

Summary of detection delays relative to first detection using real time clinical microbiology results from all facilities statewide (14 simulation runs)



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540. The Impact of Diet and Oral Hygiene on the Risk of Multidrug-Resistant Organism Carriage in the Mouth and Gut

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Background. Little is known about the relationship between oral hygiene and multidrug-resistant organism in the mouth and gut. We aimed to assess the relationship of oral hygiene and diet with multidrug-resistant organism (MDRO) carriage in the oral cavity and gut.

Methods. Participants were adults over age 18 from the 2016–2017 Survey of the Health of Wisconsin (SHOW) and its ancillary Wisconsin Microbiome Study. SHOW surveys residents of Wisconsin, collecting health determinants including a food frequency questionnaire, oral health, as well as biologic specimens. MDROs were defined as the presence of methicillin-resistant *Staphylococcus aureus*, Vancomycin-resistant *Enterococcus*, and Fluoroquinolone-resistant Gram-negative bacteria identified via culture from saliva, oral swabs, and stool samples. Statistical analysis was performed in R v3.5.1. Univariate analyses were conducted for all variables in the data set. Any variable with a P-value < 0.2 in the univariate analysis was considered for the logistic regression. Logistic regression using the glm function was done modeling MDRO carriage in either the saliva, oral swab, saliva and oral samples combined, and stool against diet, oral health, and known confounders.

Results. 876 participants were included in the dataset with all 876 providing oral and stool samples and 784 providing saliva samples. Thirty-three patients were MDRO positive in the saliva (4.2%), 36 were positive in the oral swabs (4.1%), 55 were positive in either the saliva or oral swabs (6.3%), and 103 were positive in the stool (11.8%). In the logistic regression, consumption of whole grains was significantly associated with reduced MDRO carriage in the saliva (P = 0.046) and saliva and oral swab combined (P = 0.036) data sets (Table 1).

Conclusion. Consuming more whole grains was associated with a lower prevalence of MDRO carriage in the oral cavity. Higher levels of sugar consumption were associated with a higher prevalence of MDRO in the gut. Oral hygiene was not found to be associated with MDRO colonization in the mouth and a higher prevalence in the gut in this cross-sectional study. This may be due to over-reporting of hygiene practices by participants. Being positive for an MDRO in the oral cavity significantly increased the risk of MDRO carriage in the gut.

| | Saliva | Oral Swab | Any Oral MDRO | Stool |
|-----------------------|--------------------|--------------------------------|--------------------|--------------------------------|
| Exposure | N (%) | N (%) | N (%) | N (%) |
| MDRO carriage | | | | |
| Yes | 33 (4.2) | 36 (4.1) | 55 (6.3) | 103 (11.8) |
| No | 751 (95.8) | 840 (95.9) | 821 (93.7) | 773 (88.2) |
| Categorical Variables | OR (95% CI) | OR (95% CI) | OR (95% CI) | OR (95% CI) |
| Age | | | | |
| Under 50 | 1.16 (0.51-2.54) | 1.11 (0.31-3.56) | 1.09 (0.57-2.03) | 3.01 (0.05-1.16) |
| Over 50 | -Ref- | -Ref- | -Ref- | -Ref- |
| Gender | | | | |
| Female | -Ref- | -Ref- | -Ref- | -Ref- |
| Male | 0.75 (0.30-1.79) | 0.63 (0.19-1.85) | 0.70 (0.36 – 1.13) | 1.03 (0.49-2.14) |
| Smoker | | | | |
| Yes | NA | 0.81 (0.23 – 2.53) | NA | 0.95 (0.33-2.49) |
| No | NA | -Ref- | NA | NA |
| Antibiotic Use | | | | |
| Yes | 0.86 (0.13-3.10) | 1.63 (0.23-7.01) | 1.68 (0.61 – 3.96) | 1.74 (0.45-5.46) |
| No | -Ref- | -Ref- | -Ref- | -Ref- |
| BMI | | | | |
| Underweight | 0.00 (0.00-2.72) | 2.03 (0.0-1.1e ³³) | 4.74 (0.22-44.05) | 0.00 (0.0-2.1e ⁴⁵) |
| Normal | -Ref- | -Ref- | -Ref- | -Ref- |
| Overweight | 2.06 (0.55-9.88) | 2.20 (0.47-15.8) | 0.99 (0.39-2.58) | 1.19 (0.49-3.07) |
| Obese | 3.59 (1.16-15.83)* | 1.56 (0.36-10.80) | 1.34 (0.63-3.16) | 0.48 (0.19-1.28) |
| Oral Hygiene | | | | |
| Good | -Ref- | 1.47 (0.36-5.02) | 0.79 (0.32-1.69) | 2.76 (1.19 -6.34)* |
| Poor | 1.17 (0.44-3.67) | -Ref- | -Ref- | -Ref- |
| Continuous Variables | OR (95% CI) | OR (95% CI) | OR (95% CI) | OR (95% CI) |
| Fiber (grams) | 1.25 (0.92-1.64) | 1.17 (0.92-1.43) | 1.10 (0.93-1.21) | NA |
| Calcium (milligrams) | 0.99 (0.99-1.002) | NA | NA | NA |
| Whole grains (ounces) | 0.43 (0.17-0.93)* | 0.41 (0.12-1.03) | 0.56 (0.14-0.93)* | NA |
| Produce (cups) | 0.43 (0.29-1.71) | 0.44 (0.13-1.29) | 0.59 (0.31-1.09) | NA |
| Dairy (cups) | 2.49 (0.25-30.32) | NA | NA | NA |
| Sugar (tsp) | NA | NA | NA | 1.05 (1.01-1.1)* |

