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Klebsiella pneumoniae carriage in low-income countries: antimicrobial resistance, genomic diversity and risk factors

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Abstract

Background

Klebsiella pneumoniae (hereafter, *Kp*) is a major public health threat responsible for high levels of multidrug resistant (MDR) human infections. Besides, Kp also causes severe infections in the community, especially in Asia and Africa. Although most Kp infections are caused by endogenous intestinal carriage, little is known about the prevalence and microbiological characteristics of Kp in asymptomatic human carriage, and attached risk factors including environmental sources exposure.

Methods

Here, 911 pregnant women from communities in Madagascar, Cambodia, and Senegal were screened for gut colonization by Kp. Characteristics of Kp strains (antimicrobial susceptibility, genomic diversity, virulence, and resistance genes) were defined, and associated risk factors were investigated.

Results

Kp carriage rate was 55.9%, and Kp populations were highly heterogeneous (6 phylogroups, 325 sequence types, Simpson index 99.6%). One third of Kp isolates had acquired antimicrobial resistance genes. MDR-Kp (11.7% to 39.7%) and extended spectrum beta-lactamase (ESBL)-producing Kp (0.7% to 14.7%) varied among countries. Isolates with virulence genes were detected (14.5%). Environmental exposure factors including food, animal contacts, or hospitalization of household members were associated with carriage of Kp, antimicrobial resistance and hypervirulence. However, risk factors were country-specific and Kp subpopulation-specific.

Conclusion

This large-scale multicenter study uncovers the huge diversity of Kp in human gut carriage, demonstrates that antimicrobial resistance is widespread in communities of three low-income countries, and underlines the challenges posed by Kp colonization to the control of antimicrobial resistance.

Key words: *Klebsiella pneumoniae,* carriage*,* antibiotic resistance*,* genomic diversity, community, low-income countries

BACKGROUND

Klebsiella pneumoniae (Kp) represents an increasing threat to public health. Kp strains that produce extended spectrum beta-lactamases (ESBLs) and carbapenemases often exhibit cross-resistance to other available agents, and pan-resistant *Klebsiella* are increasingly described.[1] In low-income countries (LICs), Kp is responsible for a large part of early neonatal infections and for severe community-acquired infections.[2] The latter can occur in previously healthy persons and are caused by Kp strains that are regarded as hypervirulent (HV-Kp).[1] In LICs, multidrug resistant (MDR)-Kp is one important driver of unfavorable outcome in infections because appropriate therapy is often not available nor affordable. Worryingly, the convergence of MDR and HV phenotypes in single Kp strains is being increasingly reported.[3]

The taxonomy of Kp has been recently updated, highlighting the existence of five different species distributed in seven phylogroups (Kp1 to Kp7): *K. pneumoniae sensu stricto* (phylogroup Kp1), *K. quasipneumoniae* [subsp. *quasipneumoniae* (Kp2) and subsp. *similipneumoniae* (Kp4)], *K. variicola* [subsp. *variicola* (Kp3) and subsp. *tropica* (Kp5)], '*K. quasivariicola'* (Kp6) and *K. africana* (Kp7).[4] In the manuscript, 'Kp' abbreviation refers to the *K. pneumoniae* species complex ('*sensu lato',* including the five species/seven phylogroups).

Kp is a well-established bacteria of the gut microbiota, and most Kp infections are caused by endogenous strains that previously colonize the host asymptomatically.[5,6] However, Kp carriage has been mostly analyzed within health-care facilities and with a focus on antimicrobial resistant strains. Currently, little is known about naturally occurring human carriage Kp populations, and on the prevalence and diversity of MDR-Kp or HV-Kp among these.

Kp is a ubiquitous bacteria present in animals, environmental sources, and food.[7] Therefore, environmental exposures or behavioral factors may impact individual Kp carriage. Understanding the determinants of Kp carriage may lead to novel strategies to control the spread of this pathogen. To our knowledge, risk factors associated with Kp carriage have not been investigated in the community, nor in LICs.

The objectives of this study were to define the prevalence, antimicrobial resistance, genomic diversity, and virulence potential of Kp isolates carried in pregnant women from three LICs, and to identify risk factors associated with colonization of Kp and its resistant or virulent subpopulations.

METHODS

Study design

This cross-sectional study was nested within the BIRDY program.[8] Briefly, it consists of a cohort of pregnant women and their newborns in Madagascar, Senegal, and Cambodia with an urban and rural site in each country (Figure S1). Pregnant women enrolled between January 2015 and December 2016 were invited to participate in the present *Klebsiella* carriage study. A maternal stool sample was taken at delivery or, in case of home delivery, shortly after delivery. Data on maternal socio-demographic characteristics, medical history, and exposures, possibly related to Kp and its resistant or virulent subpopulations carriage, including dietary habits, antibiotic consumption, and contacts with animals, were collected.

Klebsiella pneumoniae isolation

Stool was retrieved using swabs or stool samples, inoculated in a Luria-Bertani broth with amoxicillin (10 mg/L final concentration) and incubated 18 h at 37°C.[9] The enrichment was performed with amoxicillin because Kp isolates carry a constitutively expressed class A beta-lactamase (of *bla*$_{SHV}$, *bla*$_{OKP}$ or *bla*$_{LEN}$ type) that confers intrinsic resistant to aminopenicillins (such as ampicillin and amoxicillin), whereas many other bacteria including *E. coli* (the most abundant potential competitor) are susceptible to amoxicillin. 100 microliters of the enrichment culture were plated onto selective Simmons citrate with inositol medium agar plates.[10] Large, yellow, glossy colonies suspected of being *Klebsiella* were identified using either API20E or mass spectrometry (MALDI-ToF, Bruker). The first isolate identified as either *Klebsiella pneumoniae* or *Klebsiella variicola* was kept. For 7 carriers, two isolates genetically distinct based on 7-gene MLST were retained.[11]

Antimicrobial susceptibility testing

The susceptibility of Kp isolates to 16 antimicrobial agents (amoxicillin + clavulanic acid, ticarcillin + clavulanic acid, piperacillin + tazobactam, cephalothin, cefotaxime, ceftazidime, cefepime, aztreonam, imipenem, gentamicin, amikacin, tobramycin, nalidixic acid, ciprofloxacin, tetracycline, and trimethoprim + sulfamethoxazole) was defined using the agar disk diffusion method and interpreted according to EUCAST 2015 guidelines, except for cephalothin, nalidixic acid and tetracycline (CLSI M100-S25). ESBL isolates were identified using the double-disk method.

Genomic sequencing and bioinformatics analyses

NextSeq-500 sequencing of Nextera XT 2×150 nt libraries was performed. Genomic assemblies (Table S1) were obtained using SPAdes v3.9.[12] Multilocus sequence typing (MLST) was performed using the BIGSdb-Kp database (https://bigsdb.pasteur.fr).[11,13] This resource was also used for detecting quinolone target genes mutations, and variants of the *wzi* and intrinsic class A beta-lactamases.[13,14] Novel variants were submitted to BIGSdb (for *bla*$_{SHV}$, *bla*$_{OKP}$, and *bla*$_{LEN}$ variants) and to NCBI beta-lactamases database (*bla*$_{SHV-206}$ to *bla*$_{SHV-228}$). Other beta-lactamases and resistance gene families were detected using Kleborate (https://github.com/katholt/Kleborate). Isolates that carried only *bla*$_{\text{SHV}}$ (or *bla*$_{\text{OKP}}$ or *bla*$_{\text{LEN}}$), *fosA* and *oqxAB* genes were considered as having an ancestral resistome. Other antimicrobial resistance genes were considered acquired. To evaluate the correlation between the antimicrobial resistance phenotype and genotype, and to depict co-resistance networks, we constructed a correlation matrix for binary variables (in the case of resistance genes: 1, presence; 0, absence; in the case of antimicrobial drugs: 1, resistant/intermediate; 0, susceptible) using the 'corr.test' function (Pearson method, which for a pair of binary variables equates to the Phi coefficient) from the 'corrplot' R package. Significant correlations were visualized utilizing the 'corrplot' function from the same package.

Plasmids were detected using PlasmidFinder (https://cge.cbs.dtu.dk/services/PlasmidFinder/).[15] Kleborate (https://github.com/katholt/Kleborate) was used to search for yersiniabactin, colibactin, aerobactin, and salmochelin clusters, and to predict the capsular types.[16,17] BIGSdb-Kp was used to define the presence of other virulence-associated genes (Table S1).[18] Isolates harboring at least one of the genes *rmpA* and *rmpA2,* and/or at least one complete gene cluster among *iucABCD-iutA* (aerobactin), *iroBCDN* (salmochelin), *ybtAEPQSTUX-fuyA-irp1-irp2* (yersiniabactin), *clbABCDEFGHIJKLMNOPQR* (colibactin) and *allABCDRS* (allantoinase) were considered virulent. Hypervirulent Kp were defined as isolates harboring at least one of the genes *rmpA* and *rmpA2,* and/or at least one complete gene cluster among *iucABCD-iutA* (aerobactin) and *iroBCDN* (salmochelin). We defined 'high-risk clones' as clones harboring 7-gene MLST sequence types (ST) represented at least 10 times in NCBI genomes (April 2019: 6,258 genomes available) and mentioned in the title or abstract of at least five publications in NCBI PubMed ("Klebsiella" + "pneumoniae" + "STxxx", April 2019).

Phylogenetic and statistical analyses

Genome phylogeny was derived from MASH distances using JolyTree (https://gitlab.pasteur.fr/GIPhy/JolyTree) and visualized using iTOL (https://itol.embl.de/).[19] Unique strains were defined with a ≤ 10 allelic mismatch cutoff within allelic variation recorded using BIGSdb genome comparator function based on the 5,073 protein-coding genes of strain Kp616 (GCA_003076555.1; 90% identity and 90% length coverage).

Statistical analyses were performed using Stata version 15 (Stata Corp., College Station, TX). We defined multidrug resistant (MDR) strains as being resistant to at least one antimicrobial agent in at least 3 antibacterial categories. Chi square or Fisher exact test was used to compare the prevalence of Kp subsets (all, MDR, ESBL) and antibiotic resistance patterns among countries. Risk factor analysis was performed separately for each country given the inter-country variation of the pregnant women's characteristics. We constructed univariate analysis to examine associations between women's environmental exposures, and overall Kp, MDR-, ESBL-, and virulent Kp carriage. All variables with a univariate p-value ≤0.2 were included in multivariate analysis. We used a logistic regression model for all, MDR, and ESBL-Kp subsets. We conducted backwards stepwise elimination of non-significant parameters ($p<0.05$). All multivariate models were adjusted for site (urban/rural). For the seven women from whom 2 Kp were isolated, both were kept in the multivariate analysis; sensitivity analyses performed with and without these duplicates led to identical results. [4,20–22]

Ethics

The study was approved by the ethics committees of Madagascar (068-MSANP/CE), Senegal (SEN 14-20), Cambodia (132 NEHCR) and was authorized by the Institut Pasteur in Paris. Written informed consent was given by all participants.

RESULTS

Kp carriage

A total of 911 pregnant women from Madagascar (n=423), Cambodia (n=152), and Senegal (n=336) were enrolled. For 874 (95.9%) of these, both epidemiological data and a fecal sample were obtained (Figure S2). Women enrolled in the urban sites represented 32.6%, 55.5%, and 35.2% of the total in Madagascar, Cambodia, and Senegal, respectively. The study population (Table 1) was young (mean 27 years; SD 6.4) and underprivileged, as a large majority (79.3%-88.9%) did not complete secondary school and an important fraction did not have toilets within the housing (Madagascar: 93.1%; Cambodia: 49.3%; and Senegal: 29.9%).

Kp colonization was detected in 489 of 874 (55.9%) women. Carriage rate per country (Figure 1A) was significantly lower in Senegal (40.2%, 95% CI [36.3-46.9]; p<0.001) compared to Madagascar (64.7%, CI [59.9-69.2]) and Cambodia (66.4%, [58.3-73.7]). Carriage rate was lower in the urban area than in the rural area (Figure 1A) in Senegal (29.5% *versus* 45.4%, p=0.006) but not in Madagascar (63.6% *versus* 65.2%, p= 0.7) and Cambodia (61.5% *versus* 70.4%, p=0.3).

Kp phylogenetic diversity

Genomic sequence-based phylogenetic relationships (Figure 2) revealed the presence of six deep lineages, corresponding to *K. pneumoniae* phylogroups Kp1 (70.1%), Kp2 (2%), Kp3 (10.7%), Kp4 (15.7%) and Kp5 (2.3%) and a novel phylogroup we named Kp7, described elsewhere as *K. africana*.[4] Kp1 was the most frequent phylogroup in each country (68-73.7%), but phylogroups distribution differed among countries (p<0.001) (Figure 1B): Kp4 was the second most common group in Cambodia and Senegal (27.8% and 20.4%, respectively) but not in Madagascar (Kp3: 17.2%; Kp4: 8.4%).

A remarkably high genotypic diversity was found based on MLST. There were 325 STs, a majority of which (242, 74.5%) were represented by a single isolate (Figure S3). The genotype distribution into multiple low-frequency STs was reflected by a very high (99.6%) Simpson diversity index, even within individual countries or sites (range, 98.7 – 99.7%). High-risk clones (Table S2) represented 70 (14.1%) isolates (Table S3). Among 11 STs with ≥5 isolates, six were high-risk clones and nine were isolated in two or three countries (Figure 1C). However, based on the number of allelic differences between strains within these clonal groups, only two strains were observed in more than one carrier (Figure 1C; Table S1).

Antimicrobial resistance

Antimicrobial resistance rates differed among the three countries (Figure 3A; Table S4). Low levels of resistance were observed for imipenem (0.8%) and amikacin (0.4%). Resistance rates to quinolones (15.5%), other aminoglycosides (17.5%), and third-generation cephalosporins (14.4%) were higher ($p<0.001$) in Cambodia compared to Madagascar (2.7%, 8%, and 10%, respectively) and Senegal (~3% each). ESBL-Kp were almost absent in Senegal (0.7%) but they were frequent in Cambodia (14.4%) and Madagascar (8.4%). MDR-Kp rates were higher in Madagascar (39.7%) compared to Cambodia (25.8%) and Senegal (11.7%; $p<0.001$). Multidrug-resistance was higher in the urban site compared to the rural site only in Cambodia (42.5% vs 14%, $p=0.002$; Table S4). In Cambodia, 10.3% of the isolates were resistant to at least 8 categories of antibiotics. As expected, higher resistance levels were observed for older antibiotics (amoxicillin and ticarcillin with clavulanate, tetracycline, and trimethoprim/sulfamethoxazole).

Comparisons among phylogroups showed differences only in Cambodia, with higher resistance rates against gentamicin and tetracycline in Kp1 ($p=0.04$ and $p=0.006$, respectively; Table S3).

Antimicrobial resistance genes, plasmids and sublineages

As expected, *oqxAB*, *fos*A, and the chromosomal beta-lactamase gene were ubiquitous (Table S3; Figure 3B); 117 variants of the latter were found, with *bla*$_{\text{SHV-11}}$ (n=145, 29.7%) being the most frequent (Figure S4). Remarkably, 334 (67.4%) of isolates had no acquired resistance gene nor any GyrA or ParC alterations, thus corresponding to the ancestral ("wild-type") resistome type. The median number of acquired resistance genes was 3 (similar in each country), ranging from 9 to 11 among ESBL producers. Of the 37 ESBL enzymes, CTX-M-15 was the most common (n=22, 60%). Resistance genes were strongly associated with phenotypic resistance (Figure 3C), and some gene associations were depicted, reflecting their genetic linkage on common genetic platforms (plasmids, transposons, integrons) and resulting in co-resistance phenotypes. For example, *bla*$_{\mathrm{OXA\text{-}1}}$, *aac(6')-Ib-cr*, *catB,* and *qnrB* were associated with *bla*$_{\mathrm{CTX\text{-}M\text{-}15}}$ gene, whereas *bla*$_{\mathrm{LAP\text{-}2}}$, *qnrS,* and *aac(3)-IId* were linked to *bla*$_{\mathrm{CTX\text{-}M\text{-}14/\text{-}27}}$; detection rates for both combinations were higher in Cambodia (Table S5).

Plasmid replicons were found in 70.6%, 73.9%, and 55.5% of Kp from Madagascar, Cambodia, and Senegal, respectively. Twenty-two replicon types were detected (Table S2), of which IncFIB(K) (36.1%), Col440I (27.4%), IncFII (26.4%), IncR (15.9%), and IncFIA(HI1) (15.1%) were the most frequent. However, the predominant type in Senegal was Col440I (31.4%), and plasmid distribution differed among countries ($p<0.001$).

Seventy isolates (14.1%) belonged to widespread genotypes commonly associated with ESBL or carbapenemase production (Table S3). Furthermore, among ESBL-Kp, 19 (51.4%) belonged to previously recognized MDR STs. Although ST307 is emerging as a major carbapenemase-producing sublineage[23,24], our ST307 carriage isolates did not harbor carbapenemase genes.

Virulence genes and convergence with resistance

Seventy-two (14.5%) virulent isolates were found (Figure 1), with yersiniabactin being the most frequent virulence factor (62 isolates, 12.5%; Figure S5; TableS5). The regulator of mucoid phenotype genes *rmpA* and *rmpA2* were present in six isolates (1.2%), whereas aerobactin and salmochelin clusters were present in 14 (2.8%) and 11 (2.2%) isolates, respectively; these hypervirulence-associated clusters were observed mostly in Madagascar and were associated with STs of capsular serotype K2 previously described as hypervirulent [25,26]: ST25, ST65, ST375, and ST380 (Table S3). In contrast, no isolate of the liver abscess-associated serotype K1 ST23 was found.

Virulence and antibiotic resistance elements were generally observed in distinct isolates (Table S3; Figure S6). In particular, aerobactin and salmochelin hypervirulence clusters were associated with ancestral resistome isolates (in Madagascar, p=0.05 and p=0.06, respectively). However, in one urban Cambodian isolate (SB5663, ST17), a convergence of MDR ($\textit{bla}_{\text{CTX-M-27}}$, $\textit{bla}_{\text{LAP-2}}$, *dfrA*, *sul2*, *tetA*, *floR*) and hypervirulence (*rmpA*, yersiniabactin, salmochelin/ICEKp1) was observed (Table S3; Figure S6).

Associations between environmental exposures and specific characteristics of Kp

Risk factors of Kp, MDR, ESBL, and virulent Kp carriage were investigated (Table 2; Table S7). The use of antibiotics during pregnancy was associated with a higher risk of Kp carriage (in Madagascar, adjusted odds ratio (aOR)=2.1; p=0.03), as was dry fish consumption (in Cambodia: aOR=2; p=0.05) and contact with chicken (in Senegal: aOR=1.9; p=0.008). In contrast, hands washing after using toilets (in Madagascar: aOR=0.5; p=0.02), but also manipulating animal excrement (in Madagascar, aOR=0.5; p=0.008), were associated with a reduced risk of Kp carriage.

