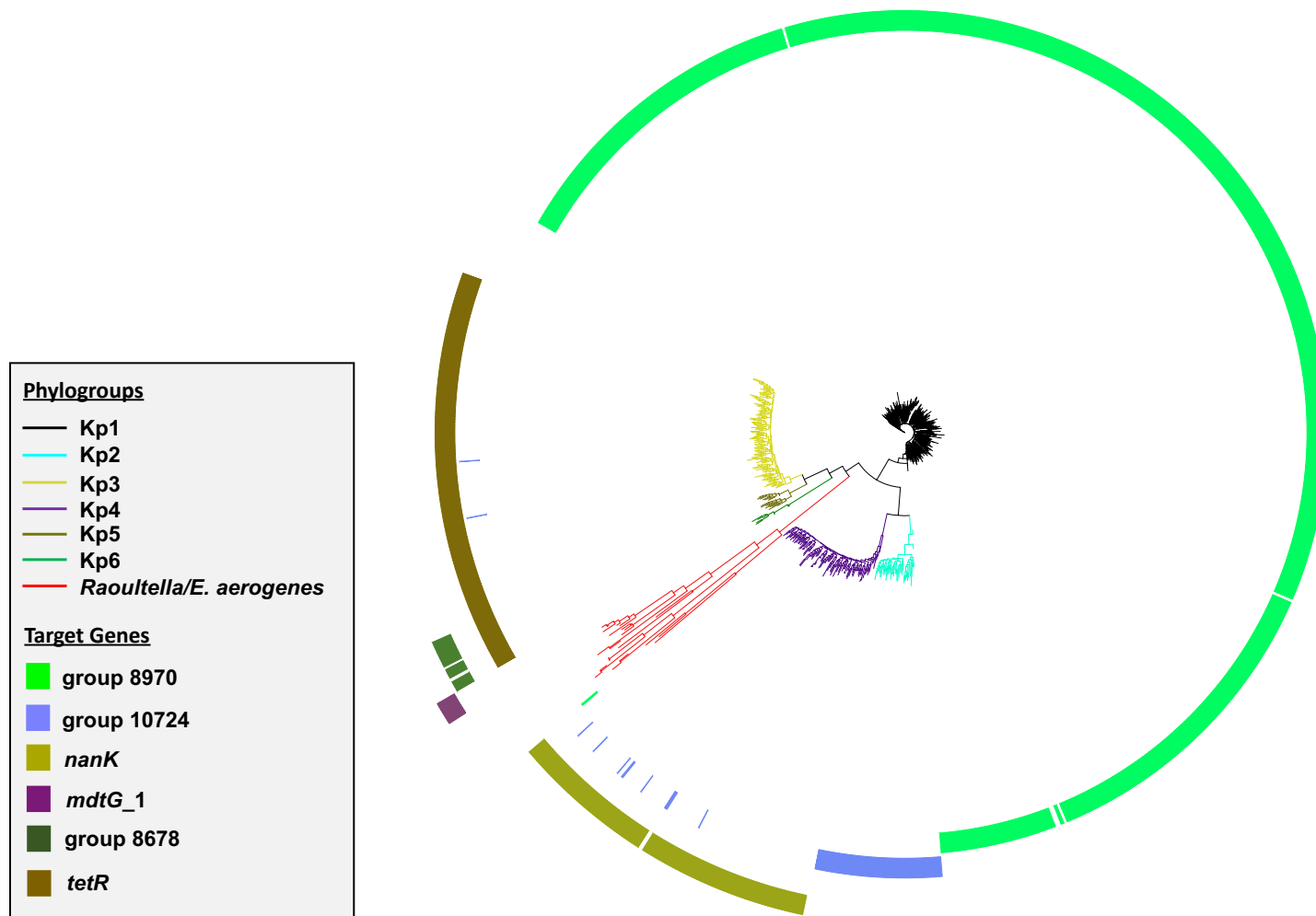


Figure 1. Phylogenetic distribution of the molecular targets selected for the identification of *K. pneumoniae* phylogroups. The branches are colored according to *K. pneumoniae* phylogroups or other closely related species (see color key). Molecular targets were considered as present in the corresponding genomes based on BLASTN, with at least 80% nucleotide identity and 80% length coverage.

