KPC and NDM-1 Genes in Related Enterobacteriaceae Strains and Plasmids from Pakistan and the United States

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To characterize the genomic context of New Delhi metallo-β-lactamase-1 (NDM-1) and Klebsiella pneumoniae carbapenemase (KPC), we sequenced 78 Enterobacteriaceae isolates from Pakistan and the United States encoding KPC, NDM-1, or no carbapenemase. High similarities of the results indicate rapid spread of carbapenem resistance between strains, including globally disseminated pathogens.

Pathogenic Enterobacteriaceae, including Escherichia coli and Klebsiella pneumoniae, are major causes of multidrug-resistant (MDR) infections in hospitals worldwide. These pathogens have recently been shown to have acquired resistance to carbapenems, and the US Centers for Disease Control and Prevention identified carbapenem-resistant Enterobacteriaceae as 1 of the 3 most urgent MDR threats (1). Among the Enterobacteriaceae, β-lactam resistance, including carbapenem resistance, is primarily caused by enzymatic degradation by β-lactamases. Two carbapenemase subclasses are especially problematic: Klebsiella pneumoniae carbapenemase (KPC) and New Delhi metallo-β-lactamase-1 (NDM-1). KPC, identified in 2001 (2), has become endemic to several noncontiguous areas of the world, including the United States, Israel, Greece, South America, and China (3). NDM-1 was first described in 2008, although retrospective studies identified NDM-1 from 2006 (4) and is abundant in New Delhi water samples (5). Most patients from whom NDM-1 is isolated have an epidemiologic link to the Indian subcontinent, but NDM-1 has also recently become endemic to the Balkans and Middle East (6).

The spread of antibiotic resistance genes such as NDM-1 and KPC is facilitated by horizontal gene transfer (HGT) between bacteria (7). Among globally disseminated pathogens, HGT facilitates combination of the most effective antibiotic resistance genes from diverse geographies into multidrug resistance plasmids that spread between strains. Recombination and transposition have created populations of these plasmids that have related architectures but vary in their composition of antibiotic drug resistance cassettes (8). This effect has enabled both KPC and NDM-1 to rapidly expand within the Enterobacteriaceae and other proteobacterial pathogens, such as Acinetobacter baumannii (9,10). Antibiotic resistance genes can also spread through clonal expansion in successful pathogenic strains, for example, KPC in K. pneumoniae sequence type (ST) 258 (11), and the extended-spectrum β-lactamase CTX-M-15 in E. coli ST131 (12). Both HGT and clonal expansion have enabled KPC and NDM-1 to rapidly spread to distant locations after their emergence (6,8).

The similarities in the spread and resistance spectra of KPC and NDM-1 (both provide resistance to nearly all β-lactam antimicrobial drugs) leads to the hypothesis that similar mobile elements will make both genes available to similar pathogen populations. We tested this hypothesis by examining clinical Enterobacteriaceae isolates from Pakistan and the United States encoding NDM-1, KPC, or no carbapenemase.

The Study
We collected 450 bacterial isolates (including 195 Enterobacteriaceae) in Pakistan during February 2012–March 2013 from Pakistan Railway General Hospital in Rawalpindi and the Pakistan Institute of Medical Sciences in Islamabad. From this collection, we randomly selected 55 Enterobacteriaceae isolates for whole-genome sequencing. We then selected 23 isolates from samples collected in the United States during January 2010–June 2013 from patients in Barnes Jewish Hospital in St. Louis, Missouri, that had similar proportions of β-lactam susceptibility and resistance to the isolates collected in Pakistan for sequencing. All isolates were de-identified and retrieved from existing strain banks. The combined set included 33 E. coli, 30 K. pneumoniae, 9 Enterobacter cloacae, and 6 Enterobacter aerogenes (online Technical Appendix Table 1, http://wwwnc.cdc.gov/EID/article/21/6/14-1504-Techapp1.pdf). We extracted plasmid DNA from 9 isolates encoding NDM-1, 11 isolates encoding KPC, and 3 isolates encoding CTX-M-15 and performed shotgun sequencing on those plasmid preparations. Detailed methods are described in the online Technical Appendix.

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Using antibiotic resistance gene predictions from the Resfams database (13) and core genome alignment, we constructed a phylogenetic tree for each species in our set, overlaid by the β-lactamases encoded by each isolate (Figure 1). Isolates from both locations were found to be members of the same subspecies clades (online Technical Appendix Figure 1) and to contain similar repertoires of β-lactamases (Figure 1), indicating that geography is not a discriminating variable for these isolates. Many of these isolates were also MDR: resistance to ciprofloxacin, trimethoprim/sulfamethoxazole, gentamicin, doxycycline, and chloramphenicol occurred in 63%, 65%, 45%, 54%, and 56% of isolates, respectively. As expected from results of previous work (8), E. coli ST131 isolates had high rates of CTX-M carriage (82%; Figure 1, panel A) and ciprofloxacin resistance (100%).

The variety of strains that we discovered encoding KPC and NDM-1 is consistent with existing evidence that HGT is a major factor in their spread. All KPC genes were proximal to Tn4401 and all NDM-1 genes were carried on ISAba125, mobile elements with which each gene has respectively been previously associated (14). We observed multiple examples of NDM-1 within the K. pneumoniae ST11 clade (15) (Figure 1, panel B; online Technical Appendix Figure 1, panel B), a close relative of ST258. This association could be caused by clonal expansion or multiple HGT events and emphasizes that lineages known to encode KPC are now also acquiring NDM-1. We also observed high rates of NDM-1 carriage in Enterobacter isolates (Figure 1, panels C and D), which in general showed a high number (maximum 8) and wide variety of β-lactamases. These isolates were also MDR: 57% of the Enterobacter isolates were resistant to all or all

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**Figure 1.** Distribution of antimicrobial drug resistance genotypes of Klebsiella pneumoniae carbapenemase (KPC) and New Delhi metallo-β-lactamase-1 (NDM-1) genes in related Enterobacteriaceae strains and plasmids in Pakistan and the United States. A) Escherichia coli; B) K. pneumoniae; C) Enterobacter cloacae; D) E. aerogenes. Phylogenetic trees have been annotated with the specific β-lactamases encoded by those isolates. *Denotes an unnamed single nucleotide variant of the named β-lactamase. Scale bars indicate nucleotide substitutions per site.
but 1 of the antimicrobial drugs tested. At best, these Enterobacter strains are a reservoir for resistance in Pakistan; at worst, they are the vanguard of an expansion of carbapenem-resistant Enterobacter infections.