Among Kp-colonized women, those who reported washing their hands after using toilets (in Madagascar: aOR=0.4; p=0.02), to eat dried meat (in Madagascar: aOR=0.4; p=0.01), or to be in contact with chicken (in Senegal: aOR=0.2; p=0.01) were less at risk of being MDR-Kp colonized. In contrast, women who reported eating raw vegetables at least once per week (in Madagascar: aOR=2.4; p=0.03) were more at risk of being MDR-Kp colonized.

Regarding virulent Kp carriage, hospitalization of a household member in the previous year (in Madagascar: aOR=4.0; p=0.001), consumption of rabbit meat (in Madagascar: aOR=3.6;

p=0.01), and use of fecal material as fertilizer (Senegal: 3.7, p=0.02) were risk factors. In contrast, fish consumption was associated with decreased virulent Kp colonization (Senegal: OR=0.2; p=0.02).

No risk factor for MDR and virulent Kp carriage in Cambodia and for ESBL Kp carriage in the 3 countries were identified.

DISCUSSION

Despite the importance of Kp carriage in the ecology and spread of this pathogen, knowledge on Kp colonization is scarce, especially in LIC communities. In previous carriage studies, other *Enterobacteriaceae* including *E. coli* were considered together with Kp, which represented a minority of studied isolates.[27,28] In addition, previous work focused on ESBL- or carbapenemase-producing *Enterobacteriaceae* carriage, overlooking the natural diversity and ecology of susceptible populations from which resistant strains evolve.

The design of our community-based multicentric study is unique in that the naturally colonizing population of Kp was investigated irrespective of antimicrobial resistance phenotypes, providing insights into the natural ecology of Kp in human carriage. We found that Kp carriage rate per country ranged from 40% to 66%. Kp community carriage studies in high-income countries found carriage rates ranging from 6% to 35%; rates were much higher in one study of Chinese volunteers living in Asian countries.[5–7,29] Although hospitalization is known to increase Kp carriage, our estimates are even higher than the prevalence of Kp carriage reported in hospital settings, typically ranging from 20 to 35%.[5,6,27] Kp abundance in the gut microbiota is low; combining an enrichment step with a *Klebsiella* selective medium may have contributed to recover Kp at higher rates here than in previous studies.[30] Of concern, pregnant women can transmit to their children during delivery or after birth, potentially leading to neonatal sepsis.[31]

Our data demonstrate that Kp1 is the most prevalent phylogroup in all sites. Currently, recognized high-risk clones all belong to Kp1, and this phylogroup is the most frequent in human infections.[26,32] Our results suggest that the clinical predominance of Kp1 might be a direct reflection of the ecological dominance of this group in carriage, rather than to a higher infectious potential compared to other phylogroups. Consistent with this hypothesis, the high rate of Kp4 carriage in Cambodia is mirrored by common Kp4 bloodstream infections in this country.[3]

A striking inter-carrier genetic diversity of Kp was found, with almost three quarters of isolates having a unique ST. Further, genomic sequencing ruled out in all cases except two, the occurrence of recent transmission. Human Kp carriage populations thus appear structured into individual carriers acting as rarely connected islands, favoring evolutionary diversification into a multitude of genotypes.

Kp isolates causing hypervirulent infections belong to recognized sublineages of capsular serotypes K1 and K2, but the source of these infections is poorly known. K1-ST23 was common among Asian healthy carriers.[33] Here, several isolates belonging to hypervirulent K2 sublineages were found, suggesting that the human gut may act as a reservoir of these strains.

Antimicrobial resistance differed among countries, likely reflecting the different levels of antibiotic use, hygiene, and infection control between the 3 countries. The proportion of MDR and ESBL-producing isolates was high in Madagascar and Cambodia. These findings are worrisome, as the gut is a well-known reservoir of infections by these strains.[5,6] Besides, the role of Kp as a source of ESBL genes and other resistance determinants that can be transmitted horizontally to other pathogens is a clear cause of concern.[34] We did not find any carbapenemase-producing Kp, indicating that its spread in the community is still limited in these countries, consistent with low carbapenem consumption.[35]

We were able to investigate for the first time, risk factors associated with natural carriage of Kp and its genetic or phenotypic subpopulations. We found that women who washed their hands after toilets use were less likely to be colonized with Kp or MDR Kp in Madagascar. Hand washing is effective in the transmission of fecal-oral infection in the community, but is often neither properly done nor practiced at key times.[36] Our finding supports that promotion of a simple hygienic behavior could contribute to the control of the spread of antimicrobial resistance in the community.

Consumption of food or contacts with some animals were found associated with Kp, MDR, or virulent Kp carriage. Raw vegetables or rabbit meat (although rabbit meat consumption was low) were associated with a higher risk of being colonized with MDR-Kp or virulent Kp, respectively, suggesting a possible food origin for these isolates. Bacteria can persist on products that are inadequately cooked prior to consumption. However, at which step of the food supply chain these products are contaminated remains an open question. This study calls for more focused investigations of the presence of Kp on food. We also found that manipulating animal excrement and having animal contacts appear protective of Kp and MDR-Kp colonization. One explanation could lie in negative ecological associations between Kp and other bacteria during animal hosts colonization. Future studies on interactions of Kp with the gut microbiota are warranted.

We acknowledge several limitations to this study. Due to the cross-sectional design, the interpretation of the risk factors must be cautious, in particular due to recall bias. Our sample size was not very large, specifically in Cambodia, which might explain that we found few risk factors associated with MDR or virulent Kp. Although the majority of the samples consisted in a stool collection (85%), endorectal swabbing was performed instead when stool was not available. However, previous studies showed that bacterial communities defined from endorectal swabbing and stool specimens are similar. [37,38] In addition, we used an enrichment step that allows the recovery of Kp isolates even when the amount of starting material is low, which could potentially be the case when using rectal swabs.

Human-to-human contact was not investigated in depth here. Characteristics reflecting a potential human transmission (number of household members) were collected and were not significantly associated with Kp carriage. We performed our carriage study in pregnant women, who represent a homogeneous and generally healthy population, with limited socioeconomic status bias. However, the immune system is modified during pregnancy, impacting the gut microbiota.[39] Whether pregnancy has an impact on Kp carriage would require dedicated studies. Finally, food or environmental sampling performed in parallel to human screening would have allowed comparing Kp populations in these niches, possibly leading to their association with human carriage, but these studies will be particularly challenging in light of the huge diversity of Kp revealed herein.[40]

CONCLUSIONS

To conclude, this multicentric study provides the most detailed picture to date of Kp colonization in human LICs communities. One important outcome is the high prevalence of Kp carriage, and high levels of antimicrobial resistance among carriage Kp isolates. Our findings also illustrate the challenges of understanding the transmission dynamics of ubiquitous pathogens. As Kp carriage risk factors were country-dependent, major drivers could not be pointed out, probably reflecting the influence of a complex combination of antibiotic use, hygienic and environmental conditions in the given local context. Consequently, our results suggest that there is “no one size fits all” intervention to tackle the Kp community burden and that public health strategies to control Kp spread may need to be defined based on local specificities.

Competing interest

The authors declare that they have no competing interests.

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Figures

Figure 1. Rates of Kp carriage and genotype diversity.

A. Prevalence of Kp carriage across countries and sites. The difference of prevalence between urban and rural sites was statistically significant in Senegal. CI, confidence interval. **B**. Phylogroup distribution in the three countries. Phylogroup Kp6 was not found; phylogroup Kp7 was only found in one isolate from Senegal. **C**. Frequency and geographic distribution of the most common carriage STs. 1% frequency corresponds to 5 isolates. Urban bar sectors are dotted with white. Within single STs, genome-wide variation ruled-out recent transmission among individual carriers, except in two instances (< 10 allelic mismatches out of 5,073 gene loci) in Madagascar (ST37: urban-rural triplet; ST48: rural pair) represented by oval shapes inside the bar sectors. High-risk clones are represented by an asterisk above the bars.

Figure 2. Phylogenetic relationships.

The scale bar corresponds to 0.01 substitutions per site. iTOL (https://itol.embl.de/) was used to visualize country of origin (circles at branch tips), phylogroups (background color in first circle comprising the isolates names), the ancestral or acquired character of isolates' resistome (second circle), ESBL phenotype (third circle), and virulence genes as indicated in front of each external circle.

Figure 3. **Antimicrobial resistance.**

A. Rates (%) of phenotypic non-susceptibility. ESBL, extended-spectrum beta-lactamases detected by the double-disk synergy test (DDST); IMI, imipenem; AMK, amikacin; GEN, gentamicin; CIP, ciprofloxacin; SXT, trimethoprim-sulfamethoxazole. **B**. Prevalence (%) of resistance genes. **C**. Correlation matrix between antimicrobial resistance genotype and phenotype (Pearson method). Blank squares represent correlations without statistical significance ($p > 0.05$). Positive correlation is depicted by blue circles, whereas red circles represent significant negative correlation. The size and strength of color represent the numerical value of the Phi correlation coefficient. Black boxes represent genes commonly found together in the same strain. The plot was created with the ‘corrplot’ R package. Antimicrobial agents: CEP, cephalothin; TOB, tobramycin; GEN, gentamicin; SXT, trimethoprim-sulfamethoxazole; TET, tetracycline; CAZ, ceftazidime; ATM, aztreonam; CTX, cefotaxime; FEP, cefepime; DDST, double-disk synergy test; CIP, ciprofloxacin; NAL, nalidixic acid; TZP, piperacillin-tazobactam; AMC, amoxicillin-clavulanic acid; TCC, ticarcillin; IMI, imipenem; AMK, amikacin.

Tables

Table 1. Characteristics of the inclusion population

	Madagascar	Cambodia	Senegal	p-value
	N=405	N=146	N=323	
		n (%) or mean (SD)		
Urban Site	132 (32.6)	81 (55.5)	105 (35.2)	<0.001
Age (years)	25.9 (6.4)	27 (5.7)	28 (6.71)	0.08
Gestity				
1	121 (29.9)	48 (32.9)	70 (21.7)	0.04
>1	284 (70.1)	119 (67.1)	253 (78.3)	
Education				
Absence/primary school	90 (22.2)	78 (53.4)	227 (70.3)	<0.001
Partial secondary school	231 (57.0)	50 (34.2)	62 (19.2)	
Complete secondary or higher	84 (20.7)	18 (12.3)	34 (11.1)	
Occupancy				
Unemployed	263 (64.9)	50 (34.3)	258 (79.9)	<0.001
Manual job	129 (31.9)	90 (61.6)	55 (17.0)	
Clerical job	13 (3.2)	6 (4.1)	10 (3.1)	
House characteristics				
Individual housing	135 (33.3)	93 (64.1)	210 (65.0)	<0.001
Housing within a compound	133 (32.8)	30 (20.7)	73 (22.6)	
Accommodation shared with other families	137 (33.8)	22 (15.2)	40 (12.4)	
Electricity	299 (73.8)	145 (99.3)	307 (95.6)	<0.001
Toilets				
Inside the house	28 (6.9)	74 (50.6)	225 (70.2)	<0.001
Outside the house	377 (93.1)	72 (49.3)	96 (29.9)	
Pregnancy follow-up				
Skilled health-care workers	384 (97.2)	142 (97.3)	322 (99.7)	0.02

Table 2. Environmental exposures and colonization with Kp, MDR KP and virulent Kp

	Kpn +	**Kpn -**	**Multivariate analysis***			**MDR Kp**	**non MDR Kp**	**Multivariate analysis***			**Virulent Kp**	**non virulent Kp**	**Multivariate analysis***	
Madagascar														
	N=262 (n, %)	N=143 (n, %)	aOR [95%CI]	p		N=104	N=158	aOR	p		N=34	N=228	aOR	p
Antibiotherapy during pregnancy	42 (16.0)	15(10.5)	2.1 [1.1-4.1]	0.03	**Hand washing after toilets use**	65(70.7)	107(81.1)	0.4 [0.2-0.9]	0.02	**Rabbit meat consumption $$**	7(20.6)	15(6.6)	3.6 [1.3-9.8]	0.01
Hand washing after toilets use	172(76.9)	115(86.4)	0.5 [0.3-0.9]	0.02	**Dry meat consumption $$**	12(11.9)	32(20.9)	0.4 [0.2-0.8]	0.01	**Hospitalization of a household member**	7(20.6)	13(5.8)	4.0 [1.4-11.2]	0.009
Manipulation of animal excrement	35(13.4))	31(21.7)	0.5 [0.2-0.8]	0.008	**Raw vegetables consumption$**	91 (88.4)	128 (82.1)	2.4 [1.1-5.5]	0.03					
Cambodia														
	N=97	N=49	aOR	p										
Dry fish consumption $	51(52.6)	17(34.7)	2.0 [1.0-4.1]	0.05										
Senegal														
	N=137	N=193	aOR	p		N=16	N=121	aOR	p		N=29	N=108	aOR	p
Contact with chicken	82(59.9)	78(40.4)	1.9 [1.2-3.1]	0.008	**Contact with chicken**	5(31.3)	77(63.6)	0.2 [0.06-0.7]	0.01	**Fish consumption $**	23 (79.3)	101(93.5.)	0.2 [0.1-0.8]	0.02
										Use of fecal material as fertilizer	8(27.6)	11(10.2)	3.7 [1.7-11.0]	0.02

. * All multivariate analyses are adjusted on site. Only significant parameters are shown

$ Consumption frequency was categorized as “at least once per week” versus “less than once per week”

$$ Consumption frequency was categorized as “ever” versus “never”

Supplementary data

Table S1. *Klebsiella* isolates and genome sequence information.

Table S2. High-risk clones.

Table S3. Characteristics of the 496 *Klebsiella* isolates: genotypes, antimicrobial susceptibility, capsular types, resistance genes, virulence genes, metal tolerance gene clusters and plasmid replicons.

Table S4. Frequencies of antimicrobial resistance phenotypes among *K. pneumoniae* isolates, by country and site.

Table S5. Frequencies of antimicrobial resistance genes among *K. pneumoniae* isolates, by country and site.

Table S6. Frequencies of virulence-associated genes among *K. pneumoniae* isolates, by country and site.

Table S7. Environmental exposures and colonization with Kp, MDR-Kp and virulent Kp among pregnant women.

Figure S1. Geographical maps with study sites.

Figure S2. Flow charts of inclusion of pregnant women and Kp isolates.

Figure S3. MLST sequence type (ST) diversity.

Figure S4. Diversity of the beta-lactamases-encoding genes (bla_{SHV}, bla_{OKP}, bla_{LEN}).

Figure S5. Rates of virulence clusters or genes, by country of isolation.

Figure S6. Details of presence per isolate of antimicrobial resistance phenotype, and of genes coding for antimicrobial resistance, virulence or plasmid replicons and metal tolerance (MT). Isolates are ordered vertically according to the same phylogeny (left) as in the main phylogeny Figure. ST, sequence type. Note that cluster *kfuABC* was conserved in non-Kp1 isolates but not within Kp1.

Table S1. Klebsiella isolates and their genomic characteristics

Isolate	Species	Phylo-group	ST	Country	Site	Isolation year	from same donor	Unique strain #	Sequencing coverage	No. Contigs	Assembly size (nt)	N50	Accession Number
SB5624	Klebsiella pneumoniae	Kp1	661	Cambodia	Rural	2016			86	72	5340922	316248	ERS3557085
SB5625	Klebsiella pneumoniae	Kp1	2643	Cambodia	Urban	2016			79	44	5107551	292488	ERS3557086
SB5627	Klebsiella pneumoniae	Kp1	2683	Cambodia	Urban	2016			78	78	5482965	243024	ERS3557087
SB5629	Klebsiella pneumoniae	Kp1	111	Cambodia	Rural	2016			49	163	5402739	129791	ERS3557088
SB5632	Klebsiella pneumoniae	Kp1	15	Cambodia	Rural	2016			65	99	5407397	195332	ERS3557091
SB5634	Klebsiella pneumoniae	Kp1	1035	Cambodia	Urban	2016			65	120	5151356	116192	ERS3556883
SB5635	Klebsiella pneumoniae	Kp1	133	Cambodia	Rural	2016			91	63	5371762	217541	ERS3557093
SB5637	Klebsiella pneumoniae	Kp1	2648	Cambodia	Urban	2016			79	92	5529200	199112	ERS3557095
SB5639	Klebsiella pneumoniae	Kp1	883	Cambodia	Urban	2016			85	92	5446274	206771	ERS3557096
SB5640	Klebsiella pneumoniae	Kp1	661	Cambodia	Urban	2016			80	70	5402508	280597	ERS3557097
SB5643	Klebsiella pneumoniae	Kp1	37	Cambodia	Urban	2016			83	70	5399978	204189	ERS3556780
SB5646	Klebsiella pneumoniae	Kp1	1574	Cambodia	Urban	2016			69	55	5269781	250108	ERS3557102
SB5647	Klebsiella pneumoniae	Kp1	2651	Cambodia	Urban	2016			76	64	5385958	312099	ERS3556894
SB5649	Klebsiella pneumoniae	Kp1	2652	Cambodia	Rural	2016			78	54	5244578	224777	ERS3557103
SB5651	Klebsiella pneumoniae	Kp1	2654	Cambodia	Urban	2016			79	66	5271961	293441	ERS3556914
SB5652	Klebsiella pneumoniae	Kp1	307	Cambodia	Urban	2016			71	93	5436326	171620	ERS3556931
SB5653	Klebsiella pneumoniae	Kp1	307	Cambodia	Urban	2016			78	87	5420162	214814	ERS3556932

