1197. Inhibitory Effect of Ursodeoxycholic Acid on Clostridioides difficile Growth

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Session: P-53. Microbial Pathogenesis

Background. Ursodeoxycholic acid (UDCA), a secondary bile acid, inhibits germination and growth of *Clostridioides difficile* in vitro, but the results from in vivo experiments have been conflicting. We evaluated the effects of UDCA on *C. difficile* in vitro and in a wax moth, *Galleria mellonella* model.

Methods. The in vitro growth and germination effects of UDCA on *C. difficile* were assessed with increased concentration of UDCA (0.001, 0.01, 0.05, and 0.1%). To assess treatment effects of UDCA, *C. difficile* spores (approximately 1x10^6-8 colony forming units (CFU)) were force fed to *G. mellonella* larvae treated with UDCA (50 mg/kg/day) 24 hours prior to *C. difficile* inoculation. Forty *G. mellonella* larvae were used for each experiment, which was repeated with two distinct strains (R20291 and CD196). Larvae were housed at 37°C and monitored for the next five days for mortality.

Results. In vitro experiment demonstrated inhibition of *C. difficile* growth at 0.1% concentration (P < 0.001 vs control). Larvae treated with UDCA had a numerically higher survival rate (60% / 24/40) compared to controls (40% / 16/40) but the results were not statistically significant (p=0.14). Identical rates of survival were observed in the control arms for both strains (40%) and similar in the treatment arms (R20291: 70%; CD 196: 50%).

Conclusion. Overall, UDCA shows inhibitory effect of growth and germination of *C. difficile* in vitro. However, in our *G. mellonella* model, a single dose of UDCA given prior to infection did not prevent CDI. Further dose dependent, and multiday studies investigating the role of UDCA in CDI is needed to better understand this in vitro / in vivo paradox.

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1198. Measurement of Pre-transplant Anti-cytomegalovirus (CMV) Immunoglobulin G Titer to Predict Risk of CMV Infection in CMV-seropositive Kidney Transplant Recipients

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Ramathibodi CMV in kidney transplant (RACK) study group

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Background. Although cytomegalovirus (CMV)-seropositive solid organ transplant recipients have a lower risk of CMV infection compared with CMV-seronegative recipients, some patients remain at risk of CMV infection after transplant. Low pre-transplant anti-CMV immunoglobulin G (IgG) titer has been reported as a predictor of CMV infection in CMV-seropositive liver and heart transplant recipients, but this association in CMV-seropositive kidney transplant (KT) recipients has not been explored. We investigated the pre-transplant anti-CMV IgG titer and other CMV infection risk factors in CMV-seropositive KT recipients.

Methods. This retrospective study was conducted on CMV-seropositive KT recipients aged >18 years old at Ramathibodi Hospital during 2017 and 2018. The cumulative incidence of CMV infection was estimated with Kaplan–Meier methodology. The pre-transplant anti-CMV IgG titer was measured with an enzyme-linked fluorescent immunoassay. Risk factors for CMV infection were analyzed with Cox proportional hazards models.

Results. Of the 340 included CMV-seropositive KT recipients (37% female; age [mean±SD]: 43±11 years), 69% and 64% received deceased-donor allograft and induction therapy, respectively. The anti-CMV IgG titer was < 20 and >20 AU/ml in 7.1% and 92.9% of patients, respectively. During a mean follow-up of 14 months, the cumulative incidence of CMV infection was 14.8%, including both asymptomatic CMV infection (69%) and tissue-invasive disease (31%). A pre-transplant anti-CMV IgG titer of < 20 AU/ml was significantly associated with CMV infection in both the univariate analysis (HR, 2.70; 95%CI, 1.21–6.05, [p=0.02]) and the multivariate analysis (HR, 2.98; 95% CI, 1.31–6.77, [p=0.009]). Other significant risk factors of CMV infection included older donor age (HR, 1.03; 95% CI, 1.01–1.06, [p=0.005]), anti-thymocyte induction therapy (HR, 2.90; 95% CI 1.09–7.74, [p=0.033]), and prolonged cold ischemic time (HR, 1.06; 95% CI, 1.02–1.10, [p=0.002]).

Conclusion. A low pre-transplant CMV-specific humoral immunity is independently associated with post-transplant CMV infection in CMV-seropositive KT recipients. The universally available anti-CMV IgG titer test could potentially stratify those at risk and target preventive strategy appropriately.

