than displaced strains, so it is critical to identify the mechanisms that enable invasion. We tested the hypothesis that invasive strains are less susceptible to RNA interference (RNAi), the major antiviral defense in mosquitoes, than displaced strains.

Methods: We knocked-down (KD) RNAi *in vivo* in *Aedes aegypti*, the DENV vector, by injecting mosquitoes with double-stranded RNA against Argonaute 2 (Ago2), a key enzyme in the RNAi pathway, or a control dsRNA. Ago2 KD and control mosquitoes were fed bloodmeals containing 1 of 3 isolates each of 3 different strains of DENV that had undergone sequential competitive displacement in Sri Lanka, termed, in order of displacement, Pre-DHF, Post-DHF and Ultra-DHF. We predicted that the Pre-DHF strain, which we have previously shown to be less infectious for mosquitoes than the other two strains, would show a greater increase in infectivity than those strains. Engorged mosquitoes were incubated for 10 days, homogenized, and assayed for virus.

Results: Ago2 KD efficiency ranged from 79% to 98%, as determined by semi-quantitative PCR and band densitometry. The percentage of mosquitoes infected following Ago2 vs. control KD was not significantly different (33% vs. 47%; paired t-test, DF = 8, $P = 0.08$). However, among infected mosquitoes, virus titer was significantly higher in Ago2 KD mosquitoes (3.98 vs. 3.38 $\log_{10}$ plaque forming units/body; t-test, DF = 14, $P = 0.02$). Contra our prediction, a two-factor ANOVA did not reveal a significant interaction between the effect of virus strain and treatment (DF = 5, $P = 0.58$), indicating that Pre-DHF viruses did not show a larger response to Ago2 KD than Post and Ultra-DHF viruses.

Conclusion: These data support the role of RNAi as a key mosquito defense against virus replication in mosquitoes but indicate that the differences in competitive success among the 3 DENV strains studied are not due to differences in interactions with Ago2 during initial stages of mosquito infection.

Disclosures. **All authors:** No reported disclosures.

2611. Enterotoxigenic *Bacteroides fragilis* Alters the Genome of Colon Epithelial Cells

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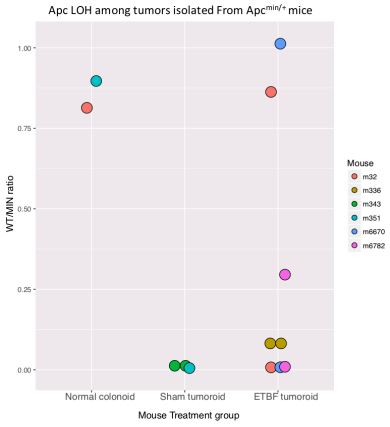
Session: 269. Pathogenesis and Host-Response Interactions
Saturday, October 5, 2019: 12:15 PM

Background: Individuals born in 1990 have twice the risk of developing colon cancer and four times the risk of developing rectal cancer as those born in 1950. The gut microbiome is being proposed as a potential contributor to this difference because of the surge in obesity in the United States, the link between obesity and gut dysbiosis, and the growing number of studies which have associated a dysbiotic gut microbiome with CRC. Enterotoxigenic *Bacteroides fragilis* (ETBF) is one of the bacteria most studied in relation to CRC development; it is found at a higher frequency in both the stool and mucosa of CRC patients, and it rapidly induces tumor formation in an $Apc^{min/+}$ mouse model of CRC. In this model, tumor formation typically occurs via loss of heterozygosity (LOH) of the *Apc* gene, the genetic mutation found in approximately 80% of sporadic CRC cases. ETBF produces a potent exotoxin (BFT) which induces E-cadherin cleavage, β-catenin nuclear localization and colonic epithelial cell proliferation. But we still do not understand how these downstream effects cause lasting changes in the genome of colon epithelial cells that then initiate tumor formation and growth. As cancer is ultimately a disease that arises and progresses via changes in the genome, understanding these interactions is essential.

Methods: We hypothesize that ETBF induces DNA mutations via BFT that encourage tumor formation, and enhance tumor growth. To test this hypothesis, we performed whole-exome sequencing on tumors and normal tissue isolated from $Apc^{min/+}$ mice after ETBF or sham inoculation. Additionally, we isolated colon organoids from $Apc^{min/+}$ mouse normal tissue (colonoids) and $Apc^{min/+}$ mouse tumors (tumoroids) after ETBF or sham inoculation. We performed in vitro DNA damage assays and qPCR for *Apc* LOH on these colon organoids.

Results: Our preliminary data indicate that ETBF-induced tumors have lower rates of *Apc* LOH and that double-stranded DNA breaks are observed as soon as 3-hours after BFT treatment of colonoids and as soon as 72-hours after ETBF inoculation.