Previous observations have predominantly found KPC and NDM-1 to be expressed from plasmids (6,11). To characterize the sequence similarity of plasmids within the NDM- and KPC-carrying plasmid populations, we purified and sequenced plasmid DNA from 9 isolates encoding NDM-1, 11 encoding KPC, and 3 encoding CTX-M-15. Sequencing showed that these plasmids include representatives from IncHI2, IncY, IncN, IncFIA, IncFIB, IncFIC, and IncI1 incompatibility groups. Using reciprocal BLAST (http://blast.ncbi.nlm.nih.gov/Blast.cgi) alignment between each pair of plasmid preparations, we calculated the percentage of each plasmid shared using a 99% identity threshold. We performed this same analysis for all sequenced plasmids containing NDM-1, KPC, or CTX-M available in the National Center for Biotechnology Information database (http://www.ncbi.nlm.nih.gov) together with our set (Figure 2) and separately (online Technical Appendix Figure 2).

Certain components, primarily mobile elements, were abundant within these plasmids: the average plasmid shared 500 contiguous bases with 58 of the other plasmids; however, median BLAST identity for this pairwise comparison was <12%, even when considering plasmids with the same β-lactamase, suggesting that both carbapenemases exist within a variety of plasmid configurations.

To visualize this comparison of carbapenemase plasmids, we generated a network diagram in which each node represented a plasmid and each line represented shared sequence between 2 plasmids (Figure 2, panel B). Node size and line width correlate to the number of nucleotides contained in the plasmid or sharing interaction. This visualization shows the abundant small, shared regions that exist between most plasmid pairs, represented as thin background lines. This visualization also highlights the larger shared regions that indicate highly similar plasmids, represented by the few wide lines. These outliers were often between pairs of plasmids encoding the same β-lactamase but were also observed between NDM-1 and KPC containing plasmids (maximum 79% of smaller plasmid length).

Figure 2. Pairwise BLAST identity (http://blast.ncbi.nlm.nih.gov/Blast.cgi) of all CTX-M genes, Klebsiella pneumoniae carbapenemase (KPC), and New Delhi metallo-β-Lactamase-1 (NDM-1) plasmids from isolates collected in Pakistan and the United States plasmid preparations, and the National Center for Biotechnology Information database complete plasmids. An all-against-all plasmid BLAST was performed and plasmid interactions were defined by the percentage of the query plasmid conserved (at ≥99% identity) in the subject plasmid. A) Plasmid interactions collected based on the defining β-lactamase of their query and subject plasmids. Box and whisker plots represent the range of pairwise sharing values within this population of plasmids. Upper and lower boundaries of the box correspond to the first and thirds quartiles; whiskers (error bars) represent 1.5 times the interquartile range; points beyond the whiskers represent outliers. B) Network map in which nodes represent individual plasmids and lines represent regions shared between plasmids. Line width is proportional to the number of nucleotides contained in fragments >500 bp in length at >99% sequence identity. Genetic elements repeated within the same plasmid DNA are represented by lines that leave and return to the same node. Plasmid sequence origin is indicated in arcs around the network.
Conclusions
Together, this evidence supports our hypothesis that strains and plasmids known to carry either carbapenemase also have access to the other. Given the similarity of carbapenemase-negative strains to those carrying KPC or NDM-1 and the high diversity of plasmids in which they can be found, we anticipate that global carbapenem usage will encourage HGT of both of these carbapenemases into additional strain and plasmid backgrounds. Because KPC and NDM-1 are poised to cross genetic and geographic boundaries, we recommend that hospitals routinely screen Enterobacteriaceae strains for both genes, even in regions where they are not yet endemic. We further advocate reduced carbapenem use to limit the selection for resistance against this vital antibiotic class.

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References
1. Centers for Disease Control and Prevention. Antibiotic resistance threats in the United States, 2013 [cited 2014 Sep 15]. http://www.cdc.gov/drugresistance/threat-report-2013/index.html
2. Yigit H, Queenan AM, Anderson GJ, Domenech-Sanchez A, Biddle JW, Steward CD, et al. Novel carbapenem-hydrolyzing beta-lactamase, KPC-1, from a carbapenem-resistant strain of Klebsiella pneumoniae. Antimicrob Agents Chemother. 2001;45:1151–61. http://dx.doi.org/10.1128/AAC.45.4.1151-1161.2001
3. Munoz-Price LS, Poirel L, Bonomo RA, Schwaber MJ, Daikos GL, Cormican M, et al. Clinical epidemiology of the global expansion of Klebsiella pneumoniae carbapenemases. Lancet Infect Dis. 2013;13:785–96. http://dx.doi.org/10.1016/S1473-3099(13)70190-7
4. Castanheira M, Deshpande LM, Mathai D, Bell JM, Jones RN, Mendes RE. Early dissemination of NDM-1 and OXA-181-producing Enterobacteriaceae in Indian hospitals: report from the SENTRY Antimicrobial Surveillance Program, 2006–2007. Antimicrob Agents Chemother. 2011;55:1274–8. http://dx.doi.org/10.1128/AAC.01497-10
5. Walsh TR, Weeks J, Livermore DM, Toleman MA. Dissemination of NDM-1 positive bacteria in the New Delhi environment and its implications for human health: an environmental point prevalence study. Lancet Infect Dis. 2011;11:355–62. http://dx.doi.org/10.1016/S1473-3099(11)70059-7
6. Dortet L, Poirel L, Nordmann P. Worldwide dissemination of the NDM-type carbapenemases in gram-negative bacteria. Biomed Res Int. 2014;2014:249856. http://dx.doi.org/10.1155/2014/249856
7. Thomas CM, Nielsen KM. Mechanisms of, and barriers to, horizontal gene transfer between bacteria. Nat Rev Microbiol. 2005;3:711–21. http://dx.doi.org/10.1038/nrmicro1234
8. Hawkey PM, Jones AM. The changing epidemiology of resistance. J Antimicrob Chemother. 2009;64(Suppl 1):13–10. http://dx.doi.org/10.1093/jac/dkp256
9. Robledo IE, Aquino EE, Vazquez GJ. Detection of the KPC gene in Escherichia coli, Klebsiella pneumoniae, Pseudomonas aeruginosa, and Acinetobacter baumannii during a PCR-based nosocomial surveillance study in Puerto Rico. Antimicrob Agents Chemother. 2011;55:2968–75. http://dx.doi.org/10.1128/AAC.01633-10
10. Sartor AL, Raza MW, Abbasi SA, Day KM, Perry JD, Paterson DL, et al. Molecular epidemiology of NDM-1 producing Enterobacteriaceae and Acinetobacter baumannii isolates from Pakistan. Antimicrob Agents Chemother. 2014;58:5589–93. http://dx.doi.org/10.1128/AAC.02425-14
11. Cuzon G, Naas T, Trioung H, Villegas MV, Wisell KT, Carmeli Y, et al. Worldwide diversity of Klebsiella pneumoniae that produce beta-lactamase blaKPC-2 gene. Emerg Infect Dis. 2010;16:1349–56. http://dx.doi.org/10.3201/eid1609.091389
12. Petty NK, Ben Zakour NL, Stanton-Cook M, Skippening E, Totsika M, Forde BM, et al. Global dissemination of a multidrug resistant Escherichia coli clone. Proc Natl Acad Sci U S A. 2014;111:5694–9. http://dx.doi.org/10.1073/pnas.1322678111
13. Gibson MKK, Dantas G. Improved annotations of antibiotic resistance functions reveals microbial resistomes cluster by ecology. ISME. 2014;106. http://dx.doi.org/10.1038/ismej.2014.106
14. Patel G, Bonomo RA. Status report on carbapenemases: challenges and prospects. Expert Rev Anti Infect Ther. 2011;9:555–70. http://dx.doi.org/10.1586/eri.11.28
15. Peña I, Picazo JJ, Rodriguez-Avial C, Rodriguez-Avial I. Carbapenemase-producing Enterobacteriaceae in a tertiary hospital in Madrid, Spain: high percentage of colistin resistance among VIM-1-producing Klebsiella pneumoniae ST11 isolates. Int J Antimicrob Agents. 2014;43:460–4 http://dx.doi.org/10.1016/j.ijantimicag.2014.01.021