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1199. Phylogenomic analysis of Campylobacter jejuni isolated from gastroenteritis cases in Michigan

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Background. *C. jejuni* is the leading cause of bacterial gastroenteritis worldwide. It has been classified as a serious antibiotic resistant threat, causing 13,000 hospitalizations and 120 deaths annually. Our goal was to describe the diversity of clinical *C. jejuni* using phylogenomics and classify resistance mechanisms.

Methods. Isolates were collected via sentinel surveillance at four hospitals, and demographic and clinical data were obtained. DNA was extracted and sequenced. Raw reads were processed with Trimmomatic and quality checked with FastQC. *De novo* genome assembly was performed in Spades. Assembled genomes were filtered for quality and completeness; samples of 1.4-2.1MB were annotated in Prokka followed by pangenome and phylogenetic analyses. Multilocus sequence typing loci and virulence and antibiotic resistance genes were extracted from each genome.

Results. Among the 214 *C. jejuni* isolates recovered, 86 unique sequence types (STs) were identified; five were novel STs with unique allele combinations. ST353 (8.3%: n=18), ST982 (7.4%: n=16), ST50 (5.1 %: n=11) and ST48 (5.1%: n=11) were the most prevalent STs identified, while the majority (50.1%: n=50) of STs were singletons. The pangenome analysis identified 8781, 615, and 1169 total, core, and shell core genes, respectively, which grouped the isolates into three major clades. Most isolates belonged to clade 1. A neighbor-net analysis detected significant recombination among all 86 STs (pairwise homoplasy index p=< 0.00001) and evidence of horizontal gene transfer across clades. The beta-lactamase gene, $bla_{OXA-605}$, was the most common resistance gene identified (58.8%: n=125) followed by *tet(O)* (56.0%: n=121), which mediate resistance to beta-lactams and tetracyclines, respectively. Resistance phenotypes were confirmed using microbroth dilution.

Conclusion: Together, these data demonstrate that the *C. jejuni* population is highly diverse and carries important resistance determinants. The phylogenomic analyses also provide insight into the evolution of this major foodborne pathogen. Future work will focus on identifying molecular and epidemiological factors associated with specific strain types and resistance and virulence profiles circulating in Michigan.

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1200. Risk of group A streptococcal Transmission Among the Pediatric Population in the Houston Area

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Session: P-53. Microbial Pathogenesis

Background. Disease due to group A *Streptococcus* (GAS) occurs frequently in children and usually manifests as pharyngitis or superficial skin infections. However, invasive disease (iGAS) such as necrotizing fasciitis or streptococcal toxic shock syndrome is responsible for significant morbidity and mortality. National-level surveillance at the Centers for Disease Control and Prevention (CDC) estimates >10,000 cases and ~1,500 deaths due to iGAS occur annually in the US. Much interest revolves around the ability to detect potential transmission events (PTEs) of GAS disease using surveillance data as such information may change recommendations for chemoprophylaxis of close contacts. Studies by the CDC have shown a secondary attack rate from 66.1 to 102 /100,000, primarily occurring among older adults with co-morbidities. However, previous studies were limited in that the GAS surveillance was limited to iGAS disease.

Methods. Retrospective study using a comprehensive GAS passive surveillance system. GAS isolates and associated metadata were obtained from 2 hospital systems in the Texas Medical Center from 2017-2019. Molecular *emm* typing of GAS isolates was performed using the CDC protocol. PTEs were defined based on GAS disease isolates originating from the same zip code, occurring within 30 days of each other, and of the same *emm* type.

Results. A total of 1291 isolates were included in the study – 94 PTEs were identified representing 168 individual GAS isolates of which 74 were defined as index cases. The 4 most common GAS *emm* types identified among PTEs were *emm1* (43/94, 45.7%), *emm12* (30/94, 31.9%), *emm4* (6/94, 6.4%), and *emm6* (5/94, 5.3%). Index cases most frequently resulted in a single PTE (n=74) with an average number of PTEs per index case of 1.3 (range 1 to 3 PTEs). From index cases, 10 GAS isolates were derived from invasive disease (10/74, 13.5%) and 6 from skin and soft tissue infections (SSTI; 6/74, 8.1%). A substantial proportion of PTEs resulted in iGAS (9/94, 9.5%) and SSTI (10/94, 10.6%).

Conclusion. Using comprehensive local surveillance, we were able to identify several potential GAS transmission events. Further analysis – including whole genome sequencing on index and PTE isolates – is needed to better define transmission events.

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