SB5654	Klebsiella pneumoniae	Kp1	2655	Cambodia	Rural	2016		84	107	5361896	248906	ERS3556822
SB5655	Klebsiella pneumoniae	Kp1	1145	Cambodia	Rural	2016		78	90	5346312	240496	ERS3557105
SB5657	Klebsiella pneumoniae	Kp1	17	Cambodia	Urban	2016		82	47	5062967	271406	ERS3557106
SB5658	Klebsiella pneumoniae	Kp1	35	Cambodia	Rural	2016		68	82	5543682	207586	ERS3557107
SB5659	Klebsiella pneumoniae	Kp1	76	Cambodia	Rural	2016		70	86	5504433	240821	ERS3557108
SB5660	Klebsiella pneumoniae	Kp1	17	Cambodia	Rural	2016		90	32	5070557	297443	ERS3557109
SB5662	Klebsiella pneumoniae	Kp1	394	Cambodia	Urban	2016		90	52	5407929	219809	ERS3556919
SB5663	Klebsiella pneumoniae	Kp1	17	Cambodia	Urban	2016		91	91	5543635	264515	ERS3556903
SB5664	Klebsiella pneumoniae	Kp1	105	Cambodia	Urban	2016		90	39	5163741	295616	ERS3556781
SB5666	Klebsiella pneumoniae	Kp1	200	Cambodia	Rural	2016		91	48	5214665	289243	ERS3557112
SB5668	Klebsiella pneumoniae	Kp1	2706	Cambodia	Rural	2016		92	44	5160021	292030	ERS3557113
SB5672	Klebsiella pneumoniae	Kp1	2709	Cambodia	Rural	2016		89	114	5155751	148981	ERS3556943
SB5673	Klebsiella pneumoniae	Kp1	2710	Cambodia	Rural	2016		91	70	5460208	317648	ERS3557117
SB5675	Klebsiella pneumoniae	Kp1	1782	Cambodia	Rural	2016		89	74	5376631	193102	ERS3556915
SB5676	Klebsiella pneumoniae	Kp1	2711	Cambodia	Rural	2016		91	84	5125733	160797	ERS3556868
SB5680	Klebsiella pneumoniae	Kp1	2713	Cambodia	Rural	2016		69	98	5359302	172998	ERS3556917
SB5681	Klebsiella pneumoniae	Kp1	1662	Cambodia	Rural	2016		74	62	5219300	233701	ERS3557121
SB5682	Klebsiella pneumoniae	Kp1	35	Cambodia	Rural	2016		88	56	5381492	245190	ERS3557122
SB5683	Klebsiella pneumoniae	Kp1	35	Cambodia	Rural	2016		90	59	5415330	240098	ERS3557123
SB5684	Klebsiella pneumoniae	Kp1	35	Cambodia	Rural	2016		80	64	5549627	204833	ERS3557124

SB5686	Klebsiella pneumoniae	Kp1	2690	Cambodia	Urban	2016	96	64	5150093	252822	ERS3556846
SB5687	Klebsiella pneumoniae	Kp1	2691	Cambodia	Rural	2016	96	50	5174574	268291	ERS3557126
SB5688	Klebsiella pneumoniae	Kp1	1662	Cambodia	Rural	2016	96	48	5226977	314174	ERS3557127
SB5690	Klebsiella pneumoniae	Kp1	ND	Cambodia	Rural	2016	94	54	5282590	306163	ERS3557128
SB5692	Klebsiella pneumoniae	Kp1	35	Cambodia	Urban	2016	92	54	5555920	283787	ERS3557130
SB5693	Klebsiella pneumoniae	Kp1	35	Cambodia	Urban	2016	91	55	5557640	285763	ERS3557131
SB5694	Klebsiella pneumoniae	Kp1	2692	Cambodia	Rural	2016	92	97	5437713	148731	ERS3556803
SB5695	Klebsiella pneumoniae	Kp1	34	Cambodia	Urban	2016	94	81	5183897	181968	ERS3556900
SB5696	Klebsiella pneumoniae	Kp1	2693	Cambodia	Urban	2016	94	77	5321489	205650	ERS3557132
SB5698	Klebsiella pneumoniae	Kp1	2504	Cambodia	Urban	2016	94	54	5314104	293448	ERS3556895
SB5699	Klebsiella pneumoniae	Kp1	111	Cambodia	Rural	2016	93	48	5193407	339667	ERS3557134
SB5701	Klebsiella pneumoniae	Kp1	2694	Cambodia	Rural	2016	95	50	5230149	298062	ERS3556847
SB5702	Klebsiella pneumoniae	Kp1	35	Cambodia	Rural	2016	95	73	5434817	258434	ERS3556908
SB5703	Klebsiella pneumoniae	Kp1	35	Cambodia	Urban	2016	95	73	5442485	285425	ERS3556909
SB5705	Klebsiella pneumoniae	Kp1	17	Cambodia	Urban	2016	95	52	5333660	310773	ERS3556918
SB5706	Klebsiella pneumoniae	Kp1	2695	Cambodia	Rural	2016	95	74	5142988	258274	ERS3557136
SB5707	Klebsiella pneumoniae	Kp1	307	Cambodia	Urban	2016	93	57	5316377	307481	ERS3556933
SB5708	Klebsiella pneumoniae	Kp1	307	Cambodia	Rural	2016	92	63	5307325	286380	ERS3556934
SB5712	Klebsiella pneumoniae	Kp1	111	Cambodia	Rural	2016	96	40	5207036	359321	ERS3557140
SB5713	Klebsiella pneumoniae	Kp1	48	Cambodia	Urban	2016	94	112	5379213	179168	ERS3556935

SB5714	Klebsiella pneumoniae	Kp1	1315	Cambodia	Urban	2016	94	102	5348903	152725	ERS3556920
SB5715	Klebsiella pneumoniae	Kp1	76	Cambodia	Urban	2016	93	57	5321869	313319	ERS3556782
SB5716	Klebsiella pneumoniae	Kp1	469	Cambodia	Urban	2016	94	48	5138345	263428	ERS3556901
SB5720	Klebsiella pneumoniae	Kp1	36	Cambodia	Urban	2016	93	47	5211442	318748	ERS3557142
SB5721	Klebsiella pneumoniae	Kp1	774	Cambodia	Rural	2016	94	40	5104795	347891	ERS3557143
SB5722	Klebsiella pneumoniae	Kp1	2701	Cambodia	Urban	2016	94	49	5195511	281539	ERS3557144
SB5723	Klebsiella pneumoniae	Kp1	631	Cambodia	Urban	2016	94	63	5314776	281221	ERS3556916
SB5724	Klebsiella pneumoniae	Kp1	2702	Cambodia	Urban	2016	90	80	5480956	225763	ERS3556869
SB5725	Klebsiella pneumoniae	Kp1	2703	Cambodia	Rural	2016	93	65	5398757	299290	ERS3557145
SB5670	Klebsiella variicola subsp. variicola	Kp3	2645	Cambodia	Rural	2016	88	50	5454754	225824	ERS3557115
SB5678	Klebsiella variicola subsp. variicola	Kp3	2645	Cambodia	Rural	2016	89	41	5446243	264614	ERS3557120
SB5691	Klebsiella variicola subsp. variicola	Kp3	2645	Cambodia	Rural	2016	94	41	5489856	314983	ERS3557129
SB5697	Klebsiella variicola subsp. variicola	Kp3	2645	Cambodia	Urban	2016	95	36	5464940	384747	ERS3557133
SB5626	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2644	Cambodia	Urban	2016	65	74	5282775	264726	ERS3556929
SB5630	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	1770	Cambodia	Urban	2016	72	193	5493483	148255	ERS3557089
SB5631	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2684	Cambodia	Rural	2016	79	38	5120402	368084	ERS3557090
SB5633	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2685	Cambodia	Urban	2016	82	36	5072270	383723	ERS3557092
SB5636	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2686	Cambodia	Urban	2016	84	30	5089222	384645	ERS3557094
SB5638	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	1584	Cambodia	Rural	2016	93	109	5429245	175660	ERS3556799
SB5641	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2689	Cambodia	Rural	2016	84	28	5044032	499401	ERS3557098

SB5642	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2689	Cambodia	Rural	2016		84	29	5043810	390857	ERS3557099
SB5644	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2649	Cambodia	Rural	2016		60	114	5365452	226173	ERS3557100
SB5645	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2650	Cambodia	Rural	2016		73	40	5092929	379605	ERS3557101
SB5648	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	1308	Cambodia	Rural	2016		59	126	5448005	180080	ERS3556867
SB5650	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2653	Cambodia	Rural	2016		73	35	5057265	379105	ERS3557104
SB5656	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2489	Cambodia	Rural	2016		81	121	5136202	144535	ERS3556942
SB5661	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2704	Cambodia	Rural	2016		91	41	5132256	270896	ERS3557110
SB5665	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2705	Cambodia	Urban	2016		89	34	5137797	371558	ERS3557111
SB5669	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2707	Cambodia	Rural	2016		89	47	5209783	394292	ERS3557114
SB5671	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2708	Cambodia	Rural	2016		89	32	5195937	342629	ERS3557116
SB5674	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2653	Cambodia	Rural	2016		90	39	5199048	370553	ERS3557118
SB5677	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2687	Cambodia	Rural	2016		61	89	5500390	248746	ERS3557119
SB5679	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2688	Cambodia	Rural	2016		87	106	5219193	237135	ERS3556944
SB5685	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2696	Cambodia	Urban	2016		96	32	5267118	580124	ERS3557125
SB5700	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	1584	Cambodia	Rural	2016		92	66	5196530	242909	ERS3557135
SB5709	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2697	Cambodia	Rural	2016		97	30	5001814	371361	ERS3557137
SB5710	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2698	Cambodia	Rural	2016		95	45	5078634	356527	ERS3557138
SB5711	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2699	Cambodia	Rural	2016		95	31	5179150	382603	ERS3557139
SB5718	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	1697	Cambodia	Rural	2016		95	86	5167614	172755	ERS3556848
SB5719	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2700	Cambodia	Rural	2016		95	29	5085967	378994	ERS3557141

SB5372	Klebsiella pneumoniae	Kp1	8	Madagascar	Urban	2015	90	76	5178652	206796	ERS3556948
SB5376	Klebsiella pneumoniae	Kp1	1621	Madagascar	Urban	2015	90	55	5330747	338002	ERS3556951
SB5378	Klebsiella pneumoniae	Kp1	1621	Madagascar	Urban	2015	78	64	5323070	288601	ERS3556953
SB5380	Klebsiella pneumoniae	Kp1	70	Madagascar	Urban	2015	86	57	5476561	305068	ERS3556954
SB5382	Klebsiella pneumoniae	Kp1	1621	Madagascar	Urban	2015	83	59	5319369	288601	ERS3556956
SB5383	Klebsiella pneumoniae	Kp1	491	Madagascar	Urban	2015	90	115	5243061	141273	ERS3556957
SB5384	Klebsiella pneumoniae	Kp1	1429	Madagascar	Urban	2015	87	87	5436056	148274	ERS3556958
SB5385	Klebsiella pneumoniae	Kp1	1873	Madagascar	Urban	2015	87	55	5222041	208934	ERS3556959
SB5389	Klebsiella pneumoniae	Kp1	873	Madagascar	Urban	2015	89	65	5416819	257302	ERS3556961
SB5390	Klebsiella pneumoniae	Kp1	111	Madagascar	Urban	2015	50	70	5429342	326979	ERS3556886
SB5391	Klebsiella pneumoniae	Kp1	1	Madagascar	Urban	2015	92	54	5334032	262838	ERS3556887
SB5392	Klebsiella pneumoniae	Kp1	2467	Madagascar	Urban	2015	92	61	5191536	329548	ERS3556962
SB5393	Klebsiella pneumoniae	Kp1	873	Madagascar	Urban	2015	91	47	5444209	355310	ERS3556963
SB5395	Klebsiella pneumoniae	Kp1	2177	Madagascar	Urban	2015	91	36	5020730	367844	ERS3556964
SB5397	Klebsiella pneumoniae	Kp1	337	Madagascar	Urban	2015	90	113	5368646	160219	ERS3556793
SB5398	Klebsiella pneumoniae	Kp1	37	Madagascar	Urban	2015	82	66	5420415	271077	ERS3556830
SB5399	Klebsiella pneumoniae	Kp1	629	Madagascar	Urban	ND	80	94	5371811	205169	ERS3556853
SB5401	Klebsiella pneumoniae	Kp1	2467	Madagascar	Urban	2015	86	58	5180397	295639	ERS3556967
SB5403	Klebsiella pneumoniae	Kp1	2471	Madagascar	Urban	2016	66	191	5367052	89127	ERS3556815
SB5404	Klebsiella pneumoniae	Kp1	45	Madagascar	Urban	2016	64	79	5396683	203125	ERS3556969

SB5406	Klebsiella pneumoniae	Kp1	2473	Madagascar	Urban	2016	65	174	5165061	70752	ERS3556970
SB5407	Klebsiella pneumoniae	Kp1	1429	Madagascar	Urban	2016	75	98	5449031	136675	ERS3556971
SB5408	Klebsiella pneumoniae	Kp1	2474	Madagascar	Urban	2016	40	157	5460594	73383	ERS3556972
SB5411	Klebsiella pneumoniae	Kp1	37	Madagascar	Urban	2016	89	114	5333761	142933	ERS3556832
SB5412	Klebsiella pneumoniae	Kp1	37	Madagascar	Urban	2016	84	142	5345078	92641	ERS3556854
SB5415	Klebsiella pneumoniae	Kp1	441	Madagascar	Urban	2016	69	102	5457548	208158	ERS3556977
SB5417	Klebsiella pneumoniae	Kp1	2480	Madagascar	Urban	2016	81	77	5418208	241277	ERS3556833
SB5418	Klebsiella pneumoniae	Kp1	2481	Madagascar	Urban	2016	72	97	5241241	172192	ERS3556834
SB5419	Klebsiella pneumoniae	Kp1	3331	Madagascar	Urban	2016	81	98	5072035	128862	ERS3556876
SB5421	Klebsiella pneumoniae	Kp1	17	Madagascar	Urban	2016	85	61	5424932	293693	ERS3556910
SB5422	Klebsiella pneumoniae	Kp1	964	Madagascar	Urban	2016	85	83	5420021	183254	ERS3556816
SB5423	Klebsiella pneumoniae	Kp1	3100	Madagascar	Urban	2016	91	130	5287089	89139	ERS3556855
SB5424	Klebsiella pneumoniae	Kp1	2482	Madagascar	Urban	2016	92	133	5084066	89186	ERS3556980
SB5425	Klebsiella pneumoniae	Kp1	2482	Madagascar	Urban	2016	88	122	5079152	92130	ERS3556981
SB5426	Klebsiella pneumoniae	Kp1	25	Madagascar	Urban	2016	89	84	5541863	192330	ERS3556982
SB5427	Klebsiella pneumoniae	Kp1	1787	Madagascar	Urban	2016	73	71	5404088	324273	ERS3556923
SB5429	Klebsiella pneumoniae	Kp1	48	Madagascar	Urban	2016	60	76	5512363	175690	ERS3556930
SB5432	Klebsiella pneumoniae	Kp1	1661	Madagascar	Urban	2016	72	45	5087071	265120	ERS3556986
SB5434	Klebsiella pneumoniae	Kp1	2484	Madagascar	Urban	2016	73	166	5230428	78973	ERS3556817
SB5435	Klebsiella pneumoniae	Kp1	872	Madagascar	Urban	ND	74	126	5250432	123643	ERS3556776

SB5436	Klebsiella pneumoniae	Kp1	2485	Madagascar	Urban	2016		92	71	5369420	203248	ERS3556987
SB5438	Klebsiella pneumoniae	Kp1	37	Madagascar	Urban	2016	strain B	93	40	5230669	284494	ERS3556989
SB5440	Klebsiella pneumoniae	Kp1	25	Madagascar	Urban	2016		92	64	5549052	211951	ERS3556990
SB5441	Klebsiella pneumoniae	Kp1	1537	Madagascar	Urban	2016		93	41	5152938	310877	ERS3556991
SB5442	Klebsiella pneumoniae	Kp1	101	Madagascar	Urban	2016		91	95	5406482	250934	ERS3556836
SB5443	Klebsiella pneumoniae	Kp1	2487	Madagascar	Urban	2016		93	94	5267782	141582	ERS3556777
SB5446	Klebsiella pneumoniae	Kp1	770	Madagascar	Urban	2016		85	41	5056940	282476	ERS3556994
SB5447	Klebsiella pneumoniae	Kp1	2938	Madagascar	Rural	2015		84	101	5314141	176731	ERS3556995
SB5450	Klebsiella pneumoniae	Kp1	1429	Madagascar	Rural	2015		93	88	5430447	148274	ERS3556997
SB5451	Klebsiella pneumoniae	Kp1	36	Madagascar	Rural	2015		83	82	5005670	133698	ERS3556998
SB5452	Klebsiella pneumoniae	Kp1	1429	Madagascar	Rural	2015		92	83	5445429	150520	ERS3556999
SB5453	Klebsiella pneumoniae	Kp1	1429	Madagascar	Rural	2015		71	115	5444588	123903	ERS3557000
SB5456	Klebsiella pneumoniae	Kp1	36	Madagascar	Rural	ND		76	153	5479592	167910	ERS3556837
SB5460	Klebsiella pneumoniae	Kp1	37	Madagascar	Rural	2015		66	109	5518271	160927	ERS3557003
SB5461	Klebsiella pneumoniae	Kp1	20	Madagascar	Rural	2015		57	74	5405677	225887	ERS3557004
SB5462	Klebsiella pneumoniae	Kp1	45	Madagascar	Rural	2015		89	34	5161179	357889	ERS3557005
SB5463	Klebsiella pneumoniae	Kp1	491	Madagascar	Rural	2015		93	106	5239597	141269	ERS3557006
SB5464	Klebsiella pneumoniae	Kp1	1303	Madagascar	Rural	2015		90	85	5018683	149691	ERS3556936
SB5466	Klebsiella pneumoniae	Kp1	2632	Madagascar	Rural	2015		68	116	5217543	173144	ERS3557007
SB5467	Klebsiella pneumoniae	Kp1	2715	Madagascar	Rural	2015		88	56	5162213	203033	ERS3556800