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KPC and NDM-1 Genes in Related *Enterobacteriaceae* Strains and Plasmids from Pakistan and the United States

**Technical Appendix**

**Methods and Materials**

**Sample Selection, Processing, and Phenotyping**

We collected 450 Pakistani bacterial isolates (PH) initially recovered from de-identified clinical samples from urinary, blood stream, genitourinary, and wound infections collected between February 2012 and March 2013 at Pakistan Railway General Hospital, Rawalpindi, Pakistan, and the Pakistan Institute of Medical Sciences in Islamabad, Pakistan. These included all ESKAPE pathogen isolates available in the Pakistani hospital strain banks during the indicated collection period. From these 450 isolates, we chose a random subset of 55 isolates from the *Enterobacteriaceae* family (from a total of 195 *Enterobacteriaceae* in this collection) for phenotypic and genotypic analysis. We also selected 48 US *Enterobacteriaceae* isolates (WU) from banked, de-identified frozen stocks of *Escherichia coli*, *Klebsiella pneumoniae*, and *Enterobacter cloacae* at Barnes Jewish Hospital/Washington University School of Medicine in Saint Louis, Missouri, United States to have beta-lactam resistance and susceptibility phenotypes in similar proportions to the Pakistani *Enterobacteriaceae* isolates, with a particular focus on the meropenem resistance phenotype (protocols for growth and phenotyping are described below). The WU strains were originally isolated from urine, respiratory, bone, and bile specimens between January 2010 and June 2013. Of the 48 WU isolates, 23 isolates were chosen for genome sequencing to generally match the species distribution of the 55 PH isolates as well as their beta-lactam resistance profiles, with the exception of *Enterobacter aerogenes*, for which none were available in the WU collection. In total, 33 *Escherichia coli* (24 PH, 9 WU), 30 *Klebsiella pneumoniae* (19 PH, 11 WU), 9 *Enterobacter cloacae* (6 PH, 3 WU), and 6 *Enterobacter aerogenes* (all 6 PH) isolates were included for the whole genome sequencing
analysis (Technical Appendix Tables 1 and 2). We cultivated all isolates on MacConkey and sheep’s blood agar (Hardy Diagnostics). We then grew single colonies in LB broth liquid culture for DNA extraction. We assessed each isolate for susceptibility to ampicillin, cefazolin, cefotetan, ceftazidime, ceftriaxone, cefepime, meropenem, ciprofloxacin, trimethoprim-sulfamethoxazole, gentamicin, doxycycline, and chloramphenicol by Kirby-Bauer disk diffusion according to Clinical and Laboratory Standards Institute guidelines and interpretive criteria (1).

Prior to whole genome sequencing, the species identity of PH and WU isolates was determined with VITEK MS MALDI-TOF MS v2.0 knowledgebase (bioMerieux) as previously described (2,3). We then extracted total DNA using the Invitrogen Charge Switch gDNA Mini Bacteria kit per the manufacturer’s protocol. We also extracted plasmid DNA from 11 KPC and 9 NDM-1 encoding isolates (as well as 3 CTX-M-15 encoding isolates), as determined by PCR and the genome sequencing, using the Qiagen Large Construct kit per the manufacturer’s protocol. We included one non-Enterobacteriaceae plasmid preparation from an Acinetobacter baumannii isolate (PH), which had been identified to contain NDM-1 by PCR.

**Illumina Library Preparation**

We sheared 500ng of total DNA from each isolate to ~300 bp fragments fragments in nine rounds of shearing of ten minutes each on the BioRupter XL. In each round the power setting was ‘H’ and samples were treated for 30s and allowed to rest for 30s. Each sample was concentrated using the Qiagen MinElute PCR purification kit per the manufacturer’s protocol. End Repair of the sheared DNA fragments was initiated with the addition of 2.5 µl of T4 DNA ligase buffer with 10mM ATP (NEB, B0202S), 1 µl of 1 mM dNTPs (NEB), 0.5 µl T4 Polymerase (NEB, M0203S), 0.5 µl T4 PNK (NEB M0201S), and 0.5 µl Taq Polymerase (NEB, M0267S). This mixture was incubated at 25°C for 30 min, then at 75°C for 20 min. Barcoded adapters were then added to the solution along with 0.8µl of T4 DNA ligase (NEB, M0202M), for the purpose of ligating the adapters to the DNA fragments. This solution was then incubated at 16°C for 40min, then 65°C for 10min. At this point the adapter-ligated DNA was purified using the Qiagen MinElute PCR purification kit per the manufacturer’s protocol.

