Methods. Cladophora were processed from three Indiana Lake Michigan sites (S1 and S2; Fig 1) in 2002 and 2012 (S3; Fig 1) at the USGS Lake Michigan Research Station (Chesterton, IN). In 2015, surface water samples were obtained by the USGS at four Chicago beaches (S4-S7; Fig 2), which also amass Cladophora. Bacteria were isolated shortly after collection. In 2019-2020, Ent were cultivated and susceptibilities were performed at Rush.

Results. In 2002-2003 (S1 and S2), 160 E. coli were cultured from Cladophora. There was AR to multiple classes, highest overall in tetracyclines (7.5%, range 6.2%-18.7%), cefoxitin (8%), and cefazolin (5.6%). Resistance to cefuroxime was 0.6%. Four Salmonella isolates from 2012 (S3) were pan-susceptible, while two Citrobacter isolates were resistant to penicillins, 1st and 2nd generation cephalosporins, and cephapems. Beach surface water samples from 2015 revealed more pronounced AR in E. coli (n=185) involving multiple classes, including highest in ampicillin (12.4%), tetracyclines (8.1%), piperacillin (7%); cep;pen (3.2%); cefazolin (3.8%); cephapems (3.2%) and amoxicillinclavulanate (2.7%). Resistance to 3rd-generation cephalosporins, fluoroquinolones, trimethoprim/sulamethoxazole ranged from 0.5-2%. AR Ent varied by beach site with highest percentages at S4, the only site with an associated dog beach.

Conclusion. These findings suggest that Cladophora in recreational waterways may serve as reservoirs for AR Ent. Differences in AR Ent at beach sites may reflect varying degrees of fecal contamination. Identifying community reservoirs is key to better understanding the acquisition of antibiotic resistant Ent among healthy populations and has long-term ecological and public health implications.

Disclosures. All Authors: No reported disclosures

Table 1. COVID-19 At-Home Capillary Blood Specimen Collection Pilot – Gaining Insight into Independent Self-Collection of Blood Specimens and COVID-19 Within the Veteran Population

| OUTCOMES | Neoteryx Mitra | Tasso-SST | Total |
|----------|----------------|-----------|-------|
| Invited  | 250 (42%)      | 240 (58%) | 500 (100%) |
| Consented| 196 (54%)      | 176 (50%) | 372 (52%) |
| Spec Rec’d| 129 (95%)  | 153 (87%) | 282 (90%) |

Table 2. Assess Sensitivity and Specificity Results

| Antigen | Neoteryx Mitra | Tasso-SST |
|---------|----------------|-----------|
| SARS-CoV-2 | Antibody Positive | Antibody Negative | Antibody Positive | Antibody Negative |
| Total Abs | 45 | 35 | 60 | 30 |
| | Sensitivity | 0.60 | 0.87 |
| | Specificity | 0.70 | 0.80 |

Table 3. COVID-19 At-Home Capillary Blood Specimen Collection Pilot Outcomes

| OUTCOMES | Neoteryx Mitra | Tasso-SST | Total |
|----------|----------------|-----------|-------|
| Invited  | 250 (42%)      | 240 (58%) | 500 (100%) |
| Consented| 196 (54%)      | 176 (50%) | 372 (52%) |
| Spec Rec’d| 129 (95%)  | 153 (87%) | 282 (90%) |

Figure 1. Map of Lake Michigan showing sites (S1-S3) where Cladophora samples were collected. NB, North Beach, Racine, Wisconsin; Michigan City, Indiana; PL, Portage Lakefront, Indiana Dunes National Park, Indiana.

Figure 2. Map of Lake Michigan showing sites (S4-S7) where beach surface water samples were obtained. Montrose, Foster, 63rd St, & Calumet beaches in Chicago, Illinois.
Conclusion. Veterans successfully collected their own specimens and had no strong preference for either device. The Tasso-SST combined with the InBios Spike IgG assay provided the highest combination of sensitivity and specificity. Limitations included one collection device per subject, varied timing of testing, unknown infection or vaccination status among some, and Tasso collection volume and Mitra whole blood dilution may have affected comparison across assays or performance.

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1006. Association of Development of Pneumonia and Virulence Gene Expression in Acinetobacter baumannii Isolated from Clinical Specimens

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Session: P-56. Microbial Pathogenesis

Background. Not all Acinetobacter baumannii isolated from respiratory specimens are true pathogens. Distinguishing between true pathogens and colonizers is important to initiate early treatment and to reduce the unnecessary prescription of antibiotics. To determine the microbiological factors contributing to the development of A. baumannii pneumonia, we investigated the association between the expression level of known A. baumannii virulence genes such as ompA and hisF and pneumonia.

Methods. Patients in whose respiratory specimens A. baumannii was identified between January 2018 and January 2019 in a tertiary university hospital were recruited into this study. Relevant radiologic findings and more than 3 days of susceptible antibiotic prescription started within 3 days of bacterial isolation were considered as having pneumonia. The absence of radiologic findings of pneumonia until 7 days after the isolation of A. baumannii was defined as colonization. The expression of ompA and hisF was determined with quantitative reverse-transcription polymerase chain reaction. Host factors known to be associated with pneumonia and expression levels of virulent genes were compared between the groups.

