

## UMP. 063

**Emergence of Colistin Resistance among Gram Negative Bacteria in Urinary Tract Infections from Super Specialty Hospital of North India**

S. Jain

Max Super Specialty Hospital, Shalimar Bagh,  
Microbiology, New Delhi, India

**Background:** Use of colistin is increasing due to the increasing prevalence of multi drug resistant gram negative bacteria (GNB). Increasing prevalence of carbapenem resistant GNB is a serious clinical and public health challenge because the treatment options are limited to colistin, Tigecycline etc. Colistin resistance is being increasingly reported in Indian hospitals. Bacteria resistant to all available antibiotics (Pan Drug Resistance) are also increasing and left no treatment option. Resistance to colistin is a major threat that limits therapeutic choices for treating carbapenem-resistant *Pseudomonas aeruginosa* and *Klebsiella sp.* infections. We hereby report the prevalence of colistin resistance among gram negative bacteria from urinary tract infection.

**Methods & Materials:** This study was performed from January 2016 to December 2016 in Max Super Speciality Hospital, Shalimar Bagh, New Delhi, India. A total of 1429 out of 2273 positive urinary isolates of *Escherichia coli* (975), *Pseudomonas aeruginosa* (201) and *Klebsiella sp.* (253) were included in this study. Identification and sensitivity was conducted by Vitek 2 compact automated system. Susceptibility of antimicrobials were interpreted according to the Clinical Laboratory Standards Institute (CLSI 2016) guidelines.

Results: Organism	Number of isolates	Percentage (%) Resistance		
		Meropenem	Imipenem	Colistin
<i>Escherichia coli</i>	975	18.66	18.66	0.67
<i>Klebsiella sp.</i>	253	45.33	43.66	12.67
<i>Pseudomonas sp.</i>	201	63.66	60	18

**Conclusion:** Colistin resistance was 18%, 12.67% and 0.67% for *Pseudomonas aeruginosa*, *Klebsiella sp.* and *Escherichia coli* respectively. Carbapenem resistance was 63.66%, 45.33% and 18.66% for *Pseudomonas aeruginosa*, *Klebsiella sp.* and *Escherichia coli* respectively. Colistin resistance was highest for *Pseudomonas aeruginosa* followed by *Klebsiella sp.* among the gram negative bacteria from urinary tract infection. Resistance of colistin against *Pseudomonas aeruginosa* is increasing which is alarming and it is the right time to use colistin judiciously. Isolation of *Pseudomonas aeruginosa* may be colonization and should be differentiate from true infection before starting treatment. In place of colistin, carbapenems should be the choice of treatment for multi drug resistant gram negative bacteria if sensitive.

<https://doi.org/10.1016/j.ijid.2018.04.3716>

## UMP. 064

**Antimicrobial drug resistance in Salmonella Typhi and Paratyphi isolates worldwide, 1990 to 2017: A systematic review of the literature**

A. Browne<sup>1,\*</sup>, P. Rao<sup>2</sup>, J. Longbottom<sup>1</sup>, E. Harriss<sup>3</sup>, B. Basnyat<sup>4</sup>, S. Baker<sup>5</sup>, N. Day<sup>6</sup>, S. Hay<sup>2</sup>, C. Dolecek<sup>7</sup>

<sup>1</sup> Global Burden of Disease-Antimicrobial Resistance Project, Big Data Institute, Li Ka Shing Centre for Health Information and Discovery, University of Oxford, Oxford, United Kingdom

<sup>2</sup> Institute of Health Metrics and Evaluation, University of Washington, Seattle, WA, United States

<sup>3</sup> Bodleian Libraries, University of Oxford, Oxford, United Kingdom

<sup>4</sup> Oxford University Clinical Research Unit Nepal, Patan Academy of Health Sciences, Kathmandu, Nepal

<sup>5</sup> Oxford University Clinical Research Unit - Hospital for Tropical Diseases, Enteric Infections, Ho Chi Minh, Vietnam

<sup>6</sup> Mahidol-Oxford Tropical Medicine Research Unit, Faculty of Tropical Medicine, Mahidol University, Bangkok, Thailand

<sup>7</sup> Centre for Tropical Medicine and Global Health, University of Oxford, Oxford, United Kingdom

**Background:** *Salmonella* Typhi and Paratyphi are WHO priority pathogens that cause serious bloodstream infections. Antimicrobial resistance presents a significant public health burden as it negatively impacts our ability to treat and control enteric fever.