The DNA fragments were then size selected on a 2% agarose gel in 1X TBE buffer stained with Biotium GelGreen dye (Biotium). DNA fragments were combined with 2.5uL 6X Orange loading dye before loading on to the gel. Adaptor-ligated DNA was extracted from gel
slices corresponding to DNA of 250-300bp using a QIAGEN MinElute Gel Extraction kit per the manufacturer’s protocol. The purified DNA was enriched by PCR using 12.5µL 2X Phusion HF Master Mix and 1µL of 10µM Illumina PCR Primer Mix in a 25µL reaction using 1µL of purified DNA as template. DNA was amplified at 98°C for 30 seconds followed by 18 cycles of 98°C for 10 seconds, 65°C for 30 seconds, 72°C for 30 seconds with a final extension of 5min. at 72°C. Afterwards, the DNA concentration was measured using the Qubit fluorometer and 10nmol of each sample (up 106 per lane of sequencing) were pooled. Subsequently, samples were submitted for Illumina HiSeq-2500 Pair-End (PE) 101bp sequencing at GTAC (Genome Technology Access Center, Washington University in St. Louis) at 9pmol per lane.

**Genome Sequence Assembly**

All sequencing reads were de-multiplexed by barcode into separate genome bins. Reads were quality trimmed to remove adapter sequence and bases on either end with a quality score below 19. Any reads shorter than 31bp after quality trimming were not used in further analysis. The best reference sequence was chosen for each isolate or plasmid by mapping 10000 reads chosen randomly from that isolate against all reference genomes (from NCBI Genome, downloaded July 14th 2014) of the same species as the isolate (in the case of genomic DNA assembly) or against all plasmid sequences containing NDM-1, KPC, or CTX-M (in the case of plasmid DNA assembly). Reads were mapped using Bowtie 2 (4) (command: bowtie2 –x <reference_genome_index_name> -1 <forward_read_file> -2 <reverse_read_file> -q --phred33 -v--very-fast –I 100 –X 600 --no-discordant --no-mixed --no-unal --no-hd --no-sq --omit-sec-strand). The genome or plasmid against which the highest percentage of reads mapped was used as the reference sequence for that assembly. It was empirically determined that if this first mapping included fewer than 60% of the reads, then the assembly would be best done completely de novo. For isolates with >60% of reads matching a reference sequence, all reads were mapped to that sequence (command: bowtie2 –x <reference_genome_index_name> -1 <forward_read_file> -2 <reverse_read_file> -q --phred33 --very-sensitive-local -I 200 -X 1000 - S <sam_output>). Variants from the reference were called using samtools (commands: samtools view -buS <sam_file> | samtools sort -m 4000000000 - <sample_prefix> ### samtools index <bam_file> ### samtools mpileup -uD -f <reference_genome> <bam_file> | bcftools view -bcv - > <bcf_file> ### bcftools view <bcf_file>). The variant call format file was then filtered to
remove SNPs with a quality score lower than 70 or coverage greater than twice the average coverage expected per base. Custom scripts were then used to extract DNA sequences from the reference genome with > three independent reads, to create a fragment file of regions in the sample genome matching the reference genome modified with high-quality variant information.

*De novo* assembly of the reads from each isolate was completed using Velvet (5) (commands: velveth <output_directory> 51 -fastq -shortPaired <interleaved_reads> ### velvetg <output_directory> -ins_length 400 -exp_cov <kmer_coverage> -cov_cutoff <coverage_cutoff>). Kmer coverage was calculated as: total read coverage*0.50 (because the kmer length was approximately half the read length), and the coverage cutoff was calculated as the kmer coverage divided by eight. If a complete reference mapping was performed, then contigs from the *de novo* assembly and reference mapping were put in an additional velvet assembly step as long reads with the original reads files (commands: velveth <output_directory> 51 -fastq -shortPaired -separate <forward_reads> <reverse_reads> -fasta -long <de_novo_fragments> <reference_fragments> ### velvetg <output_directory> -ins_length 400 -clean yes -conserveLong yes -exp_cov <kmer_coverage> -cov_cutoff <coverage_cutoff> - scaffolding yes -long_mult_cutoff 0). Finally all fragments were collapsed on nucleotide identity using cd-hit (command: cd-hit-est -I <fragment_file> -o <collapsed_file> -d 0 -M 0). All fragments smaller than 500bp were partitioned to a separate file by a custom script. Plasmid sequences were assembled by this same method, with the sequences of all complete plasmids encoding, NDM-1, KPC, or CTX-M used as references.

**ORF Prediction and Annotation**

ORF prediction for each genome was performed separately using GeneMark (6) models based on the closest reference genome (command: gmhmmp -m <model_name> -o <outfile> -a <contig_name_file>). Each ORF was compared to three databases of profile hidden Markov models using HMRR (7): Pfam (command: hmmscan --cut_ga -o /dev/null --tblast <target_out_file> --domtblast <domain_out_file> <Pfam_database_file> <protein_input_file>), TIGRFAMs (command: hmmscan --cut_ga -o /dev/null --tblast <target_out_file> --domtblast <domain_out_file> <database_file> <protein_input_file>), and Resfams (dantaslab.wustl.edu/resfams/) (8) (command: hmmscan --cut_ga -o /dev/null --tblast <target_out_file> --domtblast <domain_out_file> <database_file> <protein_input_file>). All
functional annotations were concatenated into a single file by a custom script. 756 E. coli and 54 K. pneumoniae completed and draft genomes were downloaded from the National Center for Biotechnology Information (NCBI) on April 15th 2014, for the purpose of comparing to the isolate set. GeneMark models from the completed genomes were used to predict ORFs for those genomes, while for draft genomes models created from E. coli K12 MG1655 (for E. coli draft genomes) or K. pneumoniae KCTC 2242 (for K. pneumoniae draft genomes) were used for ORF prediction. All genome and plasmid sequences were deposited into NCBI (BioProject accession number: PRJNA261540).