SB5468	Klebsiella pneumoniae	Kp1	2177	Madagascar	Rural	2015	83	53	5015760	261489	ERS3557008
SB5470	Klebsiella pneumoniae	Kp1	1978	Madagascar	Rural	2015	91	55	5264571	269053	ERS3556888
SB5471	Klebsiella pneumoniae	Kp1	36	Madagascar	Rural	2015	91	47	5228028	318470	ERS3557009
SB5472	Klebsiella pneumoniae	Kp1	1198	Madagascar	Rural	2015	62	81	5347913	264893	ERS3556838
SB5473	Klebsiella pneumoniae	Kp1	2473	Madagascar	Rural	2015	91	149	5136430	83330	ERS3557010
SB5478	Klebsiella pneumoniae	Kp1	2504	Madagascar	Rural	2015	76	66	5247596	260223	ERS3557011
SB5479	Klebsiella pneumoniae	Kp1	22	Madagascar	Rural	2015	68	120	5405462	169554	ERS3556839
SB5480	Klebsiella pneumoniae	Kp1	337	Madagascar	Rural	2015	70	94	5304577	173154	ERS3556937
SB5481	Klebsiella pneumoniae	Kp1	2505	Madagascar	Rural	2015	64	102	5479015	166616	ERS3556788
SB5482	Klebsiella pneumoniae	Kp1	2506	Madagascar	Rural	2015	73	76	5260234	227988	ERS3556889
SB5483	Klebsiella pneumoniae	Kp1	399	Madagascar	Rural	2015	73	99	5496447	174799	ERS3556840
SB5486	Klebsiella pneumoniae	Kp1	1966	Madagascar	Rural	2016	90	53	5215468	277324	ERS3557013
SB5489	Klebsiella pneumoniae	Kp1	1429	Madagascar	Rural	2016	91	99	5559122	136788	ERS3557016
SB5491	Klebsiella pneumoniae	Kp1	491	Madagascar	Rural	2016	79	163	5275772	88615	ERS3557017
SB5492	Klebsiella pneumoniae	Kp1	491	Madagascar	Rural	2016	82	158	5258941	90365	ERS3557018
SB5494	Klebsiella pneumoniae	Kp1	831	Madagascar	Rural	2016	82	76	5426956	204301	ERS3556856
SB5497	Klebsiella pneumoniae	Kp1	432	Madagascar	Rural	2016	88	41	5038579	269791	ERS3557022
SB5498	Klebsiella pneumoniae	Kp1	2552	Madagascar	Rural	2016	88	47	5204652	277765	ERS3557023
SB5499	Klebsiella pneumoniae	Kp1	22	Madagascar	Rural	2016	87	86	5304984	226309	ERS3556849
SB5500	Klebsiella pneumoniae	Kp1	873	Madagascar	Rural	2016	88	46	5302640	296215	ERS3557024

SB5501	Klebsiella pneumoniae	Kp1	45	Madagascar	Urban	2016	91	48	5183010	207611	ERS3557146
SB5502	Klebsiella pneumoniae	Kp1	8	Madagascar	Rural	2016	77	53	5175960	230593	ERS3557025
SB5506	Klebsiella pneumoniae	Kp1	2554	Madagascar	Rural	2016	76	54	5259561	293683	ERS3557027
SB5507	Klebsiella pneumoniae	Kp1	2555	Madagascar	Rural	ND	78	65	5212584	169101	ERS3557028
SB5508	Klebsiella pneumoniae	Kp1	2938	Madagascar	Rural	2016	70	92	5323442	183578	ERS3557029
SB5509	Klebsiella pneumoniae	Kp1	337	Madagascar	Rural	2016	83	125	5384152	123057	ERS3556938
SB5510	Klebsiella pneumoniae	Kp1	1429	Madagascar	Rural	2016	84	82	5429075	163610	ERS3557030
SB5511	Klebsiella pneumoniae	Kp1	1429	Madagascar	Rural	2016	86	97	5444987	148885	ERS3557031
SB5512	Klebsiella pneumoniae	Kp1	2408	Madagascar	Rural	2016	87	90	5300346	194594	ERS3557032
SB5513	Klebsiella pneumoniae	Kp1	17	Madagascar	Rural	2016	90	79	5180162	264563	ERS3556858
SB5514	Klebsiella pneumoniae	Kp1	1087	Madagascar	Rural	2016	89	87	5332857	129436	ERS3557033
SB5515	Klebsiella pneumoniae	Kp1	1296	Madagascar	Rural	2016	91	89	5407577	163767	ERS3556852
SB5516	Klebsiella pneumoniae	Kp1	337	Madagascar	Rural	ND	90	119	5536122	107851	ERS3556841
SB5518	Klebsiella pneumoniae	Kp1	500	Madagascar	Rural	2016	89	60	5320291	259971	ERS3556802
SB5521	Klebsiella pneumoniae	Kp1	307	Madagascar	Rural	2016	91	52	5303204	214814	ERS3556842
SB5522	Klebsiella pneumoniae	Kp1	2556	Madagascar	Rural	2016	84	141	5196671	99637	ERS3557035
SB5523	Klebsiella pneumoniae	Kp1	2557	Madagascar	Rural	2016	84	80	5272792	186543	ERS3557036
SB5524	Klebsiella pneumoniae	Kp1	491	Madagascar	Rural	2016	80	129	5257922	127044	ERS3557037
SB5525	Klebsiella pneumoniae	Kp1	65	Madagascar	Rural	2016	87	58	5284478	180289	ERS3556939
SB5526	Klebsiella pneumoniae	Kp1	43	Madagascar	Rural	2016	90	88	5378527	219565	ERS3557038

SB5529	Klebsiella pneumoniae	Kp1	1263	Madagascar	Rural	2016		80	60	5371814	263011	ERS3556878
SB5530	Klebsiella pneumoniae	Kp1	2560	Madagascar	Rural	2016		91	568	5444783	28573	ERS3556899
SB5532	Klebsiella pneumoniae	Kp1	37	Madagascar	Rural	2016	strain B	90	38	5234949	329374	ERS3557039
SB5534	Klebsiella pneumoniae	Kp1	36	Madagascar	Rural	2016		90	66	4986713	170149	ERS3557040
SB5535	Klebsiella pneumoniae	Kp1	215	Madagascar	Rural	2016		82	60	5250714	197167	ERS3556794
SB5538	Klebsiella pneumoniae	Kp1	441	Madagascar	Rural	2016		83	98	5440818	204880	ERS3557042
SB5540	Klebsiella pneumoniae	Kp1	337	Madagascar	Rural	2016		70	128	5370903	172812	ERS3556795
SB5546	Klebsiella pneumoniae	Kp1	29	Madagascar	Rural	2016		70	64	5272828	303990	ERS3556924
SB5547	Klebsiella pneumoniae	Kp1	12	Madagascar	Rural	2016		72	56	5189532	207116	ERS3557046
SB5548	Klebsiella pneumoniae	Kp1	1213	Madagascar	Rural	2016		84	71	5142388	197728	ERS3557047
SB5549	Klebsiella pneumoniae	Kp1	2570	Madagascar	Rural	2016		54	125	5153262	146750	ERS3557048
SB5550	Klebsiella pneumoniae	Kp1	14	Madagascar	Rural	2016		62	94	5454149	195101	ERS3557049
SB5551	Klebsiella pneumoniae	Kp1	36	Madagascar	Rural	2016		78	74	4967818	159973	ERS3557050
SB5555	Klebsiella pneumoniae	Kp1	872	Madagascar	Rural	2016		90	93	5307910	121429	ERS3556818
SB5557	Klebsiella pneumoniae	Kp1	76	Madagascar	Rural	2016		92	58	5318119	231978	ERS3557053
SB5558	Klebsiella pneumoniae	Kp1	17	Madagascar	Rural	2016		88	70	5433470	369399	ERS3556911
SB5559	Klebsiella pneumoniae	Kp1	1787	Madagascar	Rural	2016		90	78	5406219	287551	ERS3556925
SB5560	Klebsiella pneumoniae	Kp1	101	Madagascar	Rural	2016		63	87	5391103	174864	ERS3556890
SB5562	Klebsiella pneumoniae	Kp1	1787	Madagascar	Rural	2016		66	104	5389669	197174	ERS3556926
SB5563	Klebsiella pneumoniae	Kp1	1787	Madagascar	Rural	2016		59	105	5376845	204126	ERS3556927

SB5564	Klebsiella pneumoniae	Kp1	1447	Madagascar	Rural	2016	61	109	5344587	165070	ERS3556819
SB5565	Klebsiella pneumoniae	Kp1	337	Madagascar	Rural	2016	65	150	5262563	75592	ERS3556820
SB5568	Klebsiella pneumoniae	Kp1	186	Madagascar	Rural	2016	53	76	5291083	172920	ERS3557056
SB5569	Klebsiella pneumoniae	Kp1	337	Madagascar	Rural	2016	60	136	5376455	129567	ERS3556796
SB5571	Klebsiella pneumoniae	Kp1	60	Madagascar	Rural	2016	76	58	5141680	215109	ERS3557057
SB5572	Klebsiella pneumoniae	Kp1	234	Madagascar	Rural	2016	67	76	5245852	234973	ERS3556891
SB5573	Klebsiella pneumoniae	Kp1	2473	Madagascar	Rural	2016	74	157	5153367	89574	ERS3557058
SB5574	Klebsiella pneumoniae	Kp1	1429	Madagascar	Rural	2016	74	93	5432728	150523	ERS3557059
SB5575	Klebsiella pneumoniae	Kp1	2718	Madagascar	Rural	2016	78	89	5028703	190544	ERS3557060
SB5576	Klebsiella pneumoniae	Kp1	2053	Madagascar	Rural	2016	88	140	5275264	112499	ERS3556941
SB5578	Klebsiella pneumoniae	Kp1	375	Madagascar	Rural	2016	77	83	5302597	141350	ERS3557061
SB5579	Klebsiella pneumoniae	Kp1	375	Madagascar	Rural	2016	52	101	5323233	112422	ERS3557062
SB5580	Klebsiella pneumoniae	Kp1	375	Madagascar	Rural	2016	89	84	5427086	185754	ERS3557063
SB5581	Klebsiella pneumoniae	Kp1	48	Madagascar	Rural	2016	86	63	5246421	218973	ERS3556907
SB5583	Klebsiella pneumoniae	Kp1	22	Madagascar	Rural	2016	89	71	5470530	264543	ERS3557064
SB5584	Klebsiella pneumoniae	Kp1	2484	Madagascar	Rural	2016	86	129	5144991	83161	ERS3557065
SB5585	Klebsiella pneumoniae	Kp1	39	Madagascar	Rural	2016	91	69	5184265	222065	ERS3556892
SB5588	Klebsiella pneumoniae	Kp1	2596	Madagascar	Rural	2016	71	106	5356391	193137	ERS3557067
SB5589	Klebsiella pneumoniae	Kp1	904	Madagascar	Rural	2016	64	94	5317193	176576	ERS3556862
SB5590	Klebsiella pneumoniae	Kp1	2612	Madagascar	Rural	2016	88	125	5293431	173362	ERS3556779

SB5592	Klebsiella pneumoniae	Kp1	904	Madagascar	Rural	ND		81	58	5315102	355285	ERS3556864
SB5593	Klebsiella pneumoniae	Kp1	2505	Madagascar	Rural	2016		86	78	5462273	205884	ERS3556789
SB5594	Klebsiella pneumoniae	Kp1	449	Madagascar	Rural	2016		91	55	5501182	240090	ERS3556912
SB5595	Klebsiella pneumoniae	Kp1	449	Madagascar	Rural	2016		87	50	5495265	274270	ERS3556913
SB5596	Klebsiella pneumoniae	Kp1	394	Madagascar	Rural	2016		84	64	5411353	271878	ERS3556865
SB5597	Klebsiella pneumoniae	Kp1	39	Madagascar	Rural	2016		90	99	5365389	195528	ERS3556928
SB5599	Klebsiella pneumoniae	Kp1	831	Madagascar	Rural	2016		76	64	5451335	348667	ERS3556893
SB5601	Klebsiella pneumoniae	Kp1	394	Madagascar	Rural	2016		89	57	5454291	288135	ERS3556866
SB5602	Klebsiella pneumoniae	Kp1	2595	Madagascar	Rural	2016		91	136	5311261	91065	ERS3557070
SB5603	Klebsiella pneumoniae	Kp1	337	Madagascar	Rural	2016		93	100	5386562	138910	ERS3557071
SB5604	Klebsiella pneumoniae	Kp1	2596	Madagascar	Rural	2016		93	74	5343235	316377	ERS3557072
SB5605	Klebsiella pneumoniae	Kp1	2597	Madagascar	Rural	2016		68	111	5199001	154482	ERS3557073
SB5606	Klebsiella pneumoniae	Kp1	2598	Madagascar	Rural	2016		88	80	5270663	266403	ERS3557074
SB5608	Klebsiella pneumoniae	Kp1	2599	Madagascar	Rural	2016		92	100	5442784	175920	ERS3556880
SB5609	Klebsiella pneumoniae	Kp1	60	Madagascar	Rural	2016		90	52	5332478	240663	ERS3557076
SB5611	Klebsiella pneumoniae	Kp1	2599	Madagascar	Rural	2016		89	97	5415046	242755	ERS3556881
SB5612	Klebsiella pneumoniae	Kp1	2599	Madagascar	Rural	2016		90	100	5427357	176452	ERS3556882
SB5613	Klebsiella pneumoniae	Kp1	380	Madagascar	Rural	2016		91	57	5424628	284246	ERS3557077
SB5614	Klebsiella pneumoniae	Kp1	37	Madagascar	Rural	2016	strain B	88	33	5236602	349311	ERS3557078
SB5616	Klebsiella pneumoniae	Kp1	2459	Madagascar	Rural	2016		91	51	5218771	254988	ERS3557080

SB5618	Klebsiella pneumoniae	Kp1	39	Madagascar	Rural	2016		73	77	5291111	225946	ERS3556797
SB5619	Klebsiella pneumoniae	Kp1	2601	Madagascar	Rural	2016		85	88	5203937	293846	ERS3557082
SB5620	Klebsiella pneumoniae	Kp1	37	Madagascar	Rural	2016		94	51	5095900	204195	ERS3556790
SB5622	Klebsiella pneumoniae	Kp1	2602	Madagascar	Rural	2016		88	57	5488160	286870	ERS3557083
SB5623	Klebsiella pneumoniae	Kp1	1609	Madagascar	Rural	2016		90	57	5341447	204176	ERS3557084
SB5952	Klebsiella pneumoniae	Kp1	2442	Madagascar	Urban	2016		92	47	5221079	263464	ERS3557149
SB5953	Klebsiella pneumoniae	Kp1	337	Madagascar	Urban	2016		91	115	5316117	121259	ERS3557150
SB5954	Klebsiella pneumoniae	Kp1	441	Madagascar	Urban	2016		90	67	5309293	227038	ERS3557151
SB5955	Klebsiella pneumoniae	Kp1	1689	Madagascar	Urban	2016		83	60	5213238	263118	ERS3556823
SB5956	Klebsiella pneumoniae	Kp1	76	Madagascar	Urban	2016		91	56	5248702	323844	ERS3557152
SB5958	Klebsiella pneumoniae	Kp1	3102	Madagascar	Urban	2016		91	88	5199514	125901	ERS3556806
SB5959	Klebsiella pneumoniae	Kp1	3102	Madagascar	Rural	2016		92	89	5215526	132250	ERS3556807
SB5961	Klebsiella pneumoniae	Kp1	48	Madagascar	Rural	2016	strain A	91	79	5535868	184773	ERS3556921
SB5962	Klebsiella pneumoniae	Kp1	48	Madagascar	Rural	2016	strain A	90	84	5505160	218871	ERS3556922
SB5963	Klebsiella pneumoniae	Kp1	380	Madagascar	Rural	2016		92	85	5579823	283581	ERS3556824
SB5964	Klebsiella pneumoniae	Kp1	22	Madagascar	Rural	2016		92	94	5411793	176235	ERS3556808
SB5965	Klebsiella pneumoniae	Kp1	37	Madagascar	Rural	2016		92	48	5196099	255524	ERS3557155
SB5969	Klebsiella pneumoniae	Kp1	1741	Madagascar	Rural	2016		90	70	5256203	172898	ERS3556825
SB5970	Klebsiella pneumoniae	Kp1	45	Madagascar	Rural	2016		90	52	5368046	245611	ERS3556826
SB5973	Klebsiella pneumoniae	Kp1	2445	Madagascar	Rural	2016		90	65	5380953	202741	ERS3556871

SB5974	Klebsiella pneumoniae	Kp1	3106	Madagascar	Rural	2016	90	78	5247712	187053	ERS3556791
SB5487	Klebsiella quasipneumoniae subsp. quasipneumoniae	Kp2	2507	Madagascar	Rural	2016	89	39	5161973	386493	ERS3557014
SB5517	Klebsiella quasipneumoniae subsp. quasipneumoniae	Kp2	2507	Madagascar	Rural	2016	91	46	5164377	280690	ERS3557034
SB5542	Klebsiella quasipneumoniae subsp. quasipneumoniae	Kp2	526	Madagascar	Rural	2016	50	77	5128810	218655	ERS3557043
SB5543	Klebsiella quasipneumoniae subsp. quasipneumoniae	Kp2	526	Madagascar	Rural	2016	61	84	5125768	190557	ERS3557044
SB5545	Klebsiella quasipneumoniae subsp. quasipneumoniae	Kp2	2604	Madagascar	Rural	2016	66	112	5146606	123181	ERS3557045
SB5617	Klebsiella quasipneumoniae subsp. quasipneumoniae	Kp2	526	Madagascar	Rural	2016	90	82	5390302	184454	ERS3557081
SB5621	Klebsiella quasipneumoniae subsp. quasipneumoniae	Kp2	526	Madagascar	Rural	2016	93	109	5417037	177026	ERS3556845
SB5373	Klebsiella variicola subsp. variicola	Kp3	2462	Madagascar	Urban	2015	89	47	5458458	365116	ERS3556949
SB5374	Klebsiella variicola subsp. variicola	Kp3	1615	Madagascar	Urban	2015	90	80	5657557	190187	ERS3556798
SB5375	Klebsiella variicola subsp. variicola	Kp3	2463	Madagascar	Urban	2015	76	58	5554336	270995	ERS3556950
SB5377	Klebsiella variicola subsp. variicola	Kp3	2464	Madagascar	Urban	2015	76	158	5644723	142194	ERS3556952
SB5379	Klebsiella variicola subsp. variicola	Kp3	906	Madagascar	Urban	2015	77	72	5767679	316215	ERS3556874
SB5381	Klebsiella variicola subsp. variicola	Kp3	925	Madagascar	Urban	2015	88	65	5639770	337248	ERS3556955
SB5386	Klebsiella variicola subsp. variicola	Kp3	2465	Madagascar	Urban	2015	88	55	5440752	341428	ERS3556960
SB5388	Klebsiella variicola subsp. variicola	Kp3	906	Madagascar	Urban	2015	90	68	5755776	262066	ERS3556875
SB5396	Klebsiella variicola subsp. variicola	Kp3	2468	Madagascar	Urban	2015	91	106	5685191	175804	ERS3556965
SB5400	Klebsiella variicola subsp. variicola	Kp3	2469	Madagascar	Urban	2015	77	40	5602483	404425	ERS3556966
SB5402	Klebsiella variicola subsp. variicola	Kp3	2470	Madagascar	Urban	2016	72	81	5487184	274238	ERS3556968
SB5405	Klebsiella variicola subsp. variicola	Kp3	2472	Madagascar	Urban	2016	56	135	5602972	151911	ERS3556831