Conclusion: These data suggest that in vivo, ETBF may induce mutations in cancer-driver genes which cause tumor formation via pathways other than somatic recombination at the *Apc* locus, a result we are now testing with additional ($N = 19$) whole-exome tumor sequencing in-progress.



Disclosures. **All authors:** No reported disclosures.

2612. Molecular Evidence of *Ureaplasma urealyticum* and *Ureaplasma parvum* Colonization in Preterm Infants with Respiratory Distress

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Session: 270. Pediatric Respiratory Infections
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Background: *Ureaplasma urealyticum* and *Ureaplasma parvum* have been associated with respiratory diseases in premature newborns, but their role in the pathogenesis of the respiratory distress syndrome (RDS) is unclear. The present study was conducted to investigate preterm newborns with respiratory distress for colonization of *U. urealyticum* and *U. parvum* in endotracheal fluid (TF)/nasopharyngeal aspirates (NPA) specimens employing culture and polymerase chain reaction (PCR).

Methods: Sixty preterm infants, presenting with respiratory distress persisting for more than 24 hours were investigated. Endotracheal fluid or nasopharyngeal aspirates specimens were inoculated in 2mL Ureaplasma broth and Ureaplasma agar for culture identification assay and PCR. DNA extracts were processed for a genus specific PCR (429 base pair region) on urease gene of *U. urealyticum*/*U. parvum* and species specific PCR (1305 base pair region) on 16S rRNA gene in *U. parvum*.

Results: *Ureaplasma* species colonization was positive in 11 (61.11%) male patients and7 (38.89%) females but there was no statistical association between sex and *Ureaplasma*species colonization ($P = 0.771$). *Ureaplasma* spp. culture identification assay was positive in 7 (11.67%).Ureaplasma genus specific PCR was positive in 14 (23.33%) cases; species specific PCR in 9 (64.28%) infants were identified as *U. parvum.* Considering culture as diagnostic standard, sensitivity of PCR was 42.86%; specificity 79.24%; positive predictive value 21.43% and negative predictive value 91.30 %; with overall percentage agreement at 75%. Septicemia was positive in 12 (66.67%) infants colonized with *Ureaplasma*species than in 5 (11.9%) of non colonized infants which was found to be significant ($P = 0.00$). Twelve (66.67%) patients with *Ureaplasma*species colonization had lethargy with statistically significant association($P = 0.04$).

Conclusion: This study confirms that *Ureaplasma species* and particularly *U. parvum* colonization in preterm infants was related to respiratory distress.

Disclosures. **All authors:** No reported disclosures.

2613. The Epidemiology of Respiratory Syncytial Virus (RSV) in People with Immune Dysfunction Seen at a Tertiary Hospital Between 2010 and 2017

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Session: 270. Pediatric Respiratory Infections
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Background: Persons with a compromised immune system are at increased risk of complications related to respiratory syncytial virus (RSV) but the risks are not well defined. We aimed to investigate the prevalence of RSV infection, associated risk factors and complications in a large population of people with immune dysfunction.

Methods: Persons with immune dysfunction, first seen at Copenhagen University Hospital, Rigshospitalet, between January 1, 2010 and February 21, 2017, aged ≥18 were included. RSV testing and positivity (positive PCR or antigen test) was determined through the Danish Microbiology Database. Generalized estimating equations logistic regression was used to investigate the risk factors for RSV positivity; Cox regression was used to assess the impact of RSV positivity (time-updated) on mortality in the first 12 months after first visit.

Results: The study included 42,567 persons, of which 3,356 (7.9%, 95% CI 7.6%-8.1%) were tested for RSV at least once during follow-up, with 2,374 (71%) tested in the first 12 months. Stem cell transplant (HSCT) and solid-organ transplant (SOT) recipients had the highest proportion of persons tested for RSV (66.0%, 95% CI 62.9%–69.1% and 31.6%, 95% CI 29.0%–34.2%, respectively). Of those tested, 256 (7.6%, 95% CI 6.7%–8.5%) had ≥1 positive RSV test (figure). After adjustment, HSCT and SOT recipients, as well as other hematologic and rheumatologic patient groups were more likely to have a positive RSV test compared with persons seen in the infectious disease department. Fifty-seven RSV-related complications were identified in 53/256 (20.7%, 95% CI 15.7%-25.7%) persons positive for RSV (table), of which 24 (45.3%) were HSCT recipients and 18 (34.0%) were other hematologic patients. In the 12 months after first department visit, 9,451 (22%) patients died; persons with RSV had an increased risk of short-term mortality (aHR 1.77, 95% CI 1.19–2.64), adjusting for sex, age, patient group and flu positivity.

Conclusion: Patients with a hematological or rheumatological condition and SOT recipients had the highest odds of contracting RSV, with hematological patients in particular at an excess risk of RSV-related complications. RSV was associated with an increased risk of death in the first 12 months of patient follow-up.