Design of primers and probes, and real-time PCR assays

Alignments of the five candidate gene sequences were obtained using Roary. Primers pair and probe targeting each candidate gene were designed using Primer3Plus (<http://www.bioinformatics.nl/cgi-bin/primer3plus/primer3plus.cgi>) (Table 2) and tested *in silico* using BLASTN on the GenBank nucleotide collection from the NCBI database.

All real-time PCR assays were performed on an ABI StepOne real-time thermocycler (Thermo Fischer Scientific) with the following program: 95°C for 3 min and 40 cycles at 95°C 15 s and 60°C for 1 min. For each assay, DNA was amplified in a 20- μ l PCR mix containing 12.5 μ l of Takyon Rox PROBE MasterMix 2x (Eurogentec, Belgium), 1 μ l of each primer (final concentrations, 500 nM), 0.5 μ l of the probe (final concentrations, 250 nM), 2.5 μ l of template DNA, and 2.5 μ l of PCR-grade water. The specificity of the primers and probes was experimentally tested on 2 ng of purified DNA of representatives of 47 KpSC (phylogroups Kp1 to Kp6) and 20 non-*KpSC* strains (Table 3). Concerning Kp1, Kp2, Kp3/Kp5, Kp4 and Kp6 phylogroup identification, the primers and probe amplified the target sequences in all phylogroup-related strains with a threshold cycle (Ct) value ranging from 18 to 27. In contrast, no amplification was observed on non-targeted strains or with Ct above 37 for few isolates. For Kp7 strains, *in silico* analyses showed that Kp7 reference strain (SB5857T) shared 99.05% identity with the *mdtG1* gene (Kp6 target) and 100% identity in the primer and probe sequences. For the remaining Kp7 public genomes (n=9), the same was not observed, *mdtG1* was not detected (at least using 80% nucleotide identity and 80% length coverage) in the genomic sequence, and none of the remaining four phylogroup defined targets was detected. Kp7 DNA amplification was not tested experimentally and this should be the subject of future evaluation when more Kp7 strains are available.

The corresponding protocol was released publicly on protocols.io ([dx.doi.org/10.17504/protocols.io.b4s5qwg6](https://doi.org/10.17504/protocols.io.b4s5qwg6)).

Table 2. Primers and probes designed for KpSC phylogroup identification.

Target phylogroup	Target gene	Forward primer	Reverse primer	Probe	Quencher	Reporter	Amplicon length (bp)
Kp1	group_8970	CCTCAAACACGCCAATA TGC	TACCGCGACGAGTAAAG TGG	GATCCATTGATTCCATTCGAACC GG	BHQ-1	JOE	85
Kp2	group_10724	TTGTTGATTGGCAGGCC TTC	AAATGCTGTGACCACCG TTG	CGCCTGGCGTCAGTGGCCCCGAG C	BHQ-1	JOE	70
Kp3/Kp5	<i>tetR</i>	GCGGGCCGGCTTTTC	CGCATCCCAGGGTATAT TCG	AGGCCGAAGCCGCAATGATATT ACTCA	BHQ-1	FAM	71
Kp4	<i>nanK</i>	AAACAGCGGATGCTCTG AAC	ATGAGTCCGCCAAGATT CTG	ATAGCCTCGACCGGGATTATTCG TGA	BHQ-2	TAMRA	145
Kp6	<i>mdtG_1</i>	GCGTTTCAATGATCCTG TCC	ATCTGCGTCTGGAAAAC AG	GTGCGCTGATTGGTATTGGATAT GGC	BHQ-2	TAMRA	76

Table 3. Bacterial isolates used to test the specificity of the qPCR assays.