SB5409	Klebsiella variicola subsp. variicola	Kp3	2475	Madagascar	Urban	2016	68	102	5349267	106221	ERS3556973
SB5413	Klebsiella variicola subsp. variicola	Kp3	2477	Madagascar	Urban	2016	88	74	5357522	162652	ERS3556975
SB5416	Klebsiella variicola subsp. variicola	Kp3	2479	Madagascar	Urban	2016	75	113	5704285	286204	ERS3556978
SB5430	Klebsiella variicola subsp. variicola	Kp3	919	Madagascar	Urban	2016	56	192	5385660	93766	ERS3556984
SB5433	Klebsiella variicola subsp. variicola	Kp3	1562	Madagascar	Urban	2016	73	194	5952617	114346	ERS3556835
SB5437	Klebsiella variicola subsp. variicola	Kp3	919	Madagascar	Urban	2016	83	165	5346358	108291	ERS3556988
SB5444	Klebsiella variicola subsp. variicola	Kp3	2488	Madagascar	Urban	2016	92	44	5634621	373402	ERS3556992
SB5445	Klebsiella variicola subsp. variicola	Kp3	1843	Madagascar	Urban	2016	81	45	5365236	375469	ERS3556993
SB5449	Klebsiella variicola subsp. variicola	Kp3	2490	Madagascar	Rural	2015	75	52	5477885	212986	ERS3556996
SB5454	Klebsiella variicola subsp. variicola	Kp3	2491	Madagascar	Rural	2015	85	73	5442774	219515	ERS3557001
SB5465	Klebsiella variicola subsp. variicola	Kp3	906	Madagascar	Rural	2015	92	71	5763616	199460	ERS3556877
SB5485	Klebsiella variicola subsp. variicola	Kp3	2475	Madagascar	Rural	2016	67	60	5373490	222789	ERS3557012
SB5488	Klebsiella variicola subsp. variicola	Kp3	2508	Madagascar	Rural	2016	83	73	5425002	185824	ERS3557015
SB5493	Klebsiella variicola subsp. variicola	Kp3	2490	Madagascar	Rural	2016	66	68	5386564	216049	ERS3557019
SB5495	Klebsiella variicola subsp. variicola	Kp3	2551	Madagascar	Rural	2016	86	41	5486130	311060	ERS3557020
SB5496	Klebsiella variicola subsp. variicola	Kp3	2551	Madagascar	Rural	2016	87	37	5399987	394028	ERS3557021
SB5505	Klebsiella variicola subsp. variicola	Kp3	2553	Madagascar	Rural	2016	92	45	5575376	314335	ERS3557026
SB5519	Klebsiella variicola subsp. variicola	Kp3	697	Madagascar	Rural	2016	87	54	5529631	309412	ERS3557157
SB5520	Klebsiella variicola subsp. variicola	Kp3	919	Madagascar	Rural	2016	75	108	5514925	193275	ERS3556859
SB5552	Klebsiella variicola subsp. variicola	Kp3	2606	Madagascar	Rural	2016	61	77	5482237	209735	ERS3557051

SB5561	Klebsiella variicola subsp. variicola	Kp3	2609	Madagascar	Rural	2016	84	61	5402273	246602	ERS3557054
SB5566	Klebsiella variicola subsp. variicola	Kp3	357	Madagascar	Rural	2016	67	135	5613895	171203	ERS3557055
SB5582	Klebsiella variicola subsp. variicola	Kp3	2611	Madagascar	Rural	2016	90	75	5375242	213483	ERS3556821
SB5586	Klebsiella variicola subsp. variicola	Kp3	1984	Madagascar	Rural	2016	90	52	5332452	218499	ERS3557066
SB5600	Klebsiella variicola subsp. variicola	Kp3	2594	Madagascar	Rural	2016	92	48	5497328	281143	ERS3557069
SB5950	Klebsiella variicola subsp. variicola	Kp3	3101	Madagascar	Urban	2016	92	42	5355670	225689	ERS3557147
SB5951	Klebsiella variicola subsp. variicola	Kp3	3101	Madagascar	Urban	2016	92	37	5366750	246235	ERS3557148
SB5960	Klebsiella variicola subsp. variicola	Kp3	712	Madagascar	Rural	2016	92	78	5725724	258443	ERS3557154
SB5966	Klebsiella variicola subsp. variicola	Kp3	3103	Madagascar	Rural	2016	89	73	5700642	175109	ERS3557156
SB5967	Klebsiella variicola subsp. variicola	Kp3	3104	Madagascar	Rural	2016	89	75	5889124	220557	ERS3556904
SB5968	Klebsiella variicola subsp. variicola	Kp3	919	Madagascar	Rural	2016	90	90	5555178	172043	ERS3556870
SB5971	Klebsiella variicola subsp. variicola	Kp3	3104	Madagascar	Rural	2016	90	69	5886084	208898	ERS3556905
SB5972	Klebsiella variicola subsp. variicola	Kp3	3105	Madagascar	Rural	2016	90	58	5491854	188345	ERS3556884
SB5410	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2476	Madagascar	Urban	2016	88	60	5435462	296618	ERS3556974
SB5414	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2478	Madagascar	Urban	2016	92	58	5422494	295746	ERS3556976
SB5420	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	841	Madagascar	Urban	2016	88	69	5411541	297876	ERS3556979
SB5428	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2483	Madagascar	Urban	2016	83	32	5026681	379465	ERS3556983
SB5431	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2483	Madagascar	Urban	2016	57	44	5014161	371435	ERS3556985
SB5477	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2503	Madagascar	Rural	2015	62	97	5357585	228691	ERS3556801
SB5504	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2489	Madagascar	Rural	2016	80	127	5414623	153156	ERS3556857

SB5527	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2558	Madagascar	Rural	2016	85	101	5476532	212814	ERS3556898
SB5528	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2559	Madagascar	Rural	2016	80	94	5392586	218306	ERS3556860
SB5533	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2562	Madagascar	Rural	2016	89	143	5258337	105503	ERS3556843
SB5536	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2478	Madagascar	Rural	2016	92	64	5429262	295885	ERS3557041
SB5537	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	1224	Madagascar	Rural	2016	64	135	5249042	152411	ERS3556778
SB5554	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2607	Madagascar	Rural	2016	90	35	5124474	294335	ERS3557052
SB5556	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2608	Madagascar	Rural	2016	90	123	5135771	100881	ERS3556844
SB5570	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2610	Madagascar	Rural	2016	59	197	5188694	72423	ERS3556940
SB5577	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	283	Madagascar	Rural	2016	78	92	5387217	198227	ERS3556902
SB5587	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2592	Madagascar	Rural	2016	60	64	5164824	207974	ERS3556861
SB5591	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2592	Madagascar	Rural	ND	83	31	5116759	371534	ERS3556863
SB5598	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2593	Madagascar	Rural	2016	92	58	5222359	301855	ERS3557068
SB5607	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	1584	Madagascar	Rural	2016	93	79	5202162	195586	ERS3557075
SB5615	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2059	Madagascar	Rural	2016	91	30	5113756	364932	ERS3557079
SB5957	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2721	Madagascar	Urban	2016	90	40	5188994	363415	ERS3557153
SB5387	Klebsiella variicola subsp. tropicalensis	Kp5	2466	Madagascar	Urban	2015	87	56	5698764	279038	ERS2787526
SB5439	Klebsiella variicola subsp. tropicalensis	Kp5	2486	Madagascar	Urban	2016	92	45	5613167	311118	ERS2787527
SB5455	Klebsiella variicola subsp. tropicalensis	Kp5	2630	Madagascar	Rural	2015	86	43	5338997	298293	ERS3557002
SB5531	Klebsiella variicola subsp. tropicalensis	Kp5	2561	Madagascar	Rural	2016	89	48	5442219	339248	ERS2787528
SB5544	Klebsiella variicola subsp. tropicalensis	Kp5	2605	Madagascar	Rural	2016	65	57	5488176	302938	ERS2787529

SB5567	Klebsiella variicola subsp. tropicalensis	Kp5	2717	Madagascar	Rural	2016	89	85	5730017	378142	ERS3556879
SB5610	Klebsiella variicola subsp. tropicalensis	Kp5	2600	Madagascar	Rural	2016	82	64	5631209	376790	ERS2787530
SB5727	Klebsiella pneumoniae	Kp1	1303	Senegal	Rural	2016	89	180	5459317	93097	ERS3556805
SB5728	Klebsiella pneumoniae	Kp1	1886	Senegal	Rural	2016	89	93	5024483	105946	ERS3556774
SB5730	Klebsiella pneumoniae	Kp1	3108	Senegal	Urban	2016	91	144	5392688	126207	ERS3557158
SB5731	Klebsiella pneumoniae	Kp1	3109	Senegal	Rural	2016	89	85	5493388	203723	ERS3557159
SB5734	Klebsiella pneumoniae	Kp1	281	Senegal	Rural	2016	88	61	5248435	268545	ERS3557161
SB5735	Klebsiella pneumoniae	Kp1	3111	Senegal	Rural	2016	86	85	5259947	175089	ERS3557162
SB5736	Klebsiella pneumoniae	Kp1	17	Senegal	Rural	2016	81	72	5424208	297557	ERS3557163
SB5737	Klebsiella pneumoniae	Kp1	1119	Senegal	Rural	2016	91	146	5398689	164307	ERS3556896
SB5742	Klebsiella pneumoniae	Kp1	528	Senegal	Rural	2016	86	103	5558787	163712	ERS3556872
SB5743	Klebsiella pneumoniae	Kp1	3113	Senegal	Rural	2016	82	91	5282053	150704	ERS3557164
SB5749	Klebsiella pneumoniae	Kp1	17	Senegal	Rural	2016	89	92	5310170	171120	ERS3557166
SB5751	Klebsiella pneumoniae	Kp1	3116	Senegal	Rural	2016	90	75	5119808	174613	ERS3557168
SB5752	Klebsiella pneumoniae	Kp1	36	Senegal	Rural	2016	90	115	5306071	165411	ERS3557169
SB5753	Klebsiella pneumoniae	Kp1	17	Senegal	Rural	2016	84	48	5105070	310709	ERS3557170
SB5756	Klebsiella pneumoniae	Kp1	3118	Senegal	Rural	2016	92	67	5297658	211640	ERS3557172
SB5759	Klebsiella pneumoniae	Kp1	111	Senegal	Rural	2016	91	84	5325877	159857	ERS3557174
SB5762	Klebsiella pneumoniae	Kp1	3258	Senegal	Rural	2016	87	59	5350135	198994	ERS3557176
SB5765	Klebsiella pneumoniae	Kp1	1962	Senegal	Rural	2016	91	82	5419644	148060	ERS3557178

SB5768	Klebsiella pneumoniae	Kp1	3123	Senegal	Rural	2016		88	59	5392118	194742	ERS3557180
SB5770	Klebsiella pneumoniae	Kp1	152	Senegal	Rural	2016		89	85	5390648	176784	ERS3557181
SB5771	Klebsiella pneumoniae	Kp1	3124	Senegal	Rural	2016		86	64	5208506	196298	ERS3557182
SB5773	Klebsiella pneumoniae	Kp1	3260	Senegal	Rural	2016		91	86	5149261	130202	ERS3557184
SB5774	Klebsiella pneumoniae	Kp1	3261	Senegal	Rural	2016		90	61	5206782	172719	ERS3557185
SB5775	Klebsiella pneumoniae	Kp1	3262	Senegal	Rural	2016		88	54	5035131	205363	ERS3557186
SB5776	Klebsiella pneumoniae	Kp1	337	Senegal	Rural	2016		90	94	5180324	154063	ERS3557187
SB5777	Klebsiella pneumoniae	Kp1	397	Senegal	Rural	2016		90	127	5782991	151257	ERS3557188
SB5779	Klebsiella pneumoniae	Kp1	629	Senegal	Rural	2016		90	58	5096179	210411	ERS3557190
SB5783	Klebsiella pneumoniae	Kp1	3157	Senegal	Rural	2016		91	67	5170911	208422	ERS3557194
SB5786	Klebsiella pneumoniae	Kp1	277	Senegal	Rural	2016		88	118	5275557	178172	ERS3557195
SB5787	Klebsiella pneumoniae	Kp1	281	Senegal	Rural	2016		90	88	5178844	179779	ERS3557196
SB5788	Klebsiella pneumoniae	Kp1	3267	Senegal	Rural	2016		87	81	5029390	163848	ERS3557197
SB5789	Klebsiella pneumoniae	Kp1	3268	Senegal	Rural	2016		87	82	5156984	136129	ERS3557198
SB5790	Klebsiella pneumoniae	Kp1	151	Senegal	Rural	2016		81	119	5431801	105949	ERS3557199
SB5791	Klebsiella pneumoniae	Kp1	443	Senegal	Rural	2016		81	92	5391364	237290	ERS3557200
SB5792	Klebsiella pneumoniae	Kp1	514	Senegal	Rural	2016	Pair 1	90	113	5353868	153475	ERS3557201
SB5793	Klebsiella pneumoniae	Kp1	36	Senegal	Rural	2016	Pair 1	91	49	5091180	292649	ERS3557202
SB5794	Klebsiella pneumoniae	Kp1	1087	Senegal	Rural	2016		89	90	5275598	130550	ERS3556809
SB5798	Klebsiella pneumoniae	Kp1	3271	Senegal	Rural	2016		91	105	5407526	182184	ERS3556785

SB5800	Klebsiella pneumoniae	Kp1	2141	Senegal	Rural	2016		88	114	5182647	145161	ERS3557206
SB5801	Klebsiella pneumoniae	Kp1	225	Senegal	Rural	2016		78	146	5727134	167616	ERS3557207
SB5802	Klebsiella pneumoniae	Kp1	3273	Senegal	Rural	2016		90	68	5410521	248210	ERS3557208
SB5805	Klebsiella pneumoniae	Kp1	3275	Senegal	Rural	2016		80	94	5014660	150130	ERS3557210
SB5806	Klebsiella pneumoniae	Kp1	3030	Senegal	Rural	2016	Pair 3	89	116	5405559	169164	ERS3557211
SB5807	Klebsiella pneumoniae	Kp1	1263	Senegal	Rural	2016	Pair 3	84	147	5466219	139863	ERS3556827
SB5808	Klebsiella pneumoniae	Kp1	1189	Senegal	Rural	2016		91	74	5427900	244942	ERS3557212
SB5810	Klebsiella pneumoniae	Kp1	1189	Senegal	Urban	2016		91	80	5460049	244949	ERS3557214
SB5811	Klebsiella pneumoniae	Kp1	3277	Senegal	Urban	2016		91	56	5239790	234654	ERS3557215
SB5812	Klebsiella pneumoniae	Kp1	1661	Senegal	Urban	2016		83	52	5110071	235407	ERS3557216
SB5815	Klebsiella pneumoniae	Kp1	37	Senegal	Urban	2016	Pair 4	38	96	5513110	204218	ERS3556851
SB5816	Klebsiella pneumoniae	Kp1	3278	Senegal	Urban	2016	Pair 4	90	75	5306105	176071	ERS3557217
SB5817	Klebsiella pneumoniae	Kp1	292	Senegal	Urban	2016		90	68	5408598	248952	ERS3556811
SB5818	Klebsiella pneumoniae	Kp1	504	Senegal	Urban	2016		91	103	5414856	140340	ERS3556828
SB5819	Klebsiella pneumoniae	Kp1	45	Senegal	Urban	2016		91	64	5416349	203813	ERS3557218
SB5822	Klebsiella pneumoniae	Kp1	2108	Senegal	Urban	2016	Pair 7	91	125	5288488	144314	ERS3556812
SB5823	Klebsiella pneumoniae	Kp1	968	Senegal	Urban	2016	Pair 7	90	114	5408865	135254	ERS3556946
SB5824	Klebsiella pneumoniae	Kp1	2800	Senegal	Urban	2016		91	104	5286656	128390	ERS3556947
SB5825	Klebsiella pneumoniae	Kp1	491	Senegal	Urban	2016		92	88	5301914	144465	ERS3557219
SB5826	Klebsiella pneumoniae	Kp1	1401	Senegal	Urban	2016		92	106	5339690	158933	ERS3557220

SB5828	Klebsiella pneumoniae	Kp1	1049	Senegal	Urban	2016		92	60	5346709	328795	ERS3556873
SB5829	Klebsiella pneumoniae	Kp1	3280	Senegal	Urban	2016		92	67	5204522	215068	ERS3557221
SB5830	Klebsiella pneumoniae	Kp1	3281	Senegal	Urban	2016		92	74	5165672	174742	ERS3557222
SB5831	Klebsiella pneumoniae	Kp1	1401	Senegal	Urban	2016		89	118	5342371	195948	ERS3557223
SB5832	Klebsiella pneumoniae	Kp1	2655	Senegal	Urban	2016		89	93	5356443	234283	ERS3556906
SB5833	Klebsiella pneumoniae	Kp1	502	Senegal	Urban	2016		91	119	5261707	117110	ERS3556775
SB5834	Klebsiella pneumoniae	Kp1	2715	Senegal	Urban	2016		91	57	5290405	220671	ERS3556897
SB5836	Klebsiella pneumoniae	Kp1	1419	Senegal	Urban	2016		92	62	5123589	185639	ERS3557224
SB5837	Klebsiella pneumoniae	Kp1	3282	Senegal	Rural	2016		92	57	5321722	199551	ERS3556813
SB5838	Klebsiella pneumoniae	Kp1	3282	Senegal	Urban	2016		91	65	5316598	215700	ERS3556814
SB5839	Klebsiella pneumoniae	Kp1	411	Senegal	Urban	2016		91	68	5315616	357999	ERS3557225
SB5841	Klebsiella pneumoniae	Kp1	1666	Senegal	Urban	2016		92	126	5126909	121647	ERS3556786
SB5842	Klebsiella pneumoniae	Kp1	3283	Senegal	Rural	2016		89	105	5528949	187384	ERS3557226
SB5847	Klebsiella pneumoniae	Kp1	3286	Senegal	Rural	2016		71	108	5329435	140852	ERS3557230
SB5849	Klebsiella pneumoniae	Kp1	29	Senegal	Rural	2016	Pair 5	64	169	5672063	137034	ERS3557232
SB5850	Klebsiella pneumoniae	Kp1	3287	Senegal	Rural	2016	Pair 5	90	170	5494158	133356	ERS3556792
SB5851	Klebsiella pneumoniae	Kp1	249	Senegal	Rural	2016		82	88	5342878	130037	ERS3557233
SB5854	Klebsiella pneumoniae	Kp1	1419	Senegal	Rural	2016		79	79	5113371	156498	ERS3557236
SB5856	Klebsiella pneumoniae	Kp1	3290	Senegal	Urban	2016		83	63	5140202	237840	ERS3557237
SB5858	Klebsiella pneumoniae	Kp1	3286	Senegal	Rural	2016		87	72	5289021	162987	ERS3557238