In silico MLST

Multi-Locus Sequence Typing (MLST) profiles were downloaded from PubMLST (pubmlst.org). When an absolute MLST profile could not be identified for an organism (because of ambiguous bases or incomplete assembly of one or more loci) the remaining possible sequence types (ST) based on the incomplete information were identified. In all cases a strain could be identified as one of at most 19 ST using this methodology. MLST profiles were only applied to Escherichia coli and Klebsiella pneumoniae since the PubMLST database does not contain an Enterobacter table.

Core Genome Alignment

Command for whole genome alignment using mugsy (9): command: mugsy --directory <output_directory> --prefix <output_prefix> <genome_fasta_1> <genome_fasta_2> … <genome_fasta_N>. For E. coli, K. pneumoniae, and E. cloacae a single reference genome was included in the alignment to provide context (E. coli K12 MG1655, K. pneumoniae KCTC 2242, and E. cloacae ATCC 13047 respectively). Poorly aligned regions (i.e. plasmids or recombined regions, which could create noise in the phylogenetic signal) were removed using Gblocks (10) (command: Gblocks <input_file> -t=d -b3=24) leaving only the core genome alignment. Maximum likelihood trees made made by RaxML (11) (command: raxmlHPC-SSE3 -s <input_file> -n <output_file> -m GTRGAMMA -d -f a -N 100 -x 54321 -w <output_directory>) and FastTree (12) (command: FastTree -gtr -nt -gamma -nome <input_file> > <output_file>) were compared for agreement. When trees made by both methods were in agreement, the output from FastTree was used for visualization. Files were converted between various required formats by custom scripts.
Subspecies clades were defined as groups of branches descended from a common ancestor where no individual branch within the clade could have more than 0.005 substitutions per site. This definition yielded the same groupings as the in silico MLST described above, in all cases where all members of a clade could be assigned to a known ST (online Technical Appendix Figure 1, panels A,B).

**Specific β-lactamase Identification**

A BLAST database was constructed from the amino acid sequences of all β-lactamases cataloged in the Bush and Jacoby (13) database at www.lahey.org/Studies/ (accessed March 25th, 2014). Genes from our genomes annotated as β-lactamases were extracted and compared against this database by BLAST. Exact matches were then re-annotated with their specific β-lactamase name, while inexact matches were recorded as their closest hit plus an asterisk.

**Plasmid Comparisons**

We compared plasmid sequences by an all-against-all pairwise nucleotide BLAST alignment. For each pair of plasmids, we calculated the percentage of each plasmid that aligned at >99% identity. We then binned the percentages from each pairwise alignment into groups based on the defining β-lactamase of their query and subject plasmids. We also generated network diagrams from the pairwise BLASTs using custom Python scripts and Cytoscape (14), only including regions above 99% identity and over 500 bp.

**Isolate Characteristics**

The sampled Enterobacteriaceae isolates are phylogenetically diverse and include multiple examples of known pathogenic sequence types. We performed WGS of each isolate, totaling 33 *Escherichia coli* isolates, 30 *Klebsiella pneumoniae* isolates, 9 *Enterobacter cloacae* complex isolates, and 6 *Enterobacter aerogenes* isolates. We then used whole genome alignment of the core genomes of each species to reconstruct the phylogenetic relationships of each isolate at high resolution (Technical Appendix Figure 2). The species trees demonstrate that we sampled genomes from a variety of evolutionary clades as well as from multiple members of specific clades. They also demonstrate that clades could include isolates from both the United States and
Pakistan, allowing us to ignore the geographic variable and group the isolates by carbapenemase carriage for subsequent analyses. We also used housekeeping gene sequence from each isolate to perform in silico MLST, allowing us to compare our phylogenetic analysis to previously identified sequence types. We found that the clades on our tree include globally-disseminated pathogen sequence types, such as ST131 in *E. coli* and ST11 (single locus variant of ST258) in *K. pneumoniae*.

ST131 is noted for its virulence as well as for its frequent association with the CTX-M β-lactamases and fluoroquinolone resistance (15–17). Previous reports have found ST258, and closely related *K. pneumoniae*, to have relatively high rates of carbapenemase carriage (18,19). Despite the utility of MLST-based classification for large-scale epidemiological purposes, binning clinical isolates into sequence types masks genotypic and phenotypic variation due to HGT or single nucleotide polymorphisms, and therefore MLST cannot be used for fine-grained epidemiology or as an accurate predictor of antibiotic susceptibility. For example, two previous studies have shown that ST131 can be subdivided into three distinct lineages with different rates of antibiotic resistance (15,16). One of these studies found that the rapid global expansion of ST131 has been driven by the success of a specific subclone of ST131 that encodes fluoroquinolone resistant gyrA and parC alleles and CTX-M-15 (16), a characterization which fits 7 of our 11 ST131 isolates. We also identified a single ST131 isolate carrying KPC-2, which was resistant to all β-lactams tested. We also observed *K. pneumoniae* ST11 isolates carrying KPC-3, and others carrying NDM-1, which fits with reports characterizing ST11 as being highly common worldwide and frequently encoding carbapenemases (18,19).

**Antibiotic Resistance Phenotypes**

To establish the overall susceptibility profiles of each of our strains, we performed phenotypic tests using Kirby Bauer Disk diffusion in accordance with CLSI guidelines on all 78 clinical isolates against 12 antibiotics including 7 β-lactams (Technical Appendix Table 1). We found that 63% of all isolates were resistant to ciprofloxacin, a fluoroquinolone commonly used to treat urinary tract infections. We also found resistance to trimethoprim-sulfamethoxazole in 65% of isolates, and gentamicin, doxycycline, and chloramphenicol exhibited *in vitro* resistance in 45%, 54%, and 56% of isolates, respectively. In the β-lactams, we saw near universal resistance to ampicillin (96% of isolates) and variable resistance to the cephalosporins. A high
rate of resistance to meropenem was observed (31% of isolates), but this finding was not surprising since this was the property on which many of the isolates had been selected.

References

1. Clinical and Laboratory Standards Institute. Performance standards for antimicrobial susceptibility testing; twenty-third informational supplement. 2013.

