

Capsular serotypes and multilocus sequence types of bacteremic *Klebsiella pneumoniae* isolates associated with different types of infections

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Abstract We investigated the epidemiology of different serotypes of *Klebsiella pneumoniae* isolates causing bacteremic liver abscess (LA) using multilocus sequence typing (MLST). MLST and molecular typing were performed for 41 K1 (19 LA), 37 K2 (5 LA), and 33 non-K1/K2 (6 LA) isolates that were derived from a previous one-year *K. pneumoniae* bacteremia cohort. Capsular serotypes and *rmpA* of these isolates were determined by polymerase chain reaction (PCR) methods. Among the 41 K1 isolates, 39 were ST23 and the remaining two isolates were ST23 single-locus variant. There were 11 STs among K2 isolates. ST65 was the most common ($n=10$), followed by ST86, ST373, and ST375. Only ST65 ($n=3$), ST373 ($n=1$), and ST375 ($n=1$) caused LA, and ST65 was a three-locus variant of ST23. For non-K1/K2 isolates, the ST types varied widely. ST218 (K57) was the most common type ($n=6$, 18 %), and it was a single-locus variant of ST23 and caused two cases of LA. The existences of *rmpA* among serotypes varied (100 % for K1, 89 % for K2, and 55 % for non-K1/K2). For isolates causing LA, all of them were positive for *rmpA*. For non-K1/K2 isolates causing infections other than LA, the positivity of *rmpA* ranged from 0 % (biliary tree infection) to 67 % (pneumonia). In this one-year cohort, all K1 isolates were ST23 or its single-locus variants, but the composition of ST types among K2 isolates was quite variable. ST23 and its one- (ST1005 and ST218) and three-locus (ST65) variants comprised 80 % of isolates causing LA.

Introduction

Since the first report of *Klebsiella pneumoniae* causing liver abscess (LA) in Taiwan [1], there have been many researches focused on this special phenomenon [2–6]. Capsular serotype, both K1 and K2, were found to be an important factor for LA; however, there were some debates about the difference between K1 and K2, mainly the virulence of K2 [2, 4, 5, 7]. Some previous studies also group K1 and K2 together as virulent strains [3–5]. However, in our previous one-year prospective cohort for patients with *K. pneumoniae* bacteremia, we found that K1 was the predominant culprit for LA [8]. K2, in spite of a higher percentage of causing LA compared to non-K1/K2 isolates, the percentage is much lower than K1 (K1 vs. K2 vs. non-K1/K2: 46 % vs. 13 % vs. 4 % in causing LA).

Multilocus sequence typing (MLST) is a tool for strain phylogeny and large-scale epidemiology, and its application for *K. pneumoniae* was introduced in 2005 for nosocomial isolates [9]. The same group further analyzed *K. pneumoniae* isolates collected from different sources and demonstrated that two clones comprising isolates of capsular type K1, ST23 and ST82, were strongly associated with LA and respiratory infection, respectively [10]. On the contrary, only ST65, one of the two major disclosed K2 clones (ST14 and ST65), was highly virulent to mice [10]. These findings correlate well with our clinical observation that the clinical presentations of K2 isolates were much more diverse than K1 [8].

Most of the applications of MLST for *K. pneumoniae* were for drug-resistant strains and only a few reports were available for applying MLST to K1 [9–12]. In one large-scale Asian study, among K1 identified from LA and stool samples, MLST revealed seven sequence types: 85.1 % (40 of 47 isolates) belonged to ST23, one isolate belonged to ST163 (a single-locus variant of ST23), and two isolates were ST249 (a three-locus variant of ST23) [12]. The fecal carriage of K1

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ST23 was also reported in Korea [13]. However, there was limited information about K2 [10, 14].

The different presentations in K1 clones among different regions are interesting [10]. Furthermore, the exact epidemiology of K2 in Taiwan is also of interest. In order to delineate the epidemiology of K1 and K2 and its correlated clinical presentations, we performed MLST typing for all K1 ($n=41$) and K2 ($n=37$) isolates from a one-year cohort of *K. pneumoniae* bacteremia [15], and 33 non-K1/K2 isolates causing different infections (including six isolates causing LA) were also included for comparison.

