#136

U.S. Department of Veterans Affairs
Veterans Health Administration
Central Texas Veterans Health Care System

Prevalence of Plasmid Mediated Antibiotics Resistance Genes in *Klebsiella pneumoniae* in the United States

Munok Hwang, MS[1] ; Hosoon Choi, PhD[1] ; Chetan Jinadatha, MD, MPH[1]

[1]Central Texas Veterans Health Care System, Temple TX

Introduction

- Multidrug resistant (MDR) bacteria which resist at least three different antibiotic classes are a serious threat to public health and patient treatment.
- Antimicrobial resistant (AMR) genes are often mediated through plasmids due to their horizontal transferability from bacteria to bacteria.
- Here, we assessed the prevalence of AMR genes in the USA by analyzing *K. pneumoniae* plasmid genome data obtained from PATRIC (Pathosystems Resources Integration Center) database.

Methods

- The PATRIC database has 176 *K. pneumoniae* plasmid genome data collected in 9 states of US from 2004 to 2019. The isolation sources are various patient samples including urine, blood, etc (Table 1)
- The sequence information was downloaded from GeneBank.
- The AMR genes on plasmids of *K. pneumoniae* were identified using the open-source AMR database, ResFinder which searches AMR genes for 16 types of antibiotic classes.
- Default threshold of >90% Identity and >60% length was used.

References

Wattam AR, Davis JJ, Assaf R, Boisvert S, Brettin T, Bun C, Conrad N, Dietrich EM, Disz T, Gabbard JL, Gerdes S, Henry CS, Kenyon RW, Machi D, Mao C, Nordberg EK, Olsen GJ, Murphy Olson DE, Olson R, Overbeek R, Parrello B, Pusch GD, Shukla M, Vonstein V, Warren A, Xia F, Yoo H, Stevens RL. Nucleic Acids Res. 2017 Jan 4;45(D1):D535-D542. doi: 10.1093/nar/gkw1017. PMID: 27899627; PMCID: PMC5210524.

Acknowledgements

This project was supported by Central Texas Veterans Health Care System (CTVHCS) facility during the study period.

Results

Table 1. *Klebsiella pneumoniae* isolates used in the study.

Collection Year	States	Collection Site
2004	NY	
2010		Urine
2010	VA	Respiratory
2010	CA	Urine
2010	NJ	Urine
2011		Bronchoalveolar Lavage
2011	VA	Urine/Genitourinary
2011	VA	Perirectal
2011	PA	
2012		Blood
2012		Blood
2012	PA	Environment
2012	TX	Respiratory
2012		Throat/Groin
2012		Groin
2012		Sputum
2012	MN	Wound
2012	MN	Urine
2013	PA	Urine
2013		Perirectal
2013		Perirectal
2013		Urine
2013		Perirectal
2013		Urine
2013	MN	Wound
2014	MN	Tracheal Aspirate
2014	TX	Urine
2014	TX	Respiratory
2014	CA	Abdominal Drainage
2015	CA	Rectal
2016	NV	Wound
2019	VA	Abdominal Abscess
2019	VA	Urine
2019	VA	Urine
2019	VA	Sputum
2019	VA	Perirectal
2019	IL	Urine
	PA	Urine
	NY	
	NY	