2. Manji R, Bythrow M, Branda JA, Burnham CAD, Ferraro MJ, Garner OB, et al. Multi-center evaluation of the VITEK® MS system for mass spectrometric identification of non-Enterobacteriaceae Gram-negative bacilli. Eur J Clin Microbiol Infect Dis. 2014 2014/03/01;33(3):337-46. PubMed http://dx.doi.org/10.1007/s10096-013-1961-2

3. Richter SS, Sercia L, Branda JA, Burnham CAD, Bythrow M, Ferraro MJ, et al. Identification of Enterobacteriaceae by matrix-assisted laser desorption/ionization time-of-flight mass spectrometry using the VITEK MS system. Eur J Clin Microbiol Infect Dis. 2013 2013/12/01;32(12):1571-8. PubMed http://dx.doi.org/10.1007/s10096-013-1912-y

4. Langmead B, Salzberg SL. Fast gapped-read alignment with Bowtie 2. Nat Methods. 2012;9:357–9. PubMed http://dx.doi.org/10.1038/nmeth.1923

5. Zerbino DR, Birney E. Velvet: algorithms for de novo short read assembly using de Bruijn graphs. Genome Res. 2008;18:821–9. PubMed http://dx.doi.org/10.1101/gr.074492.107

6. Borodovsky M, Lomsadze A. Gene identification in prokaryotic genomes, phages, metagenomes, and EST sequences with GeneMarkS suite. Current protocols in bioinformatics / editorial board, Andreas D Baxevanis [et al]. 2011;Chapter 4:Unit 4.5.1-17.

7. Eddy SR. A new generation of homology search tools based on probabilistic inference. Genome Inform. 2009;23:205–11. PubMed http://dx.doi.org/10.1142/9781848165632_0019

8. Gibson MKFK, Dantas G. Improved annotations of antibiotic resistance functions reveals microbial resistomes cluster by ecology. ISME. 2014. PubMed http://dx.doi.org/10.1038/ismej.2014.106

9. Angiuoli SV, Salzberg SL. Mugsy: fast multiple alignment of closely related whole genomes. Bioinformatics. 2011;27:334–42. PubMed http://dx.doi.org/10.1093/bioinformatics/btq665

10. Talavera G, Castresana J. Improvement of phylogenies after removing divergent and ambiguously aligned blocks from protein sequence alignments. Syst Biol. 2007;56:564–77. PubMed http://dx.doi.org/10.1080/10635150701472164
11. Stamatakis A. RAxML Version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics. 2014 January 21, 2014. PubMed http://dx.doi.org/10.1093/bioinformatics/btu033

12. Price MN, Dehal PS, Arkin AP. FastTree 2–approximately maximum-likelihood trees for large alignments. PLoS ONE. 2010;5:e9490. PubMed http://dx.doi.org/10.1371/journal.pone.0009490

13. Bush K, Jacoby GA. Updated functional classification of beta-lactamases. Antimicrob Agents Chemother. 2010;54:969–76. PubMed http://dx.doi.org/10.1128/AAC.01009-09

14. Smoot ME, Ono K, Ruscheinski J, Wang P-L, Ideker T. Cytoscape 2.8: New features for data integration and network visualization. Bioinformatics. 2011;27:431–2 dx.doi.org//10.1093/bioinformatics/btg675. PubMed http://dx.doi.org/10.1093/bioinformatics/btg675

15. Petty NK, Ben Zakour NL, Stanton-Cook M, Skippington E, Totsika M, Forde BM, et al. Global dissemination of a multidrug resistant Escherichia coli clone. Proc Natl Acad Sci U S A. 2014;111:5694–9. PubMed http://dx.doi.org/10.1073/pnas.1322678111

16. Price LB, Johnson JR, Aziz M, Clabots C, Johnston B, Tchesnokova V, et al. The epidemic of extended-spectrum-beta-lactamase-producing Escherichia coli ST131 is driven by a single highly pathogenic subclone, H30-Rx. MBio. 2013;4:e00377–13. PubMed http://dx.doi.org/10.1128/mBio.00377-13

17. Rogers BA, Sidjabat HE, Paterson DL. Escherichia coli O25b-ST131: a pandemic, multiresistant, community-associated strain. J Antimicrob Chemother. 2011;66:1–14. PubMed http://dx.doi.org/10.1093/jac/dkq415

18. Cuzon G, Naas T, Truong H, Villegas MV, Wisell KT, Carmeli Y, et al. Worldwide diversity of Klebsiella pneumoniae that produce beta-lactamase blaKPC-2 gene. Emerg Infect Dis. 2010;16:1349–56. PubMed http://dx.doi.org/10.3201/eid1609.091389

19. Pena I, Picazo JJ, Rodriguez-Avial C, Rodriguez-Avial I. Carbapenemase-producing Enterobacteriaceae in a tertiary hospital in Madrid, Spain: high percentage of colistin resistance among VIM-1-producing Klebsiella pneumoniae ST11 isolates. Int J Antimicrob Agents. 2014;43:460–4. PubMed http://dx.doi.org/10.1016/j.ijantimicag.2014.01.021
Technical Appendix Figure 1. Phylogenetic trees for isolates from samples collected in Pakistan and the United States. Trees are separated by species, A) *Escherichia coli*, B) *Klebsiella pneumoniae*, C) *Enterobacter cloacae*, and D) *Enterobacter aerogenes*, but not rooted. Bootstrap values are 1 for each branch unless otherwise noted. For each species ~50% of the genome was determined to be core, and was used for phylogenetic inference. Scale bars indicate the nucleotide substitutions per site. In a) and b) sequence types (ST) as determined by in silico multilocus sequence typing are indicated by boxes grouping members of the same ST together. Unk = ST does not correspond to any reported in pubMLST, Ind = exact ST could not be determined due to sequencing error. Reference genomes included for *E. coli* (K12 MG1655), *K. pneumoniae* (KCTC 2242), and *E. cloacae* (ATCC 13047) on their respective trees.
Technical Appendix Figure 2. Sequence conservation between plasmids containing NDM-1, KPC, or CTX-M β-lactamases. All plasmids from A) NCBI and B) this study that contained a NDM-1, KPC, or CTX-M β-lactamase were analyzed by all-against-all BLAST. Plasmid interactions were defined by the percentage of the query plasmid conserved (at >99% identity) in the subject plasmid. Plasmid interactions were plotted based on the defining β-lactamase of their query and subject plasmids.