Taxon (Phylogroup)	Strain name	Strain bank (SB) ID*	Country	Isolation year
<i>Klebsiella pneumoniae</i> (Kp1)	SB4-2	SB1067	Netherlands	2002
<i>K. pneumoniae</i> (Kp1)	ATCC 13883 ^T	SB132	n.a.	n.a.
<i>K. pneumoniae</i> (Kp1)	MGH 78578	SB107	n.a.	1994
<i>K. pneumoniae</i> (Kp1)	none	SB1139	Netherlands	2002
<i>K. pneumoniae</i> (Kp1)	5-2	SB617	Netherlands	2000
<i>K. pneumoniae</i> (Kp1)	04A025	SB20	France	1997
<i>K. pneumoniae</i> (Kp1)	2-3	SB612	Netherlands	2000
<i>K. pneumoniae</i> (Kp1)	BJ1-GA	SB4496	France	2011
<i>K. pneumoniae</i> (Kp1)	MIAE07651	-	France	2015
<i>K. quasipneumoniae</i> subsp. <i>quasipneumoniae</i> (Kp2)	01A030 ^T	SB11	Austria	1997
<i>K. quasipneumoniae</i> subsp. <i>quasipneumoniae</i> (Kp2)	none	SB1124	Netherlands	2002
<i>K. quasipneumoniae</i> subsp. <i>quasipneumoniae</i> (Kp2)	U41	SB2110	Germany	1990
<i>K. quasipneumoniae</i> subsp. <i>quasipneumoniae</i> (Kp2)	10A442	SB224	Italy	1998
<i>K. quasipneumoniae</i> subsp. <i>quasipneumoniae</i> (Kp2)	99-1002	SB2478	Netherlands	1999
<i>K. quasipneumoniae</i> subsp. <i>quasipneumoniae</i> (Kp2)	18A451	SB255	Spain	1998
<i>K. quasipneumoniae</i> subsp. <i>quasipneumoniae</i> (Kp2)	11128	SB3445	n.a.	n.a.
<i>K. quasipneumoniae</i> subsp. <i>quasipneumoniae</i> (Kp2)	18A69	SB59	Spain	1997
<i>K. quasipneumoniae</i> subsp. <i>quasipneumoniae</i> (Kp2)	Kleb Ali 0320584	SB98	n.a.	n.a.
<i>K. variicola</i> subsp. <i>variicola</i> (Kp3)	01A065	SB1	Austria	1997

<i>K. variicola</i> subsp. <i>variicola</i> (Kp3)	07A058	SB31	Germany	1997
<i>K. variicola</i> subsp. <i>variicola</i> (Kp3)	IPEUC-1516	SB3278	France	1988
<i>K. variicola</i> subsp. <i>variicola</i> (Kp3)	CIP 53.24	SB3295	n.a.	n.a.
<i>K. variicola</i> subsp. <i>variicola</i> (Kp3)	Ørskov 1756/51	SB3301	n.a.	n.a.
<i>K. variicola</i> subsp. <i>variicola</i> (Kp3)	F2R9 ^T	SB48	Mexico	n.a.
<i>K. variicola</i> subsp. <i>variicola</i> (Kp3)	6115	SB489	n.a.	n.a.
<i>K. variicola</i> subsp. <i>variicola</i> (Kp3)	Ørskov 4425/51	SB497	n.a.	n.a.
<i>K. variicola</i> subsp. <i>variicola</i> (Kp3)	Kp342	SB579	USA	n.a.
<i>K. quasipneumoniae</i> subsp. <i>similipneumoniae</i> (Kp4)	09A323	SB164	Greece	1997
<i>K. quasipneumoniae</i> subsp. <i>similipneumoniae</i> (Kp4)	12A476	SB203	Netherlands	1998
<i>K. quasipneumoniae</i> subsp. <i>similipneumoniae</i> (Kp4)	07A044 ^T	SB30	Germany	1997
<i>K. quasipneumoniae</i> subsp. <i>similipneumoniae</i> (Kp4)	325	SB3233	France	1975
<i>K. quasipneumoniae</i> subsp. <i>similipneumoniae</i> (Kp4)	Ørskov 1303/50	SB3297	Turkey	n.a.
<i>K. quasipneumoniae</i> subsp. <i>similipneumoniae</i> (Kp4)	Ørskov 4463/52	SB500	n.a.	n.a.
<i>K. quasipneumoniae</i> subsp. <i>similipneumoniae</i> (Kp4)	CIP 110288	SB4697	China	2010
<i>K. quasipneumoniae</i> subsp. <i>similipneumoniae</i> (Kp4)	1-1	SB610	Netherlands	2000
<i>K. variicola</i> subsp. <i>tropica</i> (Kp5)	Gal12	SB824	Mexico	n.a.
<i>K. variicola</i> subsp. <i>tropica</i> (Kp5)	CDC 4241- 71	SB94	n.a.	n.a.
<i>K. variicola</i> subsp. <i>tropica</i> (Kp5)	885	SB5439	Madagascar	2016
<i>K. variicola</i> subsp. <i>tropica</i> (Kp5)	1266 ^T	SB5531	Madagascar	2016
<i>K. variicola</i> subsp. <i>tropica</i> (Kp5)	1283	SB5544	Madagascar	2016
<i>K. variicola</i> subsp. <i>tropica</i> (Kp5)	1375	SB5610	Madagascar	2016