SB5859	Klebsiella pneumoniae	Kp1	1015	Senegal	Rural	2016		88	76	5206159	136951	ERS3557239
SB5862	Klebsiella pneumoniae	Kp1	13	Senegal	Rural	2016		92	115	5520797	121910	ERS3557241
SB5863	Klebsiella pneumoniae	Kp1	788	Senegal	Rural	2016	Pair 6	82	49	5148220	218261	ERS3557242
SB5864	Klebsiella pneumoniae	Kp1	3293	Senegal	Rural	2016	Pair 6	92	50	5284856	299377	ERS3557243
SB5865	Klebsiella pneumoniae	Kp1	3294	Senegal	Urban	2016		93	52	5212655	203902	ERS3557244
SB5866	Klebsiella pneumoniae	Kp1	37	Senegal	Urban	2016		94	75	5288263	203773	ERS3557245
SB5867	Klebsiella pneumoniae	Kp1	3295	Senegal	Rural	2016		93	115	5290947	133375	ERS3557246
SB5869	Klebsiella pneumoniae	Kp1	3297	Senegal	Rural	2016		94	55	5227797	250406	ERS3557248
SB6073	Klebsiella pneumoniae	Kp1	152	Senegal	Rural	2016		88	99	5408575	219852	ERS3557249
SB6074	Klebsiella pneumoniae	Kp1	3337	Senegal	Rural	2016		86	62	5145564	286179	ERS3557250
SB6076	Klebsiella pneumoniae	Kp1	3338	Senegal	Rural	2016		88	48	5264137	279955	ERS3557252
SB6077	Klebsiella pneumoniae	Kp1	3339	Senegal	Rural	2016		87	33	5331978	389116	ERS3557253
SB6078	Klebsiella pneumoniae	Kp1	661	Senegal	Rural	2016		87	39	5131974	366827	ERS3557254
SB6079	Klebsiella pneumoniae	Kp1	867	Senegal	Rural	2016		89	80	5346442	180235	ERS3556787
SB6080	Klebsiella pneumoniae	Kp1	1662	Senegal	Rural	2016		86	39	5120121	380942	ERS3557255
SB6081	Klebsiella pneumoniae	Kp1	3340	Senegal	Rural	2016		87	39	5177609	303260	ERS3557256
SB6082	Klebsiella pneumoniae	Kp1	3341	Senegal	Rural	2016		86	49	5091487	225350	ERS3557257
SB6085	Klebsiella pneumoniae	Kp1	36	Senegal	Rural	2016		85	99	5307208	152475	ERS3557258
SB6086	Klebsiella pneumoniae	Kp1	1962	Senegal	Rural	2016		84	60	5152762	310294	ERS3557259
SB6087	Klebsiella pneumoniae	Kp1	397	Senegal	Rural	2016		60	120	5713771	240928	ERS3557260

SB6088	Klebsiella pneumoniae	Kp1	397	Senegal	Rural	2016		88	108	5706568	185261	ERS3556829
SB6089	Klebsiella pneumoniae	Kp1	1658	Senegal	Rural	2016		92	53	5216422	283352	ERS3557261
SB6091	Klebsiella pneumoniae	Kp1	39	Senegal	Rural	2016		88	61	5356306	213939	ERS3556885
SB5782	Klebsiella quasipneumoniae subsp. quasipneumoniae	Kp2	338	Senegal	Rural	2016		91	147	5417191	107073	ERS3557193
SB5799	Klebsiella quasipneumoniae subsp. quasipneumoniae	Kp2	3272	Senegal	Rural	2016		81	108	5268415	154994	ERS3556810
SB5803	Klebsiella quasipneumoniae subsp. quasipneumoniae	Kp2	3274	Senegal	Rural	2016		82	73	5193555	200431	ERS3557209
SB5745	Klebsiella variicola subsp. variicola	Kp3	3114	Senegal	Rural	2016		90	38	5324929	383397	ERS3557165
SB5754	Klebsiella variicola subsp. variicola	Kp3	3117	Senegal	Rural	2016		90	52	5618429	251495	ERS3557171
SB5767	Klebsiella variicola subsp. variicola	Kp3	3122	Senegal	Rural	2016		90	42	5443934	353056	ERS3557179
SB5868	Klebsiella variicola subsp. variicola	Kp3	3296	Senegal	Rural	2016		90	44	5411027	329853	ERS3557247
SB5726	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3107	Senegal	Rural	2016		88	78	5245485	185245	ERS3556804
SB5732	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3110	Senegal	Rural	2016		92	30	5017370	404872	ERS3557160
SB5739	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3112	Senegal	Rural	2016		81	171	5316922	119006	ERS3556945
SB5746	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3115	Senegal	Rural	2016		90	88	5402325	278229	ERS3556783
SB5750	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	1308	Senegal	Rural	2016		91	85	5173939	150803	ERS3557167
SB5758	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3120	Senegal	Rural	2016		86	48	5096656	259246	ERS3557173
SB5761	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3257	Senegal	Rural	2016		90	29	4912611	360617	ERS3557175
SB5764	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2685	Senegal	Rural	2016		92	22	5081748	375238	ERS3557177
SB5766	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3121	Senegal	Rural	2016		90	79	5331961	182382	ERS3556784
SB5772	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	138	Senegal	Rural	2016		87	67	5399904	223886	ERS3557183

SB5778	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3263	Senegal	Rural	2016		91	34	5027416	355298	ERS3557189
SB5780	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3264	Senegal	Rural	2016		91	85	5008109	111230	ERS3557191
SB5781	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3265	Senegal	Rural	2016		81	83	5012843	107757	ERS3557192
SB5784	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3266	Senegal	Rural	2016		90	100	5259734	124277	ERS3556850
SB5795	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3269	Senegal	Rural	2016	Pair 2	90	56	5184927	295952	ERS3557203
SB5796	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3270	Senegal	Rural	2016	Pair 2	85	73	5504592	260745	ERS3557204
SB5797	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	2559	Senegal	Rural	2016		90	47	5024763	253069	ERS3557205
SB5809	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3276	Senegal	Rural	2016		92	33	5110574	335878	ERS3557213
SB5843	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3284	Senegal	Urban	2016		92	44	5136034	265642	ERS3557227
SB5845	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	841	Senegal	Rural	2016		65	107	5277310	143617	ERS3557228
SB5846	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3285	Senegal	Rural	2016		71	86	5155621	119771	ERS3557229
SB5848	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	138	Senegal	Rural	2016		64	86	5159895	154440	ERS3557231
SB5852	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3288	Senegal	Urban	2016		59	159	5229734	108016	ERS3557234
SB5853	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3289	Senegal	Urban	2016		54	73	5065365	159405	ERS3557235
SB5860	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3292	Senegal	Urban	2016		55	87	5249338	193925	ERS3557240
SB6075	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	ND	Senegal	Rural	2016		82	38	4981468	282286	ERS3557251
SB6092	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3342	Senegal	Rural	2016		90	36	5010451	355888	ERS3557262
SB6093	Klebsiella quasipneumoniae subsp. similipneumoniae	Kp4	3342	Senegal	Rural	2016		90	33	5001859	377541	ERS3557263
SB5857	Klebsiella africanensis	Kp7	3291	Senegal	Rural	2016		87	50	5156720	195731	ERS2787533

defined as groups of isolates differing by less than 10 loci out of the 5,073 protein-coding genes of strain Kp616 (GenBank accession number GCA_003076555.1).

Table S2. High-risk clones

ST	No. of assembled	Number of publication	Multidrug resistant (MDR)	Detected in this study
ST258	1095	209	MDR	No
ST11	744	236	MDR	No
ST15	329	109	MDR	Yes
ST512	308	41	MDR	No
ST101	206	68	MDR	Yes
ST307	197	34	MDR	Yes
ST147	176	86	MDR	No
ST37	137	31	MDR	Yes
ST45	134	9	MDR	Yes
ST14	133	32	MDR	Yes
ST17	97	19	MDR	Yes
ST16	97	24	MDR	No
ST23	87	66	HV	No
ST340	86	31	MDR	No
ST231	84	8	MDR	No
ST437	71	17	MDR	No
ST405	67	29	MDR	No
ST29	60	14	MDR	Yes
ST48	59	19	MDR	Yes
ST20	45	9	MDR	Yes
ST395	43	12	MDR	No
ST3128	41	1	MDR	No
ST25	39	9	HV	Yes
ST86	37	21	HV	No
ST152	35	6	MDR	Yes
ST268	32	3	MDR	No
ST36	32	5	MDR	Yes
ST336	32	8	MDR	No
ST3010	29	0	MDR	No
ST323	29	7	MDR	No
ST392	28	8	MDR	No
ST43	22	4	MDR	Yes
ST13	21	4	MDR	Yes

ST39	20	7	MDR	Yes
ST1	20	7	MDR	Yes
ST65	15	20	HV	Yes
ST375	14	9	HV	Yes
ST274	12	5	MDR	No
ST383	12	12	MDR	No
ST76	11	5	MDR	Yes
ST273	11	9	MDR	No

[1]: As of April 2019: 6,258 available genomes

[2]: Klebsiella” + “pneumoniae” + “STxxx”, April 2019

Table S3. Characteristics of the 496 Klebsiella isolates: antimicrobial susceptibility, capular types, resistance genes, virulence genes and plasmid replicons

Please click on the link below

https://drive.google.com/open?id=1o3XQfW_EGt6ffKdNp1O_ZyZeAmndWJAU

Table S4. Resistance phenotypes in urban and rural areas in Madagascar, Cambodia, Senegal and globally

Resistance phenotype	**Madagascar**			**Cambodia**			**Senegal**				
	Urban (%) N=84	**Rural (%) N=178**	**p ***	**Urban (%) N=40**	**Rural (%) N=57**	**p ***	**Urban (%) N=32**	**Rural (%) N=105**	**p ***	**Total (%) N=496**	**p ****
AMC	45.2	42.7	0.7	27.5	5.3	0.02	6.3	13.3	0.36[§]	29.0	<0.001
TCC	70.2	50.6	0.003	37.5	10.5	0.001[§]	6.3	12.4	0.52[§]	37.3	<0.001
TZP	25.0	14.0	0.03	25.0	5.3	0.005[§]	0.0	1.0	1§	12.1	<0.001
CEF	4.8	15.2	0.02	30.0	12.3	0.03	6.3	9.5	0.73[§]	12.5	0.04
CTX	3.6	10.7	0.05	27.5	5.3	0.002	0.0	1.0	1[§]	7.5	<0.001
CAZ	3.6	9.6	0.09	27.5	5.3	0.002	3.1	2.9	1[§]	7.7	0.005
FEP	4.8	10.7	0.11	25.0	5.3	0.005	0.0	1.0	1[§]	7.5	0.001
ATM	3.6	9.0	0.11	27.5	5.3	0.002	0.0	1.0	1[§]	6.9	<0.001
IMI	1.2	1.1	1[§]	0.0	0.0	-	3.1	0.0	0.23[§]	0.8	0.82[§]
AMK	1.2	0.0	0.32[§]	0.0	0.0	-	0.0	1.0	1[§]	0.4	1[§]
GEN	2.4	5.1	0.51[§]	32.5	7.0	0.001	3.1	1.0	0.41[§]	6.0	<0.001
TOB	6.0	9.0	0.47[§]	30.0	7.0	0.003	3.1	2.9	1[§]	8.3	0.001
NAL	1.2	3.4	0.44[§]	22.5	10.5	0.1	0.0	1.9	1[§]	4.8	<0.001
CIP	0.0	7.9	0.006[§]	15.0	1.8	0.02[§]	3.1	2.9	1[§]	5.0	0.32
TET	36.9	42.7	0.37	45.0	14.0	0.001	18.8	11.4	0.37[§]	30.4	<0.001
SXT	27.4	33.7	0.3	40.0	12.3	0.002	50.0	29.5	0.03	30.8	0.21
DDST	3.6	10.7	0.05	27.5	5.3	0.002	0.0	1.0	1[§]	7.5	<0.001

* Comparison between rural and urban sites; ** Comparison between countries

§ Fisher's exact test

Table S5. Resistant genes rates among *K. pneumoniae* isolates, by country and site

	Madagascar			**Cambodia**			**Senegal**				
	Urban (%) N=84	Rural (%) N=178	**p***	Urban (%) N=40	Rural (%) N=57	**p***	Urban (%) N=32	Rural (%) N=105	**p***	**Total** (%) N=496	**p ****
CTX-M	3.6	8.4	0.15	25.0	3.5	0.003 §	0.0	0.0	-	6.0	<0.001
SHV-ESBL	0.0	2.2	0.31§	2.5	1.8	1	0.0	0.0	-	1.2	0.24§
pAmpC	1.2	1.1	1§	0.0	0.0	-	0.0	0.0	-	0.6	0.43§
TEM-1	15.5	20.8	0.31	35.0	10.5	0.003	6.3	3.8	0.62§	15.3	<0.001
LAP-2	1.2	2.8	0.67§	7.5	3.5	0.4§	0.0	0.0	-	2.2	0.02§
OXA-1	2.4	2.8	1§	15.0	3.5	0.06§	0.0	0.0	-	3.0	0.001§
SCO-1	0.0	1.1	1§	0.0	0.0	-	0.0	0.0	-	0.4	0.71§
AAC(3)-IIa/d	3.6	5.6	0.56§	32.5	7.0	0.001	3.1	0.0	0.23§	6.3	<0.001
AAC(6')-Ib-cr	2.4	3.4	1§	20.0	3.5	0.01§	0.0	0.0	-	3.6	<0.001
AAC(6')-Ib	0.0	0.0	-	2.5	0.0	0.41§	0.0	0.0	-	0.2	0.2§
AadA	9.5	11.2	0.68	20.0	3.5	0.01§	15.6	7.6	0.18§	10.3	0.9
AadB	0.0	0.0	-	0.0	0.0	-	0.0	1.0	1§	0.2	0.5§
APH(6)-Id	14.3	21.9	0.15	32.5	8.8	0.003	15.6	5.7	0.13§	16.1	0.01
APH(3'')-Ib	13.1	20.2	0.16	32.5	8.8	0.003	15.6	5.7	0.13§	15.3	0.02
APH(3')-Ia	2.4	0.6	0.24§	0.0	0.0	-	0.0	0.0	-	0.6	0.43§
QNDR	1.2	1.1	1§	7.5	1.8	0.3§	0.0	0.0	-	1.4	0.03§
QnrB	2.4	3.4	1§	15.0	1.8	0.02§	0.0	1.0	1	3.2	0.02§
QnrS	1.2	3.9	0.44§	20.0	12.3	0.3	0.0	1.0	1§	4.8	<0.001
Sul1	20.2	23.0	0.61	17.5	3.5	0.03§	21.9	7.6	0.05§	16.5	0.002
Sul2	17.9	28.1	0.07	32.5	8.8	0.003	12.5	4.8	0.21§	18.5	<0.001
Sul3	1.2	0.0	0.32§	5.0	3.5	1	0.0	0.0	-	1.0	0.001§
Dfr	27.4	35.4	0.2	37.5	14.0	0.007	25.0	9.5	0.04§	25.6	<0.001
TetA	15.5	21.3	0.26	40.0	12.3	0.002	9.4	6.7	0.7§	16.9	0.001
TetB	0.0	0.6	1§	0.0	0.0	-	0.0	0.0	-	0.2	1§
TetC	0.0	1.1	1§	0.0	1.8	1	0.0	0.0	-	0.6	0.6§
TetD	11.9	11.2	0.87	2.5	0.0	0.4§	9.4	1.9	0.08§	7.3	0.001
MefB	0.0	0.0	-	2.5	0.0	0.4§	0.0	0.0	-	0.2	0.2§
MphA	3.6	5.1	0.76§	7.5	1.8	0.3§	3.1	0.0	0.23§	3.4	0.1§
CatB	2.4	2.8	1§	15.0	3.5	0.06§	0.0	0.0	-	3.0	0.001§
CatI	2.4	5.1	0.51§	2.5	0.0	0.41§	3.1	1.0	0.41§	2.8	0.23§
CatII	0.0	0.6	1§	0.0	1.8	1§	0.0	0.0	-	0.4	0.43§
Cml	1.2	0.0	0.32§	2.5	1.8	1§	3.1	0.0	0.23§	0.8	0.24§
FloR	0.0	1.1	1§	12.5	1.8	0.07§	0.0	0.0	-	1.6	0.001§
Arr	0.0	0.6	1§	5.0	0.0	0.17§	0.0	0.0	-	0.6	0.17§
QacEΔ1	19.0	24.7	0.31	17.5	5.3	0.09§	21.9	7.6	0.05	17.1	0.001
QacL	0.0	0.0	-	2.5	1.8	1	0.0	0.0	-	0.4	0.04§

*Comparison between rural and urban sites; **Comparison between countries
§Fisher's exact test

Table S6. Virulence genes rates by country and site

	Madagascar			**Cambodia**			**Senegal**				
Virulence genes	Urban (%) N=84	Rural (%) N=178	**p***	Urban (%) N=40	Rural (%) N=57	**p***	Urban (%) N=32	Rural (%) N=105	**p ***	**Total** (%) N=496	**p ****
Yersiniabactin	5.9	11.8	0.14	22.5	12.3	0.18	6.2	17.1	0.16§	12.5	0.17
Colibactin	0	0.6	1§	0	0	-	0	0.9	1§	0.4	1§
Aerobactin	7.1	4.5	0.4§	0	0	-	0	0	-	2.8	0.001§
Salmochelin	2.4	4.5	0.51§	2.5	0	0.41§	0	0	-	2.2	0.03§
rmpA	1.2	1.1	1§	2.5	0	0.41§	0	0	-	0.8	0.53§
rmpA2	1.2	0.6	0.54§	0	0	-	0	0	-	0.4	0.71§
Allantoinase	2.4	3.4	1§	10	15.8	0.41	9.4	5.7	0.44§	6.1	0.001
kfuABC	38.1	38.2	1	27.5	61.4	0.001	18.7	40.9	0.02	39.3	0.17
Microcin	0	2.3	0.3§	7.5	8.8	1§	3.1	3.8	1§	3.4	0.01§
clpK	17.9	24.2	0.25	5	3.5	1§	25	10.5	0.07§	16.3	<0.001§

*Comparison between rural and urban sites; ** Comparison between countries

§ Fisher’s exact test

Table S7. Environmental exposures and colonization with Kp, MDR KP and virulent Kp among pregnant women in Madagascar, Cambodia and Senegal 2015-2016