Methods

Patients and setting

This study was conducted at the Far Eastern Memorial Hospital (FEMH), a 1,040-bed tertiary care facility in northern Taiwan. The identification of *K. pneumoniae* was based on colony morphology and traditional biochemical reaction [16]. The primary sites of bacteremia were determined from information supplied by the primary care physicians and medical records. The diagnosis of an infection focus of bacteremia was based on clinical, bacteriological, and radiological criteria. LA was defined as the coexistence of an intrahepatic abscess revealed by ultrasonography or computed tomography. Pneumonia was defined as a positive culture of *K. pneumoniae* in purulent sputum samples and the presence of newly developed lung infiltrates. Urinary tract infection (UTI) was defined as a positive urine culture and pyuria. Biliary tract infection (BTI) was defined as compatible clinical findings. If no infection focus could be identified, the bacteremia was classified as primary.

Bacterial isolates

In our previous *K. pneumoniae* bacteremia study, among 225 isolates, 41 (18.2 %) were identified as K1 serotype, 37 (16.4 %) as K2, 15 (6.7 %) as K57, and 8 (3.6 %) as K54 [8]. A total of 111 blood isolates of *K. pneumoniae* were included in this study. These included all K1 ($n=41$) and K2 ($n=37$) isolates and 33 non-K1/K2 isolates. All non-K1/K2 isolates ($n=6$) causing LA previously reported were included in this study. The remaining 27 isolates causing pneumonia ($n=9$), primary bacteremia ($n=9$), BTI ($n=5$), and UTI ($n=4$) were randomly selected [8]. Capsular type was determined by polymerase chain reaction (PCR) methods [17].

Molecular typing

All isolates were subjected to MLST according to the protocol described by Diancourt et al. [9]. Briefly, house-keeping genes, including *gapA*, *inf*, *mdh*, *pgi*, *phoE*, *rpoB*, and *tonB*,

were sequenced and compared to the MLST alleles profiles available at <http://www.pasteur.fr/mlst> (Genotyping of Pathogens and Public Health, Institut Pasteur, Paris, France). The detection of *magA* and *rmpA* genes was performed according to the protocol described by Yeh et al. [5].

Pulsed-field gel electrophoresis (PFGE) of XbaI-digested genomic DNAs and random amplified polymorphic DNA (RAPD) patterns of the isolates as determined by means of arbitrarily primed PCR (APPCR) were performed as previously described [18]. For APPCR, a total of four primers were used: A10, 5'-GTGATCGCAT-3'; R16, 5'-CTCTGCGCGT-3'; F4, 5'-GGTATCAGG-3'; and N9, 5'-TGCCGGCTTG-3'.

Results

Among the 111 isolates of *K. pneumoniae*, a total of 39 STs were identified (Tables 1, 2, and 3). The allelic profiles of 12 new STs of *K. pneumoniae* isolates which were not previously reported are shown in Table 4.

Of the 41 isolates with serotype K1, 39 (95.1 %) belonged to ST23, and the remaining two isolates were ST23 single-locus variants (ST1004 and ST1005). Eighteen (46 %) of the ST23 isolates caused LA. There were 11 different STs among the 37 serotype K2 isolates. ST65 ($n=10$, 27 %) was the most common, followed by ST86 ($n=8$, 22 %) and ST373 ($n=7$, 19 %). Three isolates of ST65 and one each of ST373 and ST375 caused LA. ST65 and ST364 were three-locus variants of ST23. All K1 isolates were positive for *magA* and *rmpA*. In addition, all K2 isolates were negative for *magA*, and 33 (89 %) of them were positive for *rmpA* (Table 1).

Table 1 Sequence types (ST) among bacteremic *Klebsiella pneumoniae* isolates with K1 and K2 serotypes

Serotype (no. of isolates)	ST (no. of isolates)	No. (%) of isolates causing liver abscess	No. (%) of isolates with <i>magA</i> gene	No. (%) of isolates with <i>rmpA</i> gene	
K1 (41)	23 (39)	18 (46)	39 (100)	39 (100)	
	1004* (1)	0 (0)	1 (100)	1 (100)	
	1005* (1)	1 (100)	1 (100)	1 (100)	
	K2 (37)	65 (10)	3 (30)	0	10 (100)
		86 (8)	0 (0)	0	7 (88)
373 (7)		1 (14)	0	7 (100)	
375 (3)		1 (33)	0	3 (100)	
76 (2)		0 (0)	0	2 (100)	
814 (2)		0 (0)	0	2 (100)	
15 (1)		0 (0)	0	0 (0)	
337 (1)	0 (0)	0	0 (0)		
364 (1)	0 (0)	0	0 (0)		
1000* (1)	0 (0)	0	0	1 (100)	
1002* (1)	0 (0)	0	0	1 (100)	