Technical Appendix Table 1. Antibiotic drug susceptibility profiles of clinical isolates from Pakistan and the United States*

| Species, no. | Location | Phenotype | AM | CZ | CTT | CAZ | CRO | FEP | MEM | CIP | SXT | GM | D† | Ct |
|--------------|----------|-----------|----|----|-----|-----|-----|-----|-----|-----|-----|----|----|----|
| E. coli, 9   | U.S.A    | R         | 78%| 67%| 22%| 44%| 44%| 44%| 56%| 33%| 22%| 33%| 33%|    |
|              |          | I         | 0% | 11%| 22%| 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 11%|
|              |          | S         | 22%| 22%| 56%| 56%| 56%| 56%| 44%| 67%| 78%| 11%| 0% |    |
| E. coli, 24  | Pakistan | R         | 96%| 83%| 13%| 38%| 63%| 21%| 0% | 67%| 75%| 38%| 33%| 33%|    |
|              |          | I         | 4% | 17%| 0% | 13%| 0% | 21%| 0% | 0% | 0% | 0% | 17%| 4% |
|              |          | S         | 0% | 0% | 88%| 50%| 38%| 58%| 100%| 33%| 25%| 63%| 17%| 63%|    |
| K. pneumoniae, 11 | U.S.A | R         | 100%| 36%| 0% | 36%| 36%| 36%| 27%| 36%| 9% | 18%| 27%|    |
|              |          | I         | 0% | 0% | 36%| 0% | 0% | 0% | 0% | 0% | 9% | 0% | 0% | 0% |    |
|              |          | S         | 0% | 64%| 64%| 64%| 64%| 64%| 73%| 55%| 91%| 18%| 9% |    |
| K. pneumoniae, 19 | Pakistan | R         | 100%| 68%| 21%| 63%| 63%| 42%| 16%| 63%| 68%| 58%| 32%| 58%|    |
|              |          | I         | 0% | 5% | 0% | 0% | 0% | 16%| 0% | 11%| 5% | 0% | 21%| 11%|    |
|              |          | S         | 0% | 26%| 79%| 37%| 37%| 42%| 84%| 26%| 26%| 42%| 47%| 32%|    |
| E. cloacae, 3 | U.S.A | R         | 100%| 100%| 100%| 100%| 100%| 100%| 67%| 67%| 33%| 33%| 33%|    |
|              |          | I         | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 33%| 33%| 33%|
|              |          | S         | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 33%| 33%| 33%| 33%|    |
| E. cloacae, 6 | Pakistan | R         | 83%| 100%| 67%| 100%| 100%| 83%| 67%| 83%| 83%| 100%| 50%| 83%|    |
|              |          | I         | 0% | 0% | 0% | 0% | 0% | 17%| 0% | 17%| 0% | 0% | 17%| 0% |    |
|              |          | S         | 0% | 0% | 33%| 0% | 0% | 0% | 33%| 0% | 17%| 0% | 33%| 17%|    |
| E. aerogenes, 6 | Pakistan | R         | 100%| 100%| 17%| 100%| 100%| 100%| 100%| 67%| 83%| 100%| 100%|    |
|              |          | I         | 0% | 0% | 83%| 0% | 0% | 0% | 0% | 0% | 0% | 17%| 0% | 0% |    |
|              |          | S         | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 0% | 33%| 0% | 0% |    |

*AM, ampicillin; CZ, cefazolin; CTT, cefotetan; CAZ, ceftazidime; CRO, ceftriaxone; FEP, cefepime; MEM, meropenem; CIP, ciprofloxacin; SXT, trimethoprim-sulfamethoxazole; GM, gentamicin; D, doxycycline; C, chloramphenicol; R, Resistant; I, Intermediate; S, Susceptible.

†For USA E. coli and K. pneumoniae in doxycycline and chloramphenicol selections, n=4.
## Technical Appendix Table 2. Assembly metrics for whole genome assemblies