The aim of this project is to map the spatial distribution of drug resistant *S. Typhi* and Paratyphi and to incorporate the impact of AMR into the Global Burden of Disease (GBD) study estimates.

**Methods & Materials:** We conducted a systematic review of the global published literature between 1990 and 2017 to analyse the prevalence of drug resistance in *S. Typhi* and Paratyphi blood culture isolates.

Antimicrobial susceptibility data to all tested drugs were extracted. We calculated the median prevalence (percentage) of resistance according to serotype, GBD super-region and five-year time-period.

**Results:** Data from 518 studies (1990–2015) have been analysed to date; heterogeneity was high ( $I^2 > 80\%$ ) within most subgroups.

Between 1990–1994 and 2010–2015 the median prevalence (MP) of multidrug resistant (MDR; resistance to chloramphenicol, co-trimoxazole and ampicillin) Typhi decreased in South Asia and North Africa/Middle-East from 42% [IQR 23–66] to 6% [0–19] and 43% [34–48] to 7% [0–33], respectively; remained constant in Southeast Asia, East Asia and Oceania; and increased in sub-Saharan Africa from 6% [3–8] to 33% [4–83]. The MP of MDR Paratyphi was less than 11% for all time-periods in South Asia.

The MP of nalidixic acid resistant (NAR; an indicator of fluoroquinolone resistance) Typhi increased from <5% in 1990–1994 to >80% in 2010–2015 in South Asia and Southeast Asia but remained low in sub-Saharan Africa (2% [1–3] in 1990–1994; 7% [4–28] in 2010–2015). The MP of NAR Paratyphi was >81% for all time-periods in South Asia.

**Conclusion:** Our results indicate that *Salmonella* Typhi strains in South Asia and North Africa/Middle East are regaining sensitivity to first-line drugs; fluoroquinolone resistance is now highly prevalent in South and Southeast Asia.

High heterogeneity indicates further spatial-temporal variation exists alongside multiple biases. We intend to adjust for biases and

develop a spatial-temporal model to produce accurate temporal national and subnational estimates of resistance. These results will be incorporated into the GBD study, providing a vital source of information.

<https://doi.org/10.1016/j.ijid.2018.04.3717>

#### UMP. 065

##### Rates of susceptibility of colistin and carbapenems against clinical isolates of *Pseudomonas aeruginosa*

T. Ajibade<sup>1,\*</sup>, E. Oladipo<sup>2</sup>, S. Akinade<sup>3</sup>

<sup>1</sup> Adeleke University, Microbiology, Ede, Nigeria

<sup>2</sup> Adeleke University, Microbiology, Ogbomoso, Nigeria

<sup>3</sup> Ladoke Akintola University of Technology, Pure and Applied Biology, Ogbomoso, Nigeria



**Background:** There are significant changes in microbial genetic as a result of indiscriminate use of antibiotics, the spread of antimicrobial resistance is now a global problem. Therefore the study was conducted to examine the susceptibility of clinical isolates *Pseudomonas aeruginosa* against Colistin and Carbapenems.

**Methods & Materials:** hundred *Pseudomonas aeruginosa* were isolated from samples collected from different anatomical sites from May to October 2016 in a tertiary hospital at Ibadan and Ogbomoso. Antimicrobial susceptibility test was performed by disk diffusion according to the standards of the Clinical Laboratory Standard Institute. Majority of isolates of *P. aeruginosa* were obtained from specimens of wound, sputum, urine and aspirates.