*New ST

Table 2 Sequence types (ST) of bacteremic *Klebsiella pneumoniae* isolates associated with liver abscess

Type of infection (no. of isolates)	Serotype	ST (no. of isolates)	<i>rmpA</i> (%)	<i>magA</i> (%)
Liver abscess (30)	K1	23 (18)	100	100
	K1	1005* (1)	100	100
	K2	65 (3)	100	0
	K2	373 (1)	100	0
	K2	375 (1)	100	0
	K57	218 (2)	100	0
	K20	268 (2)	100	0
	Non-K1/K2	660 (1)	100	0
	Non-K1/K2	1049* (1)	100	0

*New ST

There were 30 isolates associated with LA (19 K1, 5 K2, 6 non-K1/K2) (Table 2). For non-K1/K2 isolates causing LA, there were 2 K57/ST218 and 2 K20/ST268. All of them were positive for *rmpA*, regardless of the serotypes, but only K1 isolates were positive for *magA*. K1/ST23 is predominant and

Table 3 Sequence types (ST) of non-K1/K2 isolates associated with different infection sites, including primary bacteremia (*n*=9), pneumonia (*n*=9), biliary infection (*n*=5), and urinary tract infection (*n*=4) (liver abscess isolates not included)

Type of infections (no. of isolates)	ST (no. of isolates)	<i>rmpA</i> (%)
Primary bacteremia (<i>n</i> =9)	48 (2)	0
	660 (2)	100
	14 (1)	0
	218 (1)	100
	268 (1)	100
	420 (1)	100
	994* (1)	0
	1001* (1)	0
Pneumonia (<i>n</i> =9)	218 (3)	100
	29 (1)	100
	35 (1)	0
	36 (1)	100
	364 (1)	0
	592 (1)	100
Biliary infection (<i>n</i> =5)	36 (1)	0
	239 (1)	0
	485 (1)	0
	998* (1)	0
	999 *(1)	0
Urinary tract infection (<i>n</i> =4)	29 (1)	100
	995* (1)	0
	996* (1)	0
	997* (1)	0

*New ST

Table 4 The allelic profiles of 12 new sequence types (ST) of *Klebsiella pneumoniae* isolates reported in this study

Serotype	ST	Allelic profile						
		<i>gapA</i>	<i>inf</i>	<i>mdh</i>	<i>pgi</i>	<i>phoE</i>	<i>rpoB</i>	<i>tonB</i>
K1	1004	2	1	1	1	9	4	59
K1	1005	2	1	1	1	9	4	67
K2	1000	16	45	21	27	47	22	12
K2	1002	43	1	2	1	10	4	67
Non-K1/K2	994	0	2	6	1	1	10	4
Non-K1/K2	995	0	2	6	1	1	1	1
Non-K1/K2	996	0	3	1	2	1	10	4
Non-K1/K2	997	0	4	6	1	1	1	28
Non-K1/K2	998	0	2	1	1	1	12	1
Non-K1/K2	999	0	2	1	2	1	10	1
Non-K1/K2	1001	0	14	3	1	3	3	1
Non-K1/K2	1049	2	3	4	97	12	1	39

comprised 60 % of cases. K1/ST1005 and K57/ST218 were one-locus variants and K2/ST65 was a three-locus variant of ST23. Together, ST23 and its one- and three-locus variants comprised 80 % of isolates causing LA.

MLST was performed for 31 non-K1/K2 isolates (Tables 2 and 3). Compared to K1 and K2, the ST types varied further. K57/ST218 was the most common type (*n*=6, 18 %), causing two cases of LA, three of pneumonia, and one of primary bacteremia, followed by K20/ST268 (*n*=3), causing two cases of LA and one of primary bacteremia. There were two K54/ST29 isolates, associated with UTI and pneumonia. For isolates causing primary bacteremia and bacteremic pneumonia, there were seven ST types for both entities. All five isolates associated with bacteremic BTI and four isolates causing UTI belonged to different ST types. The existence of *rmpA* varied widely among non-K1/K2 isolates (0 % for BTI, 25 % for UTI, 56 % for primary bacteremia, and 67 % for pneumonia).

Among the 111 isolates, a total of 39 PFGE profiles were identified. Isolates possessing the same PFGE profiles had the same RAPD patterns generated by the four random primers. The typing results generated by RAPD and PFGE analysis among the isolates were compatible with those by MLST. The PFGE profiles and RAPD patterns of the isolates exhibiting different serotypes and different STs were different. Isolates with the same ST possessed identical RAPD patterns and pulsotypes.

