550. Carbapenem-Resistant E. coli and A. baumannii Among Catheter-Related Blood Stream Infection Patients in Egyptian ICUs

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Background. The spreading of E. coli and A. baumannii in hospitals is a growing concern due to increased resistance to carbapenems and Fluoroquinolones. The present study aimed to specifically evaluate the presence of mutations in the gyrA and parC genes in Egyptian ICU and their correlation with carbapenem-resistant strains of E. coli and A. baumannii isolates from patients in four tertiary care hospitals in Egypt.

Methods. A total of 120 A. baumannii and E. coli clinical isolates were isolated from ICU patients in 4 tertiary care hospitals in Egypt. The bacterial isolates were identified by VITEK-2 (Bio Merieux, France). Antimicrobial susceptibility testing was performed according to CLSI guidelines. Phenotypic detection of carbapenemase activity was done by carbapenem test. Amplification and sequencing of bla, blaoXA, and blv beta-lactamases were performed by multiplex PCR. The quinolone resistance-determining regions (QDRRs) in gyrA and parC genes were amplified by singleplex PCR followed by reverse and forward sequencing to detect the gene mutation. The DNA sequences were compared with the sequences of wild type of these genes available in GenBank database. Then, the obtained DNA sequences and their amino acid sequences were analyzed using bioinformatics tools.

Results. All isolates showed a high level of resistance among tested antimicrobial agents (cephalosporins, aminoglycosides, carbapenems, penicillins) that ranged from 36% to 100%. Carba-NP detected 43.59% of the carbapenem-resistant isolates. Multiplex PCR detected that 17.95%, 46.15% and 2.56% of isolates were harboring blaoXA, blaoXA, and blv beta-lactamases respectively. PCR and sequencing techniques showed combined gene mutation in 8 carbapenem-resistant E. coli and A. baumannii isolates. The specific substitutions observed in gyrA were Cys173Arg, Cys174 Gly, Asp80Val, Tyr718A SP, Tyr844 Gly, Gln854, Ser172Leu and Asp176Asn. While, the specific substitutions observed in parC were point mutation 62Arg, Phen60Leu, Ile66Val, Glu76Lys. Point mutation 62 Arg was observed in two A. baumannii isolates, whereas Ser172Leu mutation was observed in two E. coli isolates.

Conclusion. The presence of carbapenem resistance genes in combination with single and multiple mutations in QDRBs causes the presence of highly resistant E. coli and A. baumannii isolates in the Egyptian hospitals.

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551. Burden of Illness in Carbapenem-Resistant Acinetobacter baumannii Infections in US Hospitals (2014 to 2018)

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Background. Infections caused by Acinetobacter baumannii present a challenge for treating physicians due to the high level of antimicrobial resistance. The current analysis compared the burden of illness in patients infected with carbapenem-resistant (CR) vs. susceptible (CS) strains of A. baumannii.

Methods. Hospitalized adult patients with microbiologically confirmed A. baumannii infections (defined as a positive culture and receipt of antibiotics between 2 days prior to 3 days after the culture) included in the Premier Healthcare Database were retrospectively evaluated. Patient characteristics including demographics, comorbidities, time of infection onset and site of infection were assessed. Comparative outcomes between CR and CS patients assessed included in-hospital mortality, length of hospital stay (LOS), ICU LOS, and discharge status. Outcomes were also stratified by site of infection.

Results. A total of 3,471 patients admitted between January 1, 2014 and June 30, 2018 were included. Patients with CR strains of A. baumannii were older (62 vs. 59 years), more likely to have Charlson Comorbidity Index ≥3 (63.4% vs. 56.1%), more likely admitted from a healthcare origin (30.3% vs. 11.4%) and less likely to have the onset of infection within first 48 hours of hospitalization (58% vs. 69%) than those with CS strains. CR patients had increased inpatient mortality compared with CS patients (16.3% vs. 11.0%), driven primarily by patients with bloodstream infections (42.6% vs. 12.4%, respectively, P < 0.001). CR patients had a non-significantly increased median overall LOS from the onset of infection (9 vs. 8 days, P = 0.068), were more likely to be admitted to the ICU, and were significantly less likely to be discharged home (16% vs. 47%, P < 0.001). Hospitalization charges were considerably higher for CR patients (table). Readmission rates were high among CR patients and were similar to patients with CS infections.