Results. Overall, 246 patients in whose respiratory specimens A. baumannii was identified were recruited into this study. Among them, 17 and 24 patients were assigned to the pneumonia and colonization groups, respectively. In the univariable analysis, ompA, ICU stay, and mechanical ventilation were significantly associated with pneumonia (p < 0.03, < 0.01, < 0.01, respectively). In the multivariable analysis, mechanical ventilation was significantly associated with pneumonia (OR = 9.75, p = 0.03). ompA expression was not significantly associated with pneumonia in the multivariable analysis (OR = 1.12, p = 0.75) (Table 1). ompA and hisF were significantly associated with the 30-day in-hospital mortality (p = 0.02, < 0.01).

Table 1. Univariable and multivariable analysis of factors related to pneumonia

| Univariable analysis | Multivariable analysis |
|----------------------|------------------------|
| Expression of ompA   | 0.97 (0.96-1.00)       |
| ICU stay             | 0.00 (0.00-0.35)       |
| Mechanical ventilation| 0.12 (0.05-0.29)       |
| OmpA expression      | 0.97 (0.94-1.00)       |
| HisF expression      | 0.00 (0.00-0.45)       |

Cl, confidence interval; OR, odds ratio; ICU, intensive care unit

Conclusion. The association between increased ompA expression in A. baumannii and the development of pneumonia was not statistically significant after adjusting for patient factors. However, the relatively high expression of ompA in pneumonia patients and their association with increased mortality suggests the need for larger-scale prospective studies to draw a conclusion.

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1007. Hypermutability in Clinical Strains of Klebsiella pneumoniae: Role of the V76G Mutation in MutH

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Session: P-56. Microbial Pathogenesis

Background. Hypermutator (HM) bacteria exhibit high spontaneous mutation rates, due to DNA mismatch repair (MMR) gene mutations, which may indicate antibiotic resistance. HM is best described for chronic infections or colonization in particular with P. aeruginosa. HM K. pneumoniae (KP) and carbapenem resistant Enterobacteriales (CRE) are rarely studied.

Methods. Longitudinal isolates from 5 patients (pts) with long-term ST258 CRKP infections (median: 1.4 yr, 0.5–4.1 yr) underwent Illumina Hiseq whole genome sequencing. Strains from 1 pt were tested for HM and resistance. Mutant strains were created by complementation and CRISPR.

Results. In each pt, initial and recurrent isolates were genetically related (≤7 core genome (cg) SNP). In 1 pt, infection recurred 3.3 yrs after initial infection; baseline and recurrent (T0) isolates differed by 7–10 cgSNP. 4 cafefaldime-avibactam (CAZ) resistant isolates (T1-T4) were recovered ≤2 wks after treatment of T0 infection. Strains T1-T4 differed from T0 and each other by 109-214 and 58-137 cgSNP (Fig. 1), respectively, and carried mutations in MMR genes (mutS -14946A (ΔpmutS); mutH V76G) and blakp3 (D179Y). T1-T4 mutations were enriched for genes involved in metabolism (adjusted p<1.46e-1), ABC transport (p=4.1e-1), 2-component systems (p=9.2e-1), signal transduction (p=6.0e-1), and transcription regulation (p=2.1e-2). mutS and mutH expression was 46-49% lower in T1-T4 than in T0. T1-T4 demonstrated rifampin mutational frequency >10^-5, compared to < 10^-7 for earlier strains. Upon passage in meropenem-vaborbactam (MV), colistin and gentamicin, T1-T4 developed resistance faster and higher MICs than T0 (Fig 2). MV resistance was associated with ΔS5 ompk36 promoter insertions or point, deletion or STOP mutations in ompk36 coding region. Complementation of T1-T4 with wild-type (WT) mutH restored phenotypes. Introduction of V76G to WT mutH in T0 established HM and in vitro passage resistance phenotypes.

SNP matrix of 11 clinical isolates from a single patient with recurrent KPC-Kp infections

The first 6 isolates were recovered within 6 months of transplant (Tinital). The later 5 isolates were recovered ~40 months after initial GI colonization. Number of SNPs for each pairwise comparison on isolates are shown. Gray highlighted boxes shown SNP differences between the 5 later strains.

Serial passages of 4 clinical isolates.

Table 1. Univariable analysis of factors related to pneumonia

| Univariable analysis | Multivariable analysis |
|----------------------|------------------------|
| Expression of ompA   | 0.97 (0.96-1.00)       |
| ICU stay             | 0.00 (0.00-0.35)       |
| Mechanical ventilation| 0.12 (0.05-0.29)       |
| OmpA expression      | 0.97 (0.94-1.00)       |
| HisF expression      | 0.00 (0.00-0.45)       |

Cl, confidence interval; OR, odds ratio; ICU, intensive care unit

Conclusion. MMR mutations emerged in longitudinal CRKP, which conferred HM phenotypes and were associated with CAZ and other anti-CRE antibiotic resistance. mutH V76G is crucial in MMP. Long-term colonization or recurrent infections in HM resistant antibiotic exposure might predispose CRKP strains to HM.

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