Discussion

There are several major findings in this study. First, we found that all the K1 isolates were ST23 or a single-locus variant of

ST23. No ST82 was found. In the study of Yeh et al., they demonstrated that K1 strains from both Taiwan and Singapore were of different pulsotypes by PFGE [5]. However, in spite of the different pulsotypes, in this study, we showed that most of the K1 isolates at our institute were of the same ST type. In the report of Siu et al., 85.1 % K1 were ST23, but all LA isolates were ST23 or its variant [12]. In one French report, all the cases of LA were caused by K1/ST23 [14]. Moreover, a US case report showed that K29/ST163 with negative *rmpA* and aerobactin also caused LA. The allelic profile of ST163 was (2, 1, 1, 1, 9, 1, 12), which was a single-locus variant of ST23 [19]. K57, another serotype linked to LA, is also a single-locus variant of ST23 [17]. It is also interesting to find that the virulent K2/ST65 is also a three-locus variant of K1/ST23. These findings could correspond to the finding of Shu et al., showing that the genomic organizations are similar among different pathogenic *K. pneumoniae* strains, in spite of the genetic variation of the capsular polysaccharide [6].

In this study, serotype K2 isolates differed from K1 in several aspects. First, the distribution of STs was quite diverse among serotype K2 isolates. ST65 was the most common sequence type; in contrast to the report by Brisse et al., no ST14 types were found [10]. Interestingly, ST373 and ST375 were isolated from two patients with primary LAs. Both patients had diabetes mellitus and one of them had stroke, but none had known intra-abdominal predisposing factors indicating secondary LA [2]. Décré et al. reported on five patients with invasive infection caused by K2 (2 ST86 and 3 ST380) [14]. None of them had LA (all had positive blood cultures, two had positive sputum cultures, and one had positive CSF culture). In our series, six patients had bacteremic pneumonia caused by serotype K2, and the sequence types were ST65 ($n=2$), ST86 ($n=2$), ST76 ($n=1$), and ST814 ($n=1$). There were reports showing that the significance of K1/K2 on pneumonia was less prominent, as expected, and K2 was more prevalent than K1 for causing community-acquired extrahepatic abscess [20, 21]. More information about the correlation between serotypes and types of infection is needed.

We still do not completely understand the phenomenon of primary LA. Serotype K1 is a major factor, since it comprised 50–60 % of cases and a high prevalence of fecal carriage of K1 was found in endemic Asian countries [2, 12, 13]. However, K1 accounts for only 50–60 % of cases of LA and the role of K2 is under debate [2–8]. One explanation is that LAs caused by isolates other than K1 are secondary LA [2]. The other possibility is that ST23 and its variant with similar origin might also be an important factor, as we demonstrated that ST23 and its variants comprised 80 % of cases.

On the other hand, it is interesting that the prevalence of the *rmpA* gene varied widely among isolates causing different infections. It seems that *rmpA*, which is associated with a hypermucoviscosity phenotype, is associated with invasive infections, regardless of the serotype and sequence type [22].

Brisse et al. also showed that the virulence of *K. pneumoniae* sequence types can be quite different, in spite of having the same serotypes, and that the prevalence of *rmpA* among isolates with different sequence types could be quite varied [10]. In one Taiwanese report on *K. pneumoniae* causing UTI, there was no predominant serotype and the number of isolates harboring the *rmpA* gene was low [23], similar to this study. There was no information about serotypes or the existence of *rmpA* for *K. pneumoniae* isolates causing BTI in the literature, but we are surprised to find that no non-K1/K2 isolates randomly selected carried *rmpA*, which was in strong contrast to isolates causing LA (100 % positive for *rmpA*). Based on the above-mentioned findings, we speculate that sequence type and the existence of the *rmpA* gene might also play significant roles in the pathogenesis of LA, and there is a significant difference among K1/K2 isolates, so they should not be grouped together for analysis.

Since K1/ST23 and K2/ST65 were both virulent and had close ST types [10], we compared the three different loci that they possess in MLST. For *mdh*, ST23 is *mdh1* and ST65 is *mdh2* (nt429, ACC->ACT), and it is a silent mutation. For *phoE*, ST23 is *phoE9* and ST65 is *phoE10*. There are two mutations and both of them were silent mutations (nt54 GCG->GCA; nt372 TAC->TAT). For *tonB*, there were seven mutations; six of them were silent mutations and one was a neutral mutation (nt95 GCG->GTG Ala->Val; nt222 GCA->GCT; nt288 AGT->AGC; nt297 ACC->ACA; nt327 CCG->CCA; nt393 GGG->GGT; nt399 GGC->GGT). We can see that these two ST types were very similar among these important genes. A whole-genome comparison might help clarify the difference between these two virulent strains.