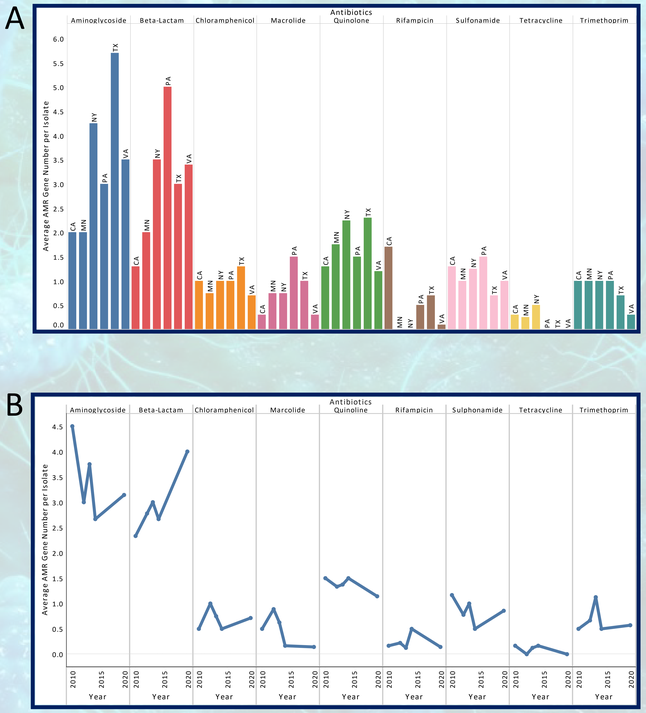

Figure 1. Changes in the number of antibiotics resistance genes over the geographical region (A) or over the years (B). Only states or time points with more than 3 isolates have been included in the analysis. Statistical analyses were performed by one-way ANOVA and Tukey's multiple comparison test. There was no statistically significant difference among the regions or no statistically significant changes over the years in any antibiotics as all p-value > 0.05.

Table 2. AMR genes detected from the isolates.

Antibiotics by Class	Generic antibiotics name	Resistance genes
Aminoglycosides	Amikacin, Gentamicin, Tobramycin, Kanamycin	*aac*(3)-IId, *aac*(3)-IV, *aac*(3)-IIa, *aac*(3)-I, *aac*(6')-Ib, *aac*(6')-Id, *aac*(6')-Ib-cr, *aac*(6')-Ib-Hanghou, *aad*A1, *aad*A2, *aad*A2b, *ant*(2")-Ia, *aph*(3')-Ib, *aph*(3')-VI, *aph*(3')- Ia, *aph*(4')-Ia, *aph*(6')-Id, *arm*A, *rmt*C
Carbapenems	Ertapenem, Doripenem, Imipenem, Meropenem	*bla*KPC-2, *bla*KPC-3, *bla*KPC-4, *bla*NDM-1, *bla*OXA-232, *bla*OXA-48
Cephalosporins	Cefoxitin, Cephalothin, Cefotaxime, Ceftazidime, Cefepime	*bla*OXA-1, *bla*OXA-9, *bla*CTX-M-15, *bla*CTX-M-2, *bla*SHV-11, *bla*SHV-12, *bla*SHV-30, *bla*SHV-1, *bla*SHV-5
Penicillin	Piperacillin, Ampicillin, Amoxicillin, Piperacillin/tazobactam, Amoxicillin/clavulanate	*bla*TEM-1A, *bla*TEM-1B, *bla*TEM-54, *bla*TEM-16, *bla*CMY-6, *bla*Fox-5, *bla*OXA-2, *bla*SHV-13, *bla*SHV-185, *bla*SHV-25, *bla*SHV-69, *bla*SHV-70, *bla*SHV-105, *bla*SHV-189
Quinolones	Ciprofloxacin, Levofloxacin, Nalidixic acid	*aac*(6')-Ib-cr, *qnr*B1, *qnr*B9, *qnr*S1, *qnr*A1
Macrolides	Erythromycin	*ere*A, *mef*B, *mph*A, *mph*E, *msr*E
Sulfonamides	Sulfamethoxazole	*sul*1, *sul*2, *sul*3
Tetracyclines	Doxycycline, Tetracycline	*tet*A, *tet*B
Chloramphenicol	Chloramphenicol	*cat*A1, *cat*A2, *cat*B3, *cml*A1
Rifampicin	Rifampin	*arr*-2, *arr*-3
Trimethoprim	Trimethoprim	*dfr*12, *dfr*1, *dfr*14

Conclusion

- AMR genes for various antibiotics were identified in most isolates (Table 2). Aminoglycoside and ß-lactam resistance genes were abundant regardless the region or time isolated (Figure 1). The prevalence of AMR genes varied by states (Figure 1A), and ß-lactam resistance increased over the year (Figure 1B).
- Multidrug resistance is present in almost all isolates, in some isolates against up to 8 different antibiotics.

CTX-R15-0922-1081