Conclusion. Patients with CR strains of A. baumannii face a greater burden of illness compared with CS patients, experiencing increased mortality, ICU admission and LOS, and incur higher hospitalization charges. Furthermore, CR patients were less likely to be discharged home after admission.

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552. Within-Host Evaluation of Colonization During Active Methicillin-Resistant S. aureus Bacteremia

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Background. Staphylococcus aureus is a common commensal pathogen and a frequent cause of bacterial infection. Our aim was to collect a contemporary set of colonizing isolates from those with methicillin-resistant S. aureus (MRSA) bloodstream infections (BSIs), evaluate the within-host diversity by whole genome sequencing (WGS), and detail the clinical features linked to colonization.

Methods. Adult patients with MRSA BSIs were screened for MRSA in the anterior nares from July 2018 to March 2019. Blood isolates underwent WGS, and spa and agr array screens were performed on three unique isolates per patient. Clinical data from the electronic medical records underwent univariant and multivariate analyses on clinical features and outcomes.

Results. Of 55 unique patients with MRSA BSIs, screening of 45 subjects revealed that 67% were colonized with MRSA. The majority (66%) were males, 32% had prior colonization, and the most common infection sources were vascular access (27%), skin (24%), and unknown (24%). For those with nasal colonization, blood isolates were composed of 57% clonal complex (CC)5/t002, 33% CC8/t008, and 10% other. 81% (24%) of nasal isolates harbored diverse spa types and 23% carried agr types. During this time frame, WGS found one transmission event involving a colonized subject. Colonization was associated with male gender (OR=4.52 95% CI [1.05–19.49], P = 0.04) and prior hospital admission within the last 3 months (OR=6.12 95% CI [1.44–26.09], P = 0.01) in multivariate analysis, with no differences in outcomes.

Conclusion. Colonization is an important component of invasive MRSA disease, and we found high rates of colonization with a predominance of the CC5. We also noted significant diversity and high proportion of agr mutants. At-risk groups included males and those with prior hospitalization. Combined molecular and clinical analyses can define the in-host and inter-host transmission dynamics of MRSA, and enables the development of targeted approaches in order to curtail disease.
555. The Burden of Invasive Staphylococcus aureus Disease Among Native Americans on the Navajo Nation

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Methods. Prospective population and laboratory-based surveillance for invasive S. aureus infections was conducted from May 2016 through April 2018. A case was defined as a Native American individual living on or around the Navajo Nation with S. aureus isolated from a normally sterile body site. Incidence rates were calculated using the Indian Health Service User Population from 2016 and 2017 as the denominators for Years 1 and 2, respectively. Age-standardized incidence rates were calculated using US Census data from 2015 as the reference group.

Results. 363 cases were identified (Year 1: 204; Year 2: 209). Most cases were adults (96.9%; median age: 56.0 years) and had ≥1 underlying medical condition (94.5%), of which the most common were diabetes (63.2%), hypertension (39.1%), and obesity (37.2%). 38.0% of cases were categorized as community acquired and 28.7% of infections were methicillin-resistant (MRSA). 83.2% of cases were hospitalization, 10.7% required amputation, and 6.5% died within 30 days of the initial culture. The overall incidence of invasive S. aureus was 74.4 per 100,000 persons (95% confidence interval [CI]: 67.1, 82.4) with a significantly higher incidence in the second year (Year 1: 64.9; Year 2: 84.0; incidence rate ratio: 1.29; 95% CI: 1.05, 1.59). The overall age-standardized incidence of invasive MRSA was 21.3 per 100,000 persons (95% CI: 17.6, 25.8) with no significant difference by year (Year 1: 21.2; Year 2: 21.4; incidence rate ratio: 1.01; 95% CI: 0.69, 1.48). The incidence of invasive S. aureus and MRSA increased with age and was highest among individuals 265 years of age. The overall age-standardized incidence of invasive MRSA was 2.9 per 100,000 persons (Year 1: 2.6; Year 2: 2.57; for comparison US 2015 general population: 18.8 per 100,000 persons).

Conclusion. The Navajo Nation has a higher burden of invasive MRSA than the general US population. Further research is needed to evaluate trends over time and identify prevention strategies and opportunities for intervention.

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