Madagascar	Kp (N=405)					MDR-Kp (N=262)					Virulent Kp (N=262)				
		Univariate analysis		Multivariate analysis			Univariate analysis		Multivariate analysis			Univariate analysis		Multivariate analysis	
	Kp + (n, %) n=262	OR	p	aOR [95%CI]	p	MDR-Kp n=104	OR	p	aOR [95%CI]	p	Virulent Kp n=34	OR	p	aOR [95%CI]	p
Rural site	178(67.9)	1.1	0.8	1.1 [0.7-1.7]	0.8	72(69.2)	1.1	0.7	1.2 [0.7-2.2]	0.5	27(79.4)	1.97	0.1	1.7 [0.7-4.1]	0.3
Education															
Absence/primary school	56(21.4)	Ref				14(13.5)	ref				6(17.7)	ref			
Partial secondary school	152(58.0)	1.2	0.6			73(70.2)	2.8	0.003			20(58.8)	0.9	0.7		
Complete secondary or higher	54(20.6)	1.1	0.8			17(16.4)	1.4	0.5			8(23.5)	0.9	0.8		
Primigravidae	180(68.7)	0.8	0.4			71(68.3)	1.0	0.9			24(70.6)	1.1	0.8		
No. of people living in household (>3)	90(34.4)	1.3	0.3			90(34.4)	0.7	0.2			22(64.7)	1.6	0.2		
Hand washing after toilets use	172(76.9)	0.5	0.03	0.5 [0.3-0.9]	0.02	65(70.7)	0.6	0.07	0.4 [0.2-0.9]	0.02	23(69.7)	0.6	0.3		
Antibiotic consumption during pregnancy	42(16.0)	1.6	0.1	2.1 [1.1-4.1]	0.03	15(14.4)	0.8	0.6			9(26.5)	2.1	0.1		
Toilets outside the house	254(97.0)	2.1	0.1			100(96.2)	0.6	0.55			33(97.1)	1.0	0.9		
Use of fecal material as fertilizer	23(8.8)	0.8	0.6			7(6.7)	0.6	0.3			2(5.9)	0.6	0.6		
Domestic animal contact															
Dog	84(32.1)	1.1	0.7			29(27.9)	0.7	0.2			10(29.4)	0.9	0.7		
Cat	84(32.1)	0.7	0.1			30(28.9)	0.8	0.4			11(32.4)	1.0	0.9		
Pet bird	40(15.3)	0.7	0.2			11(10.6)	0.5	0.1			5(14.7)	0.9	0.9		
Poultry contact															
Chicken	133(50.8)	1.1	0.6			45(43.3)	0.6	0.05			11(32.4)	0.4	0.05		

Turkey	48(18.3)	0.7	0.1			16(15.4)	0.7	0.3			3(8.8)	0.4	0.1		
Duck	52(19.9)	0.6	0.05			18(17.3)	0.8	0.4			4(11.8)	0.5	0.2		
Livestock animals contact															
Beef	66(25.2)	0.8	0.3			21(20.2)	0.6	0.1			9(26.5)	1.1	0.9		
Pig	85(32.4)	0.8	0.4			28(26.9)	0.7	0.1			10(29.4)	0.9	0.7		
Horse	62(23.66)	0.8	0.3			19(18.3)	0.6	0.1			7(20.6)	0.8	0.7		
Animals excrement manipulation	35(13.4)	0.6	0.03	0.5 [0.2-0.8]	0.008	11(10.6)	0.7	0.3			3(8.8)	0.6	0.4		
Dietary habit															
Eats chicken ≥1/week	100(38.5)	0.8	0.4			39(37.5)	0.9	0.8			17(50)	1.7	0.1		
Eats beef ≥1/week	160(61.5)	0.8	0..4			62(59.6)	0.9	0.6			18(52.9)	0.67	0.3		
Eats pork ≥1/week	122(46.9)	0.7	0.2			48(46.2)	0.9	0.8			15(44.1)	0.9	0.7		
Eats rabbit	22(8.5)	0.8	0.6			11(10.6)	1.6	0.3			7(20.6)	3.6	0.01	3.6 [1.3-9.8]	0.01
Eats fish ≥1/week	154(59.2)	0.9	0.5			58(55.8)	0.8	0.4			22(64.7)	1.3	0.5		
Eats insects	27(10.4)	0.8	0.5			15(14.4)	2.0	0.1			7(20.6)	2.7	0.04		
Eats raw meat	32(12.4)	0.8	0.5			10(9.7)	0.7	0.3			6(17.7)	1.6	0.3		
Eats raw fish	15(5.8)	0.9	0.8			4(3.9)	0.5	0.3			3(8.8)	1.7	0.4		
Eats dry meat	44(17.3)	0.7	0.3			12(11.9)	0.5	0.07	0.4 [0.2-0.8]	0.01	7(20.6)	1.3	0.6		
Eats dry fish ≥1/week	71(28.6)	0.7	0.1			34(35.8)	1.7	0.05			11(32.3)	1.2	0.6		
Eats raw vegetables ≥1/week	219(84.6)	0.8	0.4			91(88.4)	1.7	0.2	2.4 [1.1-5.5]	0.03	28(82.4)	0.8	0.7		
Hospitalization of a household member	20(7.7)	0.8	0.6			10(9.6)	1.6	0.3			7(20.6)	4.2	0.005	4.0 [1.4-11.2]	0.009
Cambodia	Kp (N=146)					MDR-KP (N=97)					Virulent Kp (N=97)				
		Univariate analysis		Multivariate analysis			Univariate analysis		Multivariate analysis			Univariate analysis		Multivariate analysis	
	Kp + (n, %) n=97	OR	p	aOR [95%CI]	p	MDR-Kp n=25	OR	p	aOR [95%CI]	p	Virulent Kp n=29	OR	p	aOR [95%CI]	p
Rural site	57(58.8)	1.5	0.26	1.4 [0.7-2.8]	0.3	8(32.0)	0.2	0.002			16(55.2)	0.8	0.6		
Education															

Absence/primary school	52(53.6)	Ref		13(52.0)	ref		16(55.2)	Ref	
Partial secondary school	29(29.9)	0.7	0.3	8(32.0)	1.1	0.8	9(31.0)	1.0	0.9
Complete secondary or higher	16(16.5)	4.0	0.1	4(16.0)	1.0	1.0	4(13.8)	0.75	0.7
Primigravidae	68(70.1)	1.5	0.3	19(76.0)	1.5	0.5	19(65.5)	0.7	0.5
No. of people living in household (>3)	68(70.1)	1.4	0.4	68(70.1)	1.1	0.8	23(79.3)	2.0	0.2
Hand washing after toilets use	81(83.5)	2.2	0.05	20(80.0)	0.7	0.6	24(82.8)	0.9	0.9
Antibiotic consumption during pregnancy	17(17.5)	0.7	0.5	4(16.0)	0.9	0.8	4(13.8)	0.7	0.5
Toilets outside the house	45(46.4)	0.8	0.6	6(24.0)	0.3	0.1	14(48.3)	1.1	0.8
Use of fecal material as fertilizer	3(3.1)	0.4	0.2	1(4)	0.3	0.3	2(6.9)	0.6	0.5
Domestic animal contact									
Dog	13(13.4)	3.6	0.1	2(8.0)	0.5	0.4	5(17.2)	1.6	0.5
Cat	8(8.3)	1.4	0.7	2(8.0)	0.9	0.9	3(10.3)	1.5	0.6
Pet bird	1(1.0)	-	-	0(0)	-	-	0(0)	-	-
Poultry contact									
Chicken	11(11.3)	2.0	0.3	4(16.0)	1.8	0.4	1(3.5)	0.2	0.1
Turkey	0(0)	-	-	0(0)	-	-	0(0)	-	-
Duck	0(0)	-	-	0(0)	-	-	0(0)	-	-
Livestock animals contact									
Beef	4(4.1)	0.7	0.6	0(0)	-	-	0(0)	-	-
Pig	0(0)	-	-	0(0)	-	-	0(0)	-	-
Horse	0(0)	-	-	0(0)	-	-	0(0)	-	-
Animals excrement manipulation	7(7.2)	0.9	0.8	0(0)	-	-	1(3.5)	0.4	0.4
Dietary habit									
Eats chicken ≥1/week	24(24.7)	0.9	0.8	7(28.0)	1.3	0.7	9(31.0)	1.6	0.4

Eats beef ≥1/week	29(29.9)	0.7	0.3			9(36.0)	1.5	0.4			7(24.1)	0.7	0.4		
Eats pork ≥1/week	76(78.4)	0.5	0.2			19(76.0)	0.8	0.7			21(72.4)	0.6	0.4		
Eats rabbit	1(1.0)	0.5	0.6			1(4.0)	-	-			1(3.5)	-	-		
Eats fish ≥1/week	83(85.6)	2.0	0.1			20(80.0)	0.6	0.4			23(79.3)	0.5	0.3		
Eats insects	59(60.8)	1.5	0.3			14(56.0)	0.8	0.6			16(55.2)	0.7	0.5		
Eats raw meat	19(19.6)	1.1	0.9			4(16.0)	0.7	0.6			4(13.8)	0.6	0.4		
Eats raw fish	7(6)	1.8	0.5			2(8.0)	1.2	0.9			0(0)	-	-		
Eats dry meat	56(57.7)	0.9	0.7			14(56.0)	0.9	0.8			18(62.1)	1.3	0.6		
Eats dry fish ≥1/week	51(52.6)	2.1	0.04	2.0 [1.0-4.1]	0.05	12(48.0)	0.8	0.6			15(51.7)	0.9	0.9		
Eats raw vegetables ≥1/week	51(52.6)	1.4	0.4			13(52.0)	1.0	0.9			13(44.8)	0.6	0.3		
Hospitalization of a household member	9(9.3)	0.9	0.9			3(12.0)	1.5	0.6			2(6.9)	0.6	0.6		

Senegal	Kp (N=330)					MDR-KP (N=137)					Virulent Kp (N=137)				
	Univariate analysis			Multivariate analysis		Univariate analysis			Multivariate analysis		Univariate analysis			Multivariate analysis	
	Kp + (n, %) n=137	OR	p	aOR [95%CI]	p	MDR-Kp n=16	OR	p	aOR [95%CI]	p	Virulent Kp n=29	OR	p	aOR [95%CI]	p
Rural site	104(75.9)	2.0	0.007	1.5 [0.9-2.6]	0.2	12(75.0)	1.9	0.9	1.8 [0.5-6.8]	0.4	24(82.8)	1.7	0.3	1.2 [0.4-3.5]	0.8
Education															
Absence/primary school	92(67.2)	ref				11(68.8)	ref				17(58.6)	ref			
Partial secondary school	31(22.6)	1.4	0.3			3(18.8)	0.8	0.7			9(31.0)	1.8	0.2		
Complete secondary or higher	14(10.2)	1.0	1			2(12.5)	1.2	0.8			3(10.3)	1.2	0.8		
Primigravidae	110(80.3)	1.2	0.6			13(81.3)	1.1	0.9			24(82.8)	1.2	0.7		
No. of people living in household (>3)	67(48.9)	1.1	0.5			67(48.9)	0.8	0.7			13(44.8)	0.8	0.6		
Hand washing after toilets use	132(96.4)	1.3	0.6			16(100)	-.	-			26(89.7)	0.2	0.05		

Antibiotic consumption during pregnancy	11(8.0)	0.7	0.4			1(6.3)	0.7	0.8			2(6.9)	0.8	0.8		
Toilets outside the house	129(94.2)	1.2	0.7			14(87.5)	0.4	0.2			29(100)	-	-		
Use of fecal material as fertilizer	19(13.9)	1.7	0.1			2(12.5)	0.9	0.9			8(27.6)	3.4	0.02	3.7 [1.7-11.0]	0.02
Domestic animal contact															
Dog	10(7.3)	1.2	0.7			2(12.5)	2.0	0.4			2(2.1)	0.9	0.9		
Cat	41(29.9)	1.0	0.9			1(6.3)	0.1	0.06			13(44.8)	2.3	0.05		
Pet bird	1(0.7)	1.4	0.8			0(0)	-	-			0(0)	-	-		
Poultry contact															
Chicken	82(59.9)	2.2	0.001	1.9 [1.2-3.1]	0.008	5(31.3)	0.3	0.02	0.2 [0.06-0.7]	0.01	23(79.3)	3.2	0.05		
Turkey	1(0.7)	0.3	0.2			0(0)	-	-			0(0)	-	-		
Duck	13(9.5)	1.2	0.7			1(6.3)	0.6	0.6			2(6.9)	0.7	0.6		
Livestock animals contact															
Beef	2(1.5)	2.8	0.4			1(6.3)	8.0	0.2			0(0)	-	-		
Pig	2(1.5)	1.4	0.7			0(0)	-	-			0(0)	-	-		
Horse	4(2.9)	5.8	0.1			1(6.3)	2.6	0.4			1(3.5)	1.3	0.8		
Animals excrement manipulation	49(35.8)	2.0	0.1			2(12.5)	0.2	0.06			13(44.8)	1.6	0.3		
Dietary habit															
Eats chicken ≥1/week	55(40.2)	1.7	0.04			4(25.0)	0.5	0.2			11(37.9)	0.9	0.8		
Eats beef ≥1/week	44(32.1)	1.5	0.1			4(25.0)	0.7	0.5			6(20.7)	0.5	0.1		
Eats pork ≥1/week	0(0)	-	-			0(0)	-	-			0(0)	-	-		
Eats rabbit	7(5.1)	1.2	0.7			0(0)	-	-			3(10.3)	3.0	0.2		
Eats fish ≥1/week	124(90.5)	1.6	0.2			15(93.8)	1.7	0.6			23(79.3)	0.3	0.03	0.2 [0.1-0.8]	0.02
Eats insects	3(2.2)	4.3	0.2			0(0)	-	-			1(3.5)	1.9	0.6		
Eats raw meat	0(0)	-	-			0(0)	-	-			0(0)	-	-		
Eats raw fish	1(0.7)	-	-			0(0)	-	-			0(0)	-	-		
Eats dry meat	37(27.0)	1.0	0.9			4(25.0)	0.9	0.8			11(37.9)	1.9	0.1		
Eats dry fish ≥1/week	135(98.5)	2.7	0.2			16(100)	-	-			29(100)	-	-		
Eats raw vegetables ≥1/week	104(75.9)	1.0	0.9			13(81.3)	1.4	0.6			23(79.3)	1.3	0.6		

Hospitalization of a household member	21(15.3)	1.8	0.1	1(6.3)	0.3	0.3	8(27.6)	2.8	0.05

