Sustained viral titer plateaus, despite antiviral ISG induction, suggests viral blocking of plateaus 24–96 hours post infection. IFN-β and IFN-λ pre- and posttreatment conditions were analyzed. Viral titers increased significantly over the first 24 hours post infection. ISGs were induced in a similar pattern to IFNs. Restriction of Rhinovirus Infection Depends on Virus Sensing and Early IFN Induction

**Results:** We found that RV infection induces IFN-β and IFN-λ production and subsequent ISG induction, including expression of IFIT1, OAS1, and MX1. RV-14 infection induced IFN-β and IFN-λ in a dose-dependent manner, with a maximum fold increase of IFN expression at 48 hours post infection. ISGs were induced in a similar pattern to IFNs. Viral titers increased significantly over the first 24 hours post infection and then plateaued through 96 hours. IFN-β and IFN-λ pre- and posttreatment conditions significantly decreased maximum viral titers achieved but continued with viral plateau 24–96 hours post infection.

**Conclusion:** We observed that RV infection induces innate immune activation and the production of type I and II IFNs during acute infection of airway cells. Sustained viral titer plateau, despite antiviral ISG induction, suggests viral blocking of IFN pathway mechanisms that can be overcome by early IFN induction to significantly restrict RV viral replication.
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 *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 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

**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 toxin (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 last changing 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 and *Apc^{min/+}* mouse tumors (tumoroids) after ETBF or sham inoculation. We performed in vitro DNA damage assays and qPCR for APO LOH on these colon organoids.

**Results:** Our preliminary data indicate that ETBF-induced tumors have lower rates of APO LOH and DNA damage. 36 colon organoids from *Apc^{min/+}* mouse normal tissue (colonoids) and 36 *Apc^{min/+}* mouse tumors (tumoroids) after ETBF or sham inoculation. We performed in vitro DNA damage assays and qPCR for APO LOH on these colon organoids.

**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.

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

**Background:** Early-onset neonatal pneumonia and sepsis are the leading causes of mortality in newborns, with their role in the pathogenesis of respiratory distress syndrome (RDS) 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 real-time PCR and double-stranded DNA breaks.

**Methods:** Sixty preterm infants, presenting with respiratory distress persisting for more than 24 hours were investigated. Endotracheal fluid and nasopharyngeal aspirates were inoculated in 2ml Ureaplasma broth and Ureaplasma agar for culture identification assay and PCR. DNA extracts were processed for a genus-specific (PCR429 base pair region) on urease of *U. urealyticum*/*U. parvum* and species specific PCR. (1305 base pair region) on 16S rDNA gene in *U. parvum*.

**Results:** *Ureaplasma* species colonization was positive in 11 (61.1%) male patients and 27 (58.8%) 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 (23.3%) cases; species specific PCR in 5 (6.48%) infants were identified as *U. parvum*. Considering culture as diagnostic standard, sensitivity of PCR was 42.86%; specificity 79.2%; positive predictive value 21.43% and negative predictive value 91.36% 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* = 0.007).

**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

**Background:** Persons with a compromised immune system are at increased risk for respiratory 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:** Patients 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 logit 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 recipients (SCT) and solid-organ transplant recipients (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, H SCT and SOT recipients, as well as other hematologic and solid-organ transplantation (SOT) recipients were more likely to have a positive RSV test compared with persons seen in the infeetious 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 SCT recipients and 18 (34.0%) were SOT recipients. In the first 12 months after first 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 increased risk of RSV-related complications. RSV was associated with an increased risk of death in the first 12 months of patient follow-up.