There are several limitations of this study. First, MLST typing and *rmpA* screening were not performed for all isolates of the one-year bacteremia cohort [15]. The major goal of this study is to investigate the role of K1 and K2 causing LA using MLST analysis. Thus, we focus on K1 and K2 and only screen part of the non-K1/K2 isolates. Second, the clinical diagnosis could be wrong or the diagnosis of LA could be missed, but we think that the possibility of this is low, since the epidemic of *K. pneumoniae* causing LA had been noted for years in Taiwan and the awareness of physicians about this disease is high [24]. Third, this is a single-institute experience; whether it could reflect the situation in Taiwan deserves further multicenter surveillance studies. Furthermore, geographic differences in *K. pneumoniae* epidemiology could be anticipated, as in one Australian study, K54 was the most common serotype [25].

In summary, in this one-year bacteremic *K. pneumoniae* cohort, all K1 isolates were ST23 or its single-locus variants, but the composition of ST types among K2 was quite variable. All isolates causing LA were positive for *rmpA*, in contrast to the low *rmpA* positivity among isolates causing UTI and BTI. The molecular epidemiology of *K. pneumoniae* determined with MLST is quite versatile and more information is needed.

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Conflict of interest The authors declare that they have no conflict of interest.

References

- Liu YC, Cheng DL, Lin CL (1986) *Klebsiella pneumoniae* liver abscess associated with septic endophthalmitis. Arch Intern Med 146:1913–1916
- Fang CT, Lai SY, Yi WC, Hsueh PR, Liu KL, Chang SC (2007) *Klebsiella pneumoniae* genotype K1: an emerging pathogen that causes septic ocular or central nervous system complications from pyogenic liver abscess. Clin Infect Dis 45:284–293
- Yu VL, Hansen DS, Ko WC, Sagnimeni A, Klugman KP, von Gottberg A, Goossens H, Wagener MM, Benedi VJ; International *Klebsiella* Study Group (2007) Virulence characteristics of *Klebsiella* and clinical manifestations of *K. pneumoniae* bloodstream infections. Emerg Infect Dis 13:986–993
- Yu WL, Ko WC, Cheng KC, Lee CC, Lai CC, Chuang YC (2008) Comparison of prevalence of virulence factors for *Klebsiella pneumoniae* liver abscesses between isolates with capsular K1/K2 and non-K1/K2 serotypes. Diagn Microbiol Infect Dis 62:1–6
- Yeh KM, Kurup A, Siu LK, Koh YL, Fung CP, Lin JC, Chen TL, Chang FY, Koh TH (2007) Capsular serotype K1 or K2, rather than *magA* and *rmpA*, is a major virulence determinant for *Klebsiella pneumoniae* liver abscess in Singapore and Taiwan. J Clin Microbiol 45:466–471
- Shu HY, Fung CP, Liu YM, Wu KM, Chen YT, Li LH, Liu TT, Kirby R, Tsai SF (2009) Genetic diversity of capsular polysaccharide biosynthesis in *Klebsiella pneumoniae* clinical isolates. Microbiology 155:4170–4183
- Fung CP, Siu LK (2007) Virulence of *Klebsiella pneumoniae* serotype K2 should not be underestimated in *K. pneumoniae* liver abscess. Clin Infect Dis 45:1530–1531
- Liao CH, Huang YT, Lai CC, Chang CY, Chu FY, Hsu MS, Hsu HS, Hsueh PR (2011) *Klebsiella pneumoniae* bacteremia and capsular serotypes, Taiwan. Emerg Infect Dis 17:1113–1115
- Diancourt L, Passet V, Verhoef J, Grimont PA, Brisse S (2005) Multilocus sequence typing of *Klebsiella pneumoniae* nosocomial isolates. J Clin Microbiol 43:4178–4182
- Brisse S, Fevre C, Passet V, Issenhuth-Jeanjean S, Tournebise R, Diancourt L, Grimont P (2009) Virulent clones of *Klebsiella pneumoniae*: identification and evolutionary scenario based on genomic and phenotypic characterization. PLoS One 4:e4982
