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 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 log10 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 animal model of CRC. In this study, we hypothesized that ETBF-induced tumors have lower rates of nuclear localization and colonic epithelial cell proliferation. But we still do not understand the mechanism of displacement of CRC. In this model, tumor formation typically occurs via loss of heterozygosity (LOH) of CRC. In this model, tumor formation typically occurs via loss of heterozygosity (LOH) of CRC. In this model, tumor formation typically occurs via loss of heterozygosity (LOH) of CRC.

**Methods:** We hypothesize that ETBF induces DNA mutations via BFT that encourage invasion. These data suggest that in vivo, ETBF may induce mutations in the genome of colon epithelial cells.

**Conclusion:** ETBF-induced tumor has lower rates of nuclear localization and colonic epithelial cell proliferation.

**Disclosures. 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 Saturday, October 5, 2019: 12:15 PM

**Background:** People with a compromised immune system are at increased risk of respiratory infections related to respiratory syncytial virus (RSV) but the risks are not well defined. We aimed to investigate the prevalence of RSV infection, association 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 (SCT) 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, HSC/T and SOT recipients, as well as other hematologic patient groups were more likely to have a positive RSV test compared with persons seen in the infecciones 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 SOT recipients and 18 (54.0%) were HSC/T recipients.

**Conclusion:** Patients with a hematologic or rheumatological condition and SOT recipients had the highest odds of contracting RSV, with hematologic 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.