Figure S1: study sites

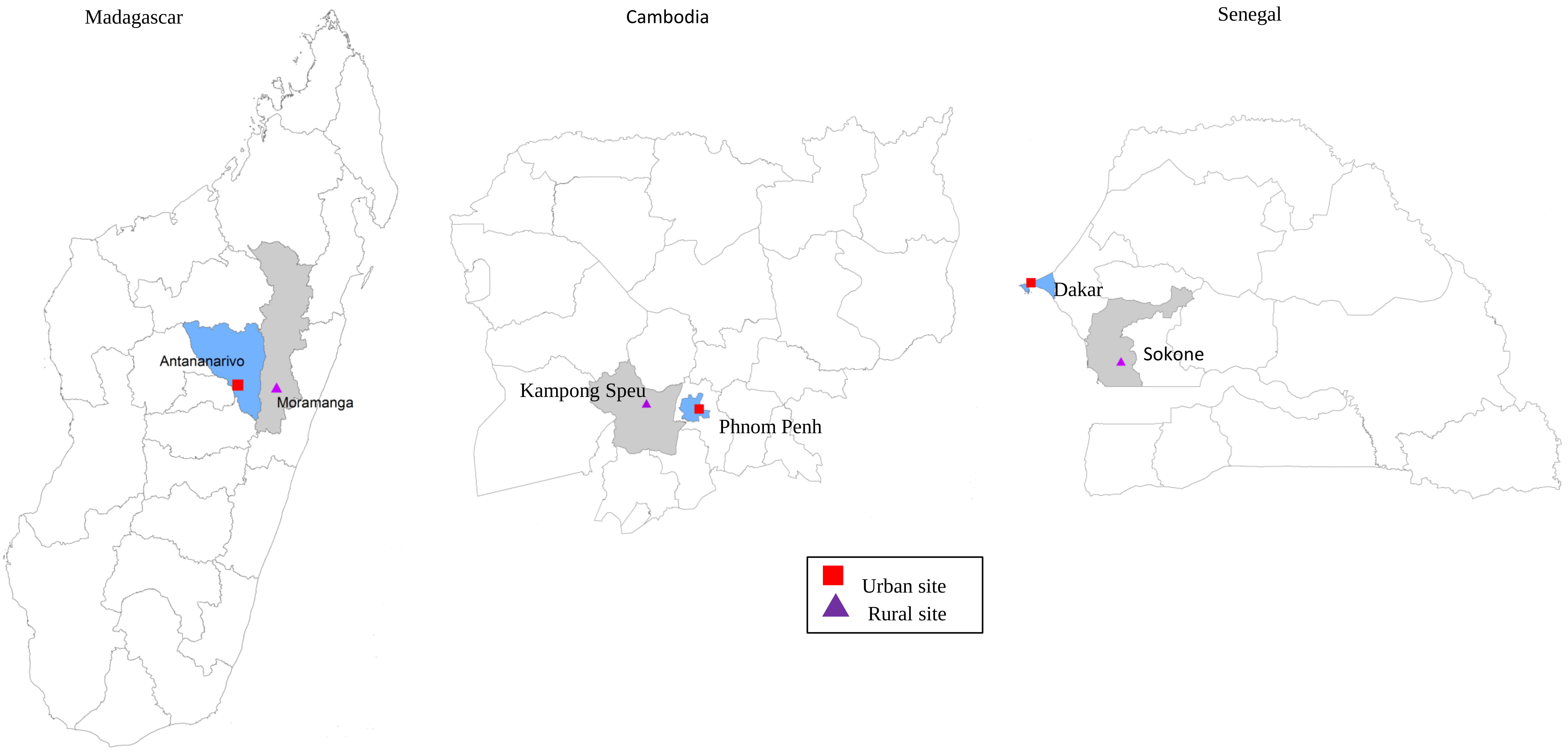


Figure S2. Flow diagram of inclusions

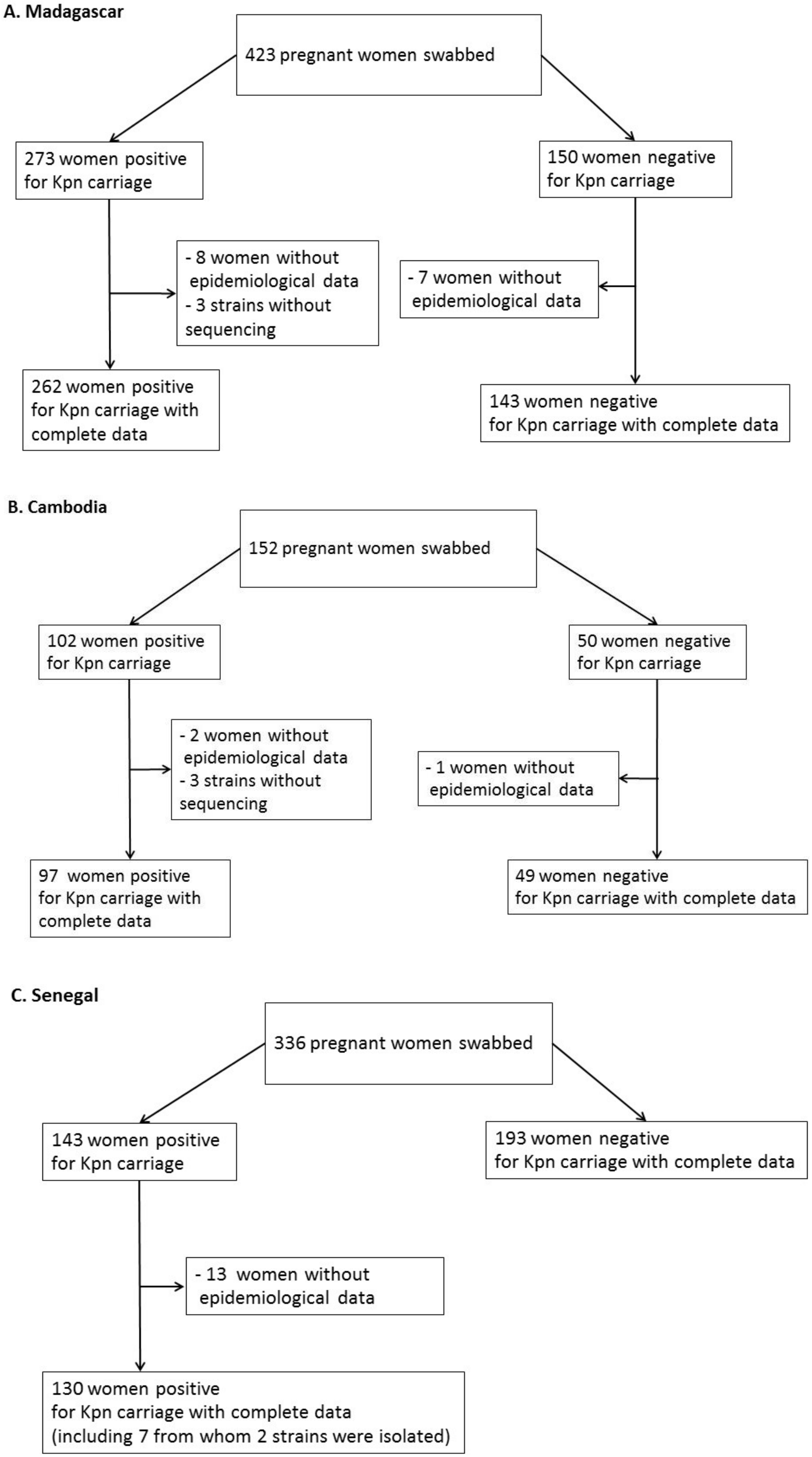


Figure S3. MLST sequence type (ST) diversity

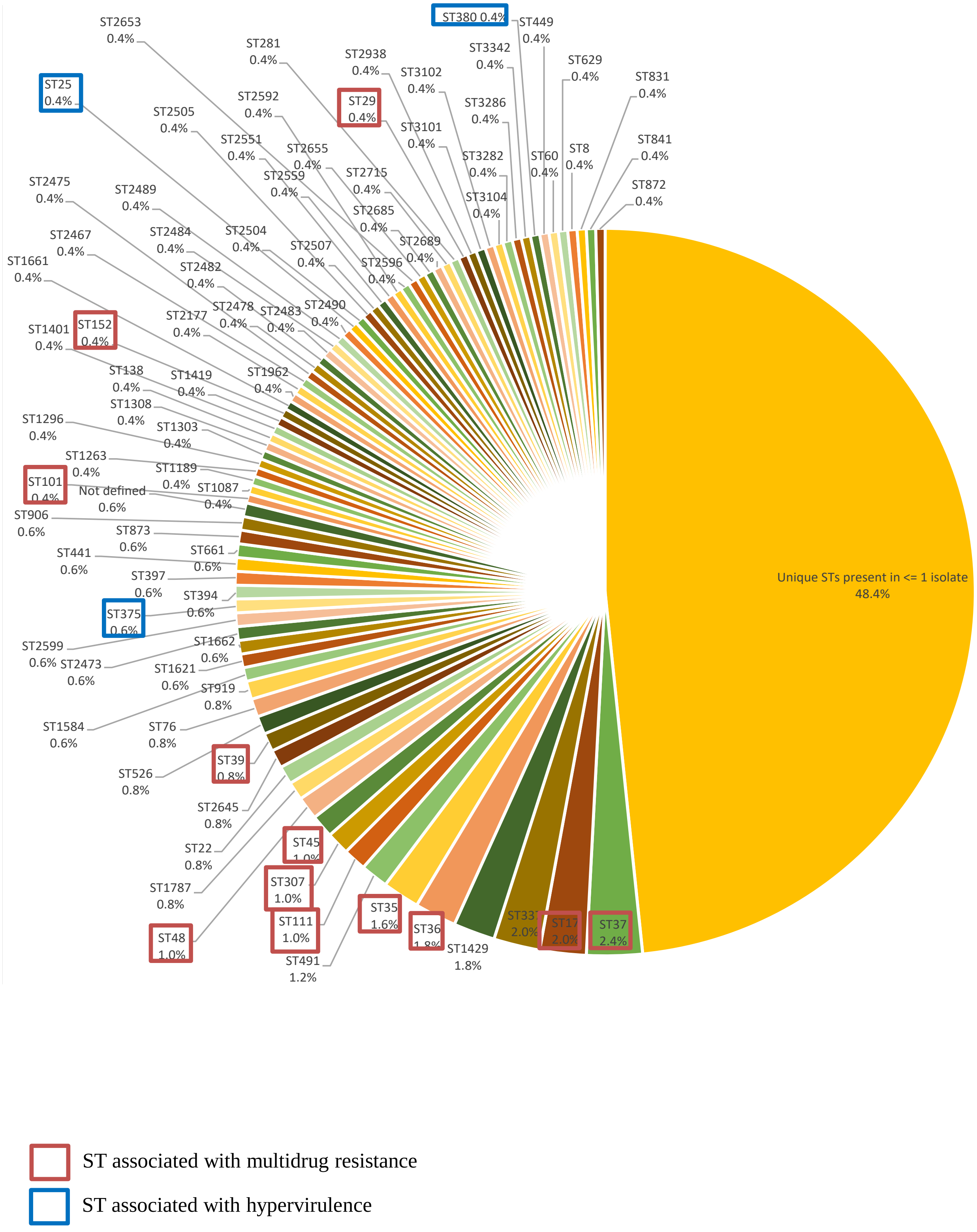
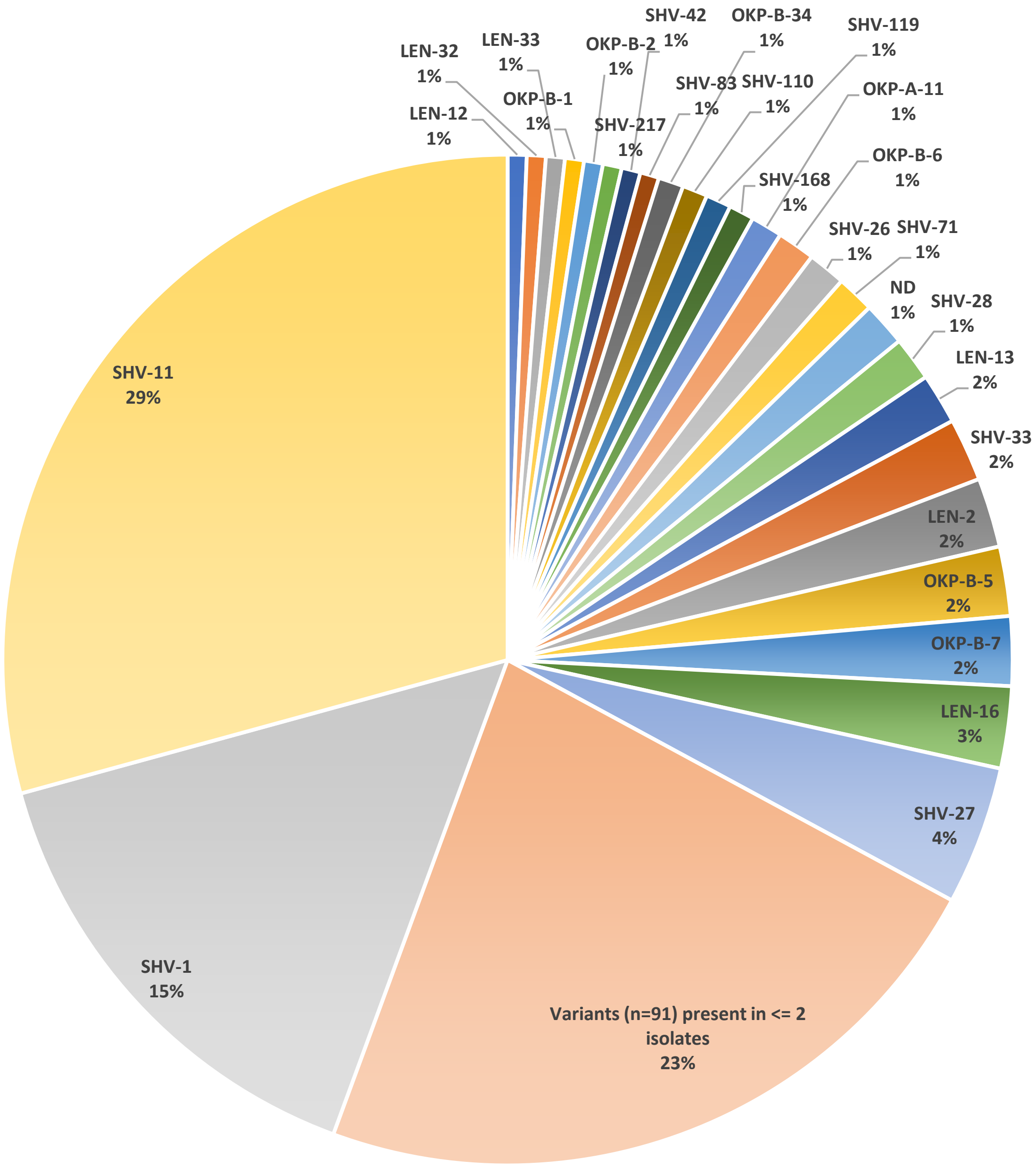


Figure S4.

Diversity of the beta-lactamases-encoding genes (*bla*$_{\mathrm{SHV,}}$ *bla*$_{\mathrm{OKP,}}$ *bla*$_{\mathrm{LEN}}$)



ND, not detected

Figure S5. Rate of virulence clusters or genes, by country of isolation

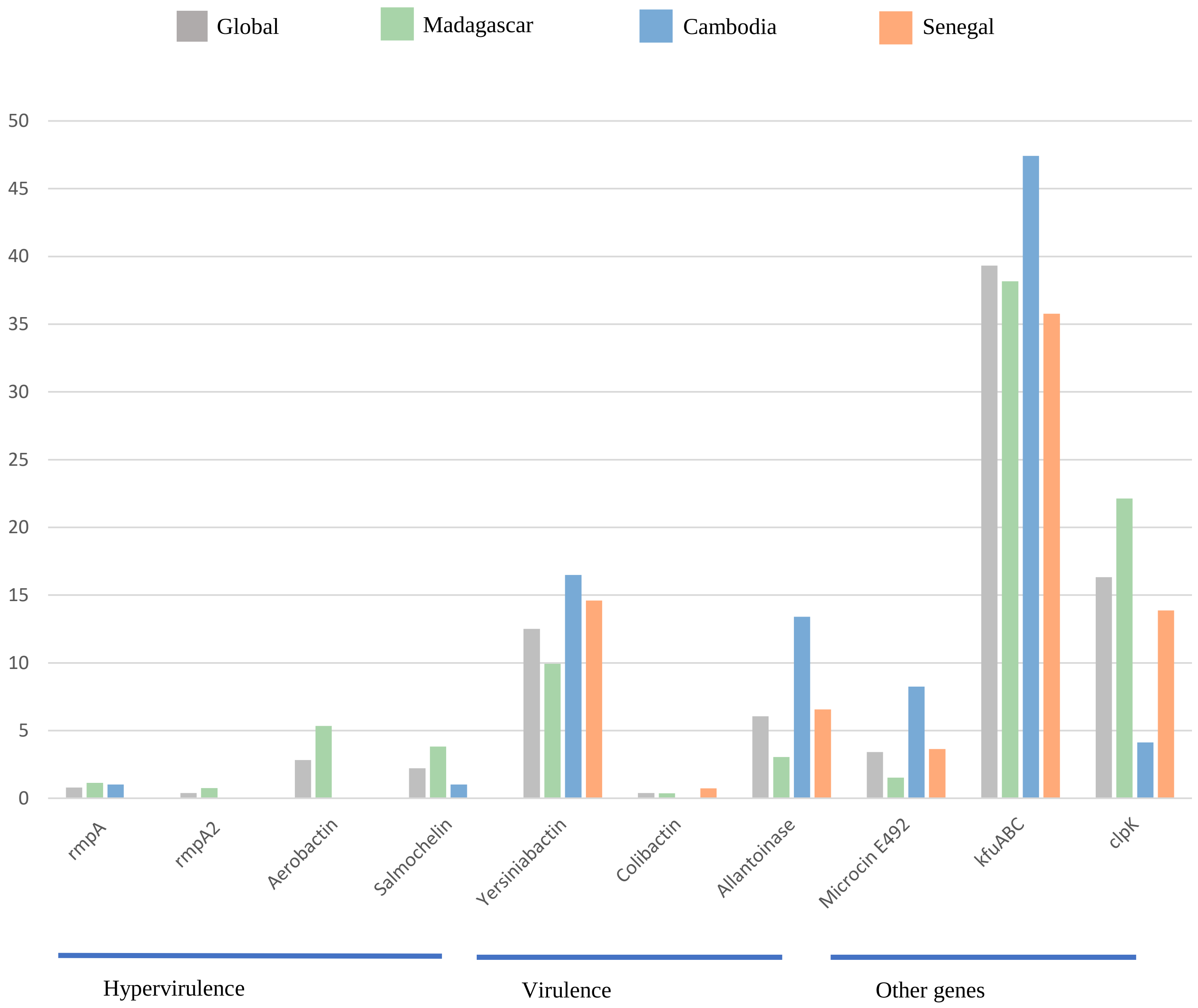
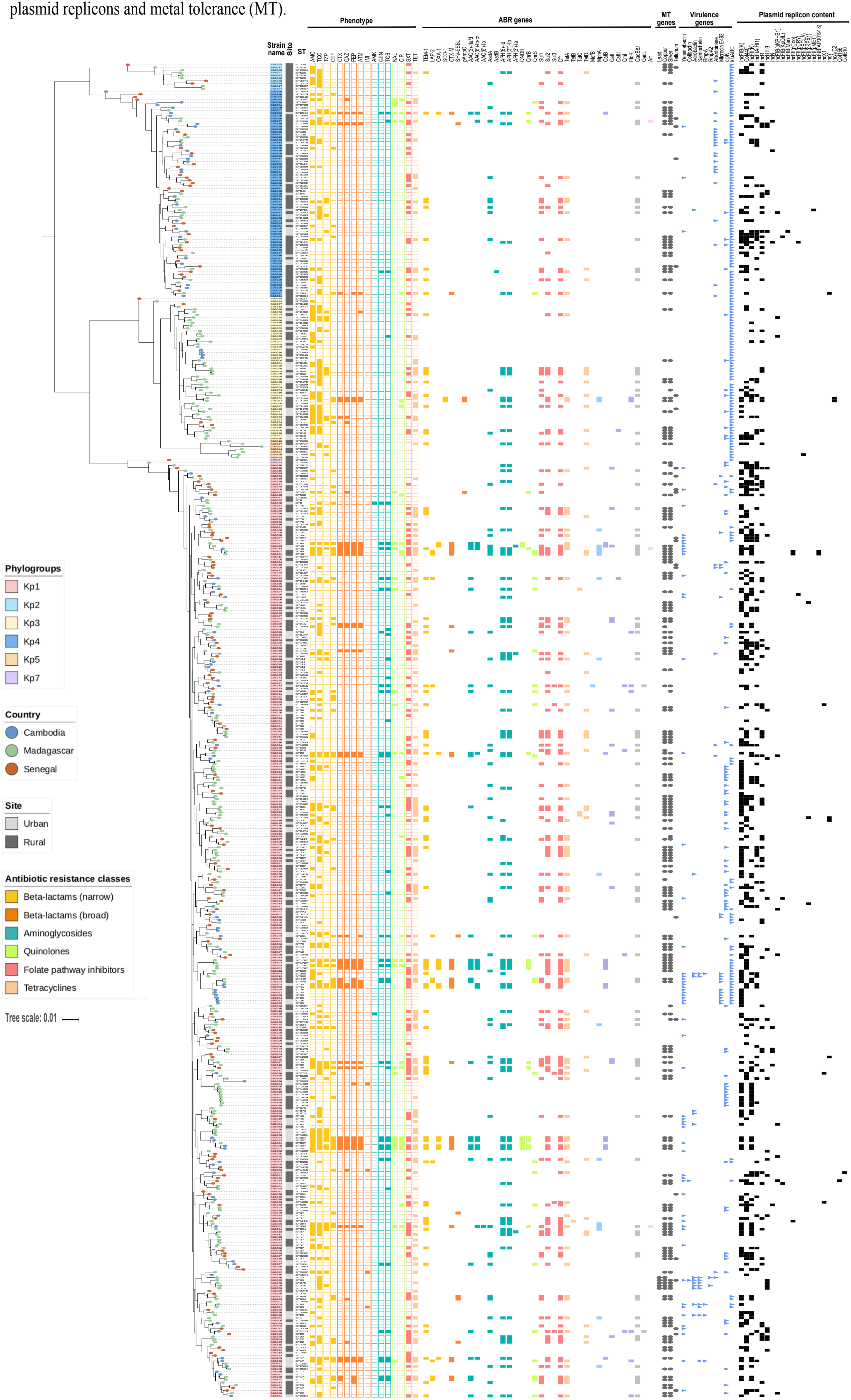


Figure S6. Details of presence per isolate of antimicrobial resistance phenotype, and of genes coding for antimicrobial resistance, virulence or plasmid replicons and metal tolerance (MT).



Isolates are ordered vertically according to the same phylogeny (left) as in the main phylogeny Figure. Note that cluster kfuABC was conserved in non-Kp1 isolates but not within Kp1.