- Lee CM, Liao CH, Lee WS, Liu YC, Mu JJ, Lee MC, Hsueh PR (2012) Outbreak of *Klebsiella pneumoniae* carbapenemase-2-producing *K. pneumoniae* sequence type 11 in Taiwan in 2011. Antimicrob Agents Chemother 56:5016–5022
- Siu LK, Fung CP, Chang FY, Lee N, Yeh KM, Koh TH, Ip M (2011) Molecular typing and virulence analysis of serotype K1 *Klebsiella pneumoniae* strains isolated from liver abscess patients and stool samples from noninfectious subjects in Hong Kong, Singapore, and Taiwan. J Clin Microbiol 49:3761–3765
- Chung DR, Lee H, Park MH, Jung SI, Chang HH, Kim YS, Son JS, Moon C, Kwon KT, Ryu SY, Shin SY, Ko KS, Kang CI, Peck KR, Song JH (2012) Fecal carriage of serotype K1 *Klebsiella pneumoniae* ST23 strains closely related to liver abscess isolates in Koreans living in Korea. Eur J Clin Microbiol Infect Dis 31:481–486
- Decré D, Verdet C, Emirian A, Le Gourrierec T, Petit JC, Offenstadt G, Maury E, Brisse S, Arlet G (2011) Emerging severe and fatal infections due to *Klebsiella pneumoniae* in two university hospitals in France. J Clin Microbiol 49:3012–3014
- Liao CH, Lai CC, Hsu MS, Huang YT, Chu FY, Hsu HS, Hsueh PR (2009) Correlation between time to positivity of blood cultures with clinical presentation and outcomes in patients with *Klebsiella pneumoniae* bacteraemia: prospective cohort study. Clin Microbiol Infect 15:1119–1125
- Abbott SL (2003) *Klebsiella*, *Enterobacter*, *Citrobacter*, *Serratia*, *Plesiomonas*, and other *Enterobacteriaceae*. In: Murray PR, Baron EJ, Pfaller MA, Tenover FC, Tenover RH (eds) Manual of clinical microbiology, 8th edn. ASM Press, Washington, DC, pp 684–700
- Pan YJ, Fang HC, Yang HC, Lin TL, Hsieh PF, Tsai FC, Keynan Y, Wang JT (2008) Capsular polysaccharide synthesis regions in *Klebsiella pneumoniae* serotype K57 and a new capsular serotype. J Clin Microbiol 46:2231–2240
- Hsueh PR, Wu JJ, Teng LJ, Chen YC, Yang PC, Ho SW, Luh KT (2002) Primary liver abscess caused by one clone of *Klebsiella pneumoniae* with two colonial morphotypes and resistotypes. Emerg Infect Dis 8:100–102
- Abate G, Koh TH, Gardner M, Siu LK (2012) Clinical and bacteriological characteristics of *Klebsiella pneumoniae* causing liver abscess with less frequently observed multi-locus sequences type, ST163, from Singapore and Missouri, US. J Microbiol Immunol Infect 45:31–36
- Lin YT, Jeng YY, Chen TL, Fung CP (2010) Bacteremic community-acquired pneumonia due to *Klebsiella pneumoniae*: clinical and microbiological characteristics in Taiwan, 2001–2008. BMC Infect Dis 10:307
- Ku YH, Chuang YC, Yu WL (2008) Clinical spectrum and molecular characteristics of *Klebsiella pneumoniae* causing community-acquired extrahepatic abscess. J Microbiol Immunol Infect 41:311–317
- Yu WL, Ko WC, Cheng KC, Lee HC, Ke DS, Lee CC, Fung CP, Chuang YC (2006) Association between *rmpA* and *magA* genes and clinical syndromes caused by *Klebsiella pneumoniae* in Taiwan. Clin Infect Dis 42:1351–1358
- Lin WH, Wang MC, Tseng CC, Ko WC, Wu AB, Zheng PX, Wu JJ (2010) Clinical and microbiological characteristics of *Klebsiella pneumoniae* isolates causing community-acquired urinary tract infections. Infection 38:459–464
- Tsai FC, Huang YT, Chang LY, Wang JT (2008) Pyogenic liver abscess as endemic disease, Taiwan. Emerg Infect Dis 14:1592–1600
- Jenney AW, Clements A, Fam JL, Wijburg OL, McGlinchey A, Spelman DW, Pitt TL, Kaufmann ME, Liolios L, Moloney MB, Wesselingh SL, Strugnell RA (2006) Seroprevalence of *Klebsiella pneumoniae* in an Australian tertiary hospital and its implications for vaccine development. J Clin Microbiol 44:102–107