<i>K. variicola</i> subsp. <i>tropica</i> (Kp5)	814	SB5387	Madagascar	2015
' <i>K. quasivariicola</i> ' (Kp6)	08A119	SB33	Germany	1997
' <i>K. quasivariicola</i> ' (Kp6)	10982	SB6071	USA	2005
' <i>K. quasivariicola</i> ' (Kp6)	01-467- 2ECBU	SB6094	Madagascar	2015
' <i>K. quasivariicola</i> ' (Kp6)	01-310A	SB6095	Madagascar	2013
' <i>K. quasivariicola</i> ' (Kp6)	KPN1705 ^T	SB6096	USA	2014
<i>K. michiganensis</i> (Ko1)	CIP 110787 ^T	SB4934	USA	2010
<i>K. michiganensis</i> (Ko1)	05A071	SB71	France	1997
<i>K. michiganensis</i> (Ko1)	09A029	SB78	Greece	1997
<i>K. grimontii</i> (Ko6)	07A479	SB324	Germany	1998
<i>K. grimontii</i> (Ko6)	06D090	SB352	France	1998
<i>K. grimontii</i> (Ko6)	06D021 ^T	SB73	France	1997
<i>K. oxytoca</i> (Ko2)	ATCC 13182 ^T	SB175	n.a.	n.a.
<i>K. oxytoca</i> (Ko2)	02A067	SB131	Belgium	1997
<i>K. oxytoca</i> (Ko2)	NCTC 49131	SB136	n.a	n.a
<i>K. aerogenes</i>	MIAE07652	-	France	n.a.
<i>K. aerogenes</i>	CIP 60.86 ^T	SB3629	France	n.a.
<i>K. aerogenes</i>	01A089	SB538	Austria	1997
<i>K. aerogenes</i>	02A002	SB539	Belgium	1997
<i>Raoultella terrigena</i>	ATCC 33257 ^T	SB170	n.a.	n.a.
<i>R. terrigena</i>	17C143	SB313	Spain	1998
<i>R. terrigena</i>	V9813596	SB2796	Netherlands	1998
<i>R. planticola</i>	01A041	SB7	Austria	1997
<i>R. planticola</i>	ATCC 33531 ^T	SB174	n.a.	n.a.
<i>R. planticola</i>	12C169	SB303	Netherlands	1998
<i>R. ornithinolytica</i>	ATCC 31898	SB171	n.a.	n.a.

n.a., information not available; T, reference strain.

* Internal strain collection number of the Biodiversity and Epidemiology of Bacterial Pathogens unit, Institut Pasteur.

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