NA= Not applicable, variable did not meet criteria to be included in final model.

*Indicates significance (p<0.05)

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541. Factors Associated with the Persistence of Colonization by Multidrug-Resistant Organisms in Cali, Colombia

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Background. Colonized patients represent a reservoir for transmission to other non-colonized patients for health institutions, so surveillance measures and contact precautions have been taken in the worldwide to mitigate transmission. However, despite the different interventions implemented, factors associated with persistence have not been evaluated in our context. This study aimed to describe the persistence of colonization in patients with multidrug-resistant organisms (MDROs) re-admitted to a health institution.

Methods. A retrospective observational study was conducted. Patients re-admitted with a previous positive rapid test for MDROs, who had received chlorhexidine bathing and contact precautions during hospitalization were included. Samples were obtained from two rectal and one nasal swap. Colonization was defined as MDRO detection in at least one anatomical site, in the absence of symptoms or signs of infection. Persistence was defined as two positive screening for the same MDRO. Laboratory tests were chromID*, CHROMID* CARBA and MacConkey agar. VITEK MS* MALDI-TOF conducted MDROs genus identification, and carbapenem-resistant was evaluated through Sensi-Disc^{**}. Logistic regression was performed to examine any association between persistence and clinical data.

Results. A total of 4,362 screening for MDROs was analyzed form July 2015 to December 2016, and 142 patients were included in the study; the median age was 39 years (IQR=12–62) and 56% were male. The most frequent MDRO was carbapenem-resistant Enterobacteriaceae. There was a statistically significant difference in length of hospitalization (P = 0.003) and ICU (P = 0.035) between non-colonized and persistence of colonization. Factor associated with persistence of colonization included liver disease [OR=3.1; 95% CI: 1.068–9.019; P = 0.037], history of infection in the last year [OR=5.37; 95% CI: 1.036–13.839; P = 0.044], use of permanent urinary catheter [OR=6.48; 95% CI: 1.314–31.975; P = 0.022], history of gastrostomy before hospitalization [OR=5.37; 95% CI: 1.547–18.638; P = 0.036], and use of nasogastric tube [OR=5.14; 95% CI: 1.108–23.861; P = 0.036].

Conclusion. It is necessary to consider the previous history of infection in the last year, and other patient's comorbidities and conditions as risk factors of persistence to colonization by MDROs.

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542. Los Angeles County Acute Care Regional Antibiogram Suggests Changing Landscape of MDRO Threats Between 2015 and 2017

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Background. National surveillance for multidrug-resistant organisms (MDRO) are limited by narrow geographic sampling, few hospitals, and failure to account for local epidemiology. A Los Angeles County (LAC) regional antibiogram was created to inform public health interventions and provide a baseline for susceptibility patterns countywide. We present data to compare the 2015 and 2017 LAC regional antibiogram.

Methods. We conducted a cross-sectional survey of cumulative facility-level antibiograms from all hospitals in LAC; 83 hospitals (AH) and 9 Long-term Acute Care (LTAC). For 2015, submission was voluntary, 2017 data were collected by public health order. Non-respondents were contacted by phone and in person. Isolates from sterile sources were pooled. Countywide susceptibility was calculated by weighting each facility's isolate count by its reported susceptibility rate with minimum-maximim observed (2015) and Interquartile range (IQR) for 2017. Change from 2015 mean susceptibility is reported.