**Results:** *Pseudomonas aeruginosa* had 48% susceptibility to Colistin, 8% to Ertapenem, 3% to Imipenem and 2% to Meropenem; no intermediate was observed for Colistin while 4% to Ertapenem and 1% to Imipenem. Colistin was found to be the most effective antimicrobial drugs.

**Conclusion:** Therefore, the use of Colistin should be encouraged for infections caused by *Pseudomonas aeruginosa* in order to achieve effective treatment. Continuous monitoring of susceptibility profile of *Pseudomonas aeruginosa* should be encouraged to appropriate antimicrobial regimens against *Pseudomonas aeruginosa* infections.

<https://doi.org/10.1016/j.ijid.2018.04.3718>

#### UMP. 066

##### First report of *Pseudomonas aeruginosa* co-harboring bla<sub>VIM-2</sub> and bla<sub>PER-1</sub> in Latin America

R. Papa<sup>1,\*</sup>, I. Bado<sup>1</sup>, L. Caiata<sup>1</sup>, V. Seija<sup>2</sup>, R. Vignoli<sup>1</sup>

<sup>1</sup> Instituto de Higiene, Facultad de Medicina, Universidad de la República, Bacteriología y Virología, Montevideo, Uruguay

<sup>2</sup> Hospital de Clínicas, Facultad de Medicina, Universidad de la República, Departamento de Laboratorio Clínico, Microbiología, Montevideo, Uruguay



**Background:** Multidrug resistant *Pseudomonas aeruginosa* is one of the most important opportunistic pathogens. *P. aeruginosa* carrying Metallo-beta-lactamases (MBL) have been described worldwide as linked to hospital outbreaks or in isolated episodes.

The association of MBL with resistance mechanisms to other antibiotic groups allows few therapeutic options, which conducts to increased morbimortality, therapy failure and high healthcare cost.

The aim of this study was to characterize the beta-lactamic resistance genes carried by a clinical isolate of *P. aeruginosa*.

**Methods & Materials:** *P. aeruginosa* 6415 was recovered from a cerebrospinal fluid sample from a 68-year-old woman, admitted to the intensive care unit of the Uruguayan University Hospital with a ventriculitis diagnosis.

The strain was identified on Vitek2 system. Susceptibility testing was performed by disk diffusion method, and double-disc synergy test was assessed for phenotypic detection of MBL, class A carbapenemase and extended spectrum beta-lactamase (ESBL).

Presence of MBL and ESBL coding genes was determined by polymerase chain reaction (PCR), with specific primers for bla<sub>VIM</sub>, bla<sub>NDM</sub>, bla<sub>IMP</sub>, bla<sub>PER-1</sub>, bla<sub>PER-2</sub> and bla<sub>CTX-M</sub>. Presence of class 1 integrons and their variable regions were assessed by PCR with class I integrase and 3' – 5' conserved sequences primers, respectively. PCR products were sequenced by Sanger method.

**Results:** *P. aeruginosa* 6415 was resistant to piperacillin-tazobactam, ceftazidime, cefepime, meropenem, imipenem, aztreonam, ciprofloxacin and amikacin, and susceptible to gentamicin, and colistin.

Double disk synergy test revealed the presence of both MBL and ESBL enzymes. PCR and sequencing results were compatible, displaying the presence of bla<sub>VIM-2</sub> and bla<sub>PER-1</sub>.

bla<sub>VIM-2</sub> was inserted in a class 1 integron, as the only gene cassette on a 1000 bp variable region.

**Conclusion:** MBL-producing *P. aeruginosa* constitutes a global public health concern, since it has a broad hydrolysis spectrum and is widely spread. The presence of both, MBL and ESBL defines a resistance profile to all antipseudomonal beta-lactams. Class 1 integrons are capable of acquiring various gene cassettes as it has been found previously in Uruguay, which leads to multidrug resistance profiles, allowing very few treatment options. To the best of our knowledge, this is the first *P. aeruginosa* isolate co-harboring both bla<sub>VIM-2</sub> and bla<sub>PER-1</sub> in Latin America.

<https://doi.org/10.1016/j.ijid.2018.04.3719>