| Species                          | Genome | Number of contigs | N50 | Largest contig | Total nucleotides |
|---------------------------------|--------|-------------------|-----|----------------|-------------------|
| **Escherichia coli**            |        |                   |     |                |                   |
| PH100                           | 1288   | 35053             | 385222 | 6309191        |
| PH101-2                        | 404    | 31119             | 177520 | 4857948        |
| PH105                           | 288    | 55979             | 220618 | 5045926        |
| PH108                           | 754    | 12427             | 95430  | 4930575        |
| PH114                           | 280    | 68389             | 450011 | 5902206        |
| PH118                           | 1028   | 13550             | 93913  | 5073129        |
| PH129                           | 235    | 76630             | 188170 | 5470109        |
| PH135                           | 156    | 87914             | 545356 | 4864787        |
| PH141                           | 656    | 14806             | 87255  | 4496903        |
| PH143                           | 355    | 33581             | 145252 | 4875919        |
| PH151-2                        | 368    | 41647             | 143184 | 5066089        |
| PH156-1                        | 720    | 24256             | 203811 | 5432228        |
| PH18                            | 357    | 39599             | 128851 | 5026978        |
| PH20                            | 513    | 20802             | 122933 | 4967604        |
| PH31                            | 394    | 40363             | 219779 | 5077941        |
| PH39                            | 465    | 28063             | 96484  | 4695860        |
| PH51                            | 1108   | 13899             | 85055  | 4986846        |
| PH5                             | 193    | 185476            | 496282 | 5367128        |
| PH85                            | 331    | 45973             | 149681 | 5118463        |
| PH90                            | 475    | 31325             | 258054 | 5169559        |
| PH92-1                          | 738    | 19526             | 90560  | 5313215        |
| PH93                            | 487    | 31876             | 685039 | 5927902        |
| PH94                            | 325    | 40628             | 218502 | 4960477        |
| PH98                            | 401    | 28050             | 272240 | 4791597        |
| PHU31                           | 502    | 21374             | 148889 | 4585305        |
| PHU32                           | 326    | 43395             | 160814 | 4866448        |
| PHU33                           | 487    | 25419             | 139243 | 4975544        |
| PHU34                           | 278    | 67976             | 229510 | 5206801        |
| PHU40                           | 145    | 202444            | 388283 | 5052711        |
| PHU43                           | 193    | 91836             | 346403 | 5033909        |
| PHU44                           | 196    | 92332             | 610815 | 5473063        |
| PHU45                           | 332    | 40224             | 155439 | 4990710        |
| **Klebsiella pneumoniae**       |        |                   |     |                |                   |
| PH102                           | 2205   | 3247              | 29455  | 4976237        |
| PH1                             | 192    | 129071            | 506496 | 5877659        |
| PH11                            | 224    | 109166            | 648719 | 5657202        |
| PH124                           | 238    | 66778             | 202869 | 5515528        |
| PH12                            | 317    | 46831             | 180775 | 5530414        |
| PH139                           | 263    | 92250             | 433917 | 5458209        |
| PH150-2                        | 487    | 40719             | 311295 | 5588393        |
| PH152                           | 354    | 74725             | 275892 | 5593335        |
| PH24-1                          | 181    | 209112            | 601209 | 5541503        |
| PH25                            | 439    | 51744             | 186964 | 5437740        |
| PH28-1                          | 302    | 72750             | 480318 | 5876774        |
| PH38-1                          | 178    | 243482            | 614325 | 6135768        |
| PH40                            | 471    | 43686             | 232550 | 6212797        |
| PH44                            | 251    | 130296            | 479083 | 6297207        |
| PH49-2                          | 273    | 84383             | 550379 | 6883299        |
| PH72                            | 2195   | 13163             | 144014 | 7250407        |
| PH73                            | 997    | 11652             | 91567  | 5804995        |
| PH88                            | 150    | 289170            | 512144 | 5630043        |
| PH9                             | 927    | 12231             | 72933  | 5207334        |
| PHU10                           | 179    | 117943            | 480943 | 5928719        |
| PHU12                           | 113    | 12084             | 59345  | 5227362        |
| PHU18                           | 961    | 14636             | 98561  | 5114063        |
| PHU21                           | 372    | 67952             | 249904 | 5556247        |
| PHU23                           | 142    | 208533            | 460529 | 5958526        |
| PHU2                            | 407    | 55286             | 345910 | 6330941        |
| PHU5                            | 705    | 94321             | 408241 | 6853166        |
| PHU6                            | 297    | 104936            | 426673 | 5919869        |
| PHU7                            | 227    | 79691             | 298801 | 5818526        |
| PHU8                            | 377    | 64077             | 729073 | 7202435        |
| PHU9                            | 141    | 120728            | 292977 | 5557123        |
| **Enterobacter aerogenes**      |        |                   |     |                |                   |
| 112-2                           | 90     | 177700            | 566534 | 5153448        |
| PH113                           | 450    | 22178             | 97515  | 4695038        |
| PH134                           | 274    | 107942            | 399309 | 5126469        |
| PH138                           | 776    | 30613             | 144769 | 9901518        |
| Species                  | Genome | Number of contigs | N50    | Largest contig | Total nucleotides |
|-------------------------|--------|-------------------|--------|----------------|-------------------|
| *Enterobacter aerogenes*| PH63   | 225               | 47345  | 184904         | 5211429           |
| *Enterobacter aerogenes*| PH84-2 | 226               | 61644  | 336177         | 5307861           |
| *Enterobacter cloacae* | PH23   | 179               | 83227  | 473778         | 5536166           |
| *Enterobacter cloacae* | PH24-2 | 1238              | 20166  | 178617         | 8756501           |
| *Enterobacter cloacae* | PH112-1| 621               | 175912 | 517857         | 9155709           |
| *Enterobacter cloacae* | PH125  | 1221              | 45282  | 215620         | 6004095           |
| *Enterobacter cloacae* | PH158  | 552               | 34922  | 172567         | 9711730           |
| *Enterobacter cloacae* | PH82   | 389               | 61644  | 336177         | 5307861           |
| *Enterobacter cloacae* | WU26   | 538               | 46418  | 208322         | 5369428           |
| *Enterobacter cloacae* | WU27   | 315               | 45300  | 178617         | 5251409           |
| *Enterobacter cloacae* | WU29   | 457               | 24866  | 86433          | 4888311           |
| Average                 | NA     | 490               | 67666  | 285311         | 5664479           |

**Technical Appendix Table 3. Assembly metrics for plasmid assemblies**

| Species                  | Genome | Number of contigs | N50    | Largest contig | Total nucleotides |
|-------------------------|--------|-------------------|--------|----------------|-------------------|
| Acinetobacter baumannii | PH147_2| 98                | 3072   | 7683           | 181370            |
| Escherichia coli        | WU31   | 41                | 16473  | 48183          | 214615            |
| Escherichia coli        | WU32   | 86                | 11069  | 31992          | 233185            |
| Escherichia coli        | WU33   | 87                | 9555   | 47149          | 168182            |
| Klebsiella pneumoniae   | PH11   | 53                | 19073  | 48703          | 230288            |
| Klebsiella pneumoniae   | PH88   | 39                | 15980  | 48463          | 218205            |
| Klebsiella pneumoniae   | WU13   | 6                 | 12943  | 12943          | 18694             |
| Klebsiella pneumoniae   | WU14   | 4                 | 12976  | 12976          | 18501             |
| Klebsiella pneumoniae   | WU17   | 374               | 4432   | 60538          | 328889            |
| Klebsiella pneumoniae   | WU18   | 40                | 18017  | 43330          | 221015            |
| Klebsiella pneumoniae   | WU19   | 37                | 22152  | 87768          | 315122            |
| *Enterobacter aerogenes*| PH112_2| 80                | 19156  | 52826          | 450788            |
| *Enterobacter aerogenes*| PH113  | 17                | 5703   | 19095          | 59909             |
| *Enterobacter aerogenes*| PH134  | 22                | 4168   | 9715           | 48836             |
| *Enterobacter aerogenes*| PH138  | 171               | 8795   | 35183          | 466555            |
| *Enterobacter aerogenes*| PH63   | 37                | 29896  | 44891          | 282470            |
| *Enterobacter cloacae*  | PH23   | 111               | 12334  | 42017          | 516173            |
| *Enterobacter cloacae*  | PH24_2 | 95                | 15201  | 41616          | 562271            |
| *Enterobacter cloacae*  | PH82   | 206               | 9384   | 37900          | 641720            |
| Average                 | NA     | 84                | 13178  | 38620          | 272463            |