Results. Seventy-five (75) facilities submitted antibiograms for 2015 and 86 facilities for 2017. Among non-respondents in 2017, two facilities could not provide an adequate antibiogram and 4 were specialty hospitals with too few cultures to create an antibiogram. Regional summmary tables are presented in Tables 1–4. *Klebsiella pneumoniae* (n = 50 hospitals/19,382 isolates) % S to meropenem was 97% (IQR 94–100%), no change from 2015. *Pseudomonas aeruginosa* (PA) (n = 52 hospitals/17,770 isolates)% S to meropenem was 84% (IQR 74–93%), no change from 2015. Susceptibility to *Acinetobacter baumannii* (AB) was reported by 48 hospitals, including 1,4361 isolates, % S to meropenem was 39% (IQR 25–75%), 14% lower than 2015. *Streptococcus agalactiae* (n = 13 hospitals/647 isolates)% S to clindamycin was 43% (IQR 13–59%), a 22% increase from 2015.

Conclusion. LAC regional antibiograms identified stable patterns of antimicrobial resistance for most pathogens, but concerning results with *AB* and *PA*. Analysis of highly drug-resistant pathogens such as AB and PA would be improved with patient-level data to generate a combination antibiogram. We favor presenting IQR %S as done for 2017. Ongoing analysis will include multivariable analysis of observed changed S controlling for hospital characteristics.



Image: state state

S interpreted using non-meningitis (e.g., pneumonia) breakpoints; meningitis specific %S reported in detailed antibiogram Intrinsically resistant Not routinebt tested or not annitrable

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543. Biocide Resistance Genes in *Klebsiella* spp. Infections from Trauma Patients in Iraq and Afghanistan

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Background. Biocides play an integral role in infection control. Paralleling concern about rising incidence of multidrug-resistant (MDR) organisms is a concern for resistance to biocides. In small studies, several genes involved in the production of efflux pump proteins have been identified as markers of biocide resistance in *Klebsiella* spp., namely *cepA*, *qacA*, *qacE*, *qacAE*, and *acrA*. This study aimed to analyze the *Klebsiella* spp. isolates of a previously defined military trauma group with a high incidence of MDR organisms for the presence of these genes and their correlation with other resistance.

Methods. All infecting *K. pneumoniae*, *K. variicola*, and *K. quasipneumoniae* isolates archived by the Trauma Infectious Disease Outcomes Study (June 2009–December 2014) were selected. Additionally, all colonizing isolates linked with infecting isolates were included; the remainder to total 50 MDR and 46 non-MDR colonizing isolates were chosen randomly. Antimicrobial identification and susceptibilities were determined by CLSI criteria using the BD Phoenix Automated Microbiology System. PCR according to published methods for *cepA*, *qacA*, *qacE*, *qacAE*, and *acrA* was accomplished in duplicate. MDR was defined as either resistance to \geq 3 classes of an ESBL or KPC.

Results. A total of 237 isolates (221 K. pneumoniae, 10 K. variicola, 6 K. quasipneumoniae) met inclusion criteria, of which 149 (63%) were MDR. All isolates had been exposed to antimicrobials prior to isolation. Of all isolates, 234 (98%) carried cepA: 218 (98%) K. pneumoniae carried cepA, 10 (100%) K. variicola carried cepA, and 6 (100%) of K. quasipneumoniae carried cepA. In addition, 148 (62%) isolates with cepA were MDR. One (10%) K. variicola isolate carried qacE along with cepA. This isolate was the only MDR K. variicola. None of the isolates carried qacA, qacAE, or acrA.

Conclusion. We confirmed the near universal presence of the *cepA* biocide resistance gene in *Klebsiella* spp. isolated from trauma patients in Iraq and Afghanistan. In the largest evaluation of biocide resistance genes in *Klebsiella* spp. to our knowledge, the presence of *qacA*, *qacE*, *qac*\Delta*E*, and *acrA* was less common than has been reported elsewhere.

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544. Clonal Spread of Two Sequence Types of Carbapenem-Resistant *Acinetobacter baumannii* Blood Isolates at a Tertiary Care Hospital in South Korea Over 2.5 Years

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