Results. 160 Veterans were diagnosed with INF from December 1, 2017 to April 26, 2018. 106 had INF A, 54 INF B. Of the 160 cases, 15 were in DEC, 61 in JAN, 69 in FEB, 13 in MAR, 2 in APRIL 10 INF A isolates subtype as 8: H3N1, 2 H1N1pdm09. 5 INF B isolates subtype as Yangata lineage. Demographics: Median age 63 years (23–93); Race: 79% Caucasian, 16% Black, 1% Asian, 1% Pacific Island, 3% Hispanic. 95% had Medical History; 61% had Chronic Illness; 41% had COPD, HTN, 24% DM, and 12% COPD. The median BMI was 29 (17–51.5). 101 tested in ER; 36 in clinics, 5 in our related adult and nursing homes, and 17 during their hospitalization. 56 (35%) had received the INF vaccine this season. The median duration from vaccination to diagnosis was 100.5 days (2–175 days), 25 required hospitalization with 5 of them in ICU; 40% of the hospitalized patients had received the INF vaccine. The median length of stay was 4.5 days. 139 received oseltamiv (OSE), 13 supportive treatment, 8 antibiotics alone, and 7 OSE-antibiotics. 5 patients expired (3 INF A, 2 INF B) 3 were not vaccinated; 2 patient developed NSTEMI and survived. Hospitalized patients were older vs. 60, P = 0.018, more likely to have COPD (P = 0.0069), CHF (P = 0.0066), and history of lung cancer. There was no difference in risk for hospitalization between vaccinated and unvaccinated Veterans, P = 0.649.

Conclusion. The months of JAN and FEB had the highest flu activity, mirroring the INF activity in our nation as reported by the CDC. The majority of our patients were not vaccinated. 5 fatalities were noted. Not surprisingly, the vaccine was incident, NIV infections were more common than IV. Understanding the high traditionally been attributed to IV, including influenza-like-illness (ILI); however, the winter months. Many viral syndromes during the height of influenza season have RSV, but without a specific virus driving the trend.

2518. The Role of Non-Influenza Viruses in the Seasonal Viral Respiratory Illness: A Epidemiologic Study From October 2016–March 2017

Methods. A retrospective analysis of all PCR test results from one hospital system, collected between October 1, 2016 and March 7, 2017, including inpatient and outpatient samples was performed. 2,047 PCR test results were tested; after removing those with undetermined results and internal control samples, 1,924 were analysed. Data points abstracted included detection and identification of virus, and date of detection. We compared the total and monthly rates of NIV with IV, throughout the study period.

Results. Of 1,924 PCR results, 985 (51%) were positive for a respiratory virus. Of these, 302 (31%) were IV, and 683 (69%) were NIV. For every month studied, the ratio of IV to NIV exceeded 50%, including the height of the season. The most commonly detected viruses were Influenza A (30%), Rhino/Enterovirus (24%), RSV (19%), followed by other respiratory viruses (10%). Most common coinfections were influenza A and enterovirus (9%) and influenza B and RSV (10%). The ratio of NIV to IV exceeded 50%, including the height of the season. The most commonly detected viruses were Influenza A (30%), Rhino/Enterovirus (24%), RSV (19%), follow

Conclusion. Non-influenza respiratory viruses cause substantial viral RI during the winter months. Many viral syndromes during the height of influenza season have RSV, but without a specific virus driving the trend.

Disclosures. All authors: No reported disclosures.

Table 1: Demographic and Laboratory Characteristics in the Patients With Crimene-Congo Hemorrhagic Fever

| Characteristic | Survival Patients | Fatal Patients | NLR ≤ 2 | NLR > 2 |
|----------------|------------------|---------------|--------|--------|
| Age (%)        | 49.1 (175)       | 64.6 (14.0)   | 0.001  | 48.6 (17.0) |
| Gender (%)     | 46.6             | 40            | 0.075  | 513     |
| Platelet count (x10⁴/µL) | 49.8 (19.4) | 178 (78.0) | 0.001  | 49.0 (35.9) |

ALU (ALT (U/L) | 230 (429.4) | 1386 (1296.0) | 0.001 | 49.0 (35.9) |

LHD (LDH (U/L) | 1785 (943.9) | 5385 (1943.0) | 0.001 | 183.0 (973.2) |

CRT (Cr (mg/dL) | 0.9 (1.5) | 2.7 (2.5) | 0.001 | 1.0 (1.5) |

NLR | 2.9 (3.5) | 4.5 (3.0) | 0.001 |

Conclusion. NLR for clinicians may be an additional test as useful as platelet count and plasma creatinine, AST, ALT, LDH, and CK levels. Our study shows that NLR might be used as a prognostic marker to predict the severity of the disease in CCHF.

Disclosures. All authors: No reported disclosures.

2520. Epidemiology, Clinical Manifestations, and Outcomes of the 2017–2018 Influenza Season Among Hospitalized Patients at a Tertiary Care Center

Methods. Retrospective chart review of patients with Influenza admitted from September 1, 2017 to April 13, 2018. Diagnosis was confirmed by rapid flu test (RIDT) or Target Enriched Multiplex PCR (TEM PCR). Demographic, clinical, lab, treatment, and outcomes data were obtained. Analysis included prevalence and relative risk (RR)

Results. 220 patients were identified (47% males, 73% White). Median age was 70 years (range 18–99). 65% had Flu A and 27% Flu B. 81% came from home, 17% from a facility (nursing home, assisted living). 49% had flu vaccination (Figure 1). Flu strain and vaccination status had no association RR 1.31 (95% CI 0.85–2.01, P = 0.21). Common comorbidities were lung disease 44%, obesity 41%, DM 36%, CAD 34%, CHF 31% (Figure 2). Common presentations were respiratory 79% and constitutional 53%. 68% were hypoxic and 4% hypotensive on arrival. 42% had new CXR/CT finding and 55% had pneumonia. Sensitivity of RIDT was 38%. 91% were treated with oseltamivir (21% within 48 hours of flu detection). Median treatment duration was 5 days. Hospitalizations peaked in January (Figure 3). Median length of hospital stay was 6 days. 23% had severe flu (needed NPPV 13%, intubation 12%, pressor 5%, ICU stay 16%) which showed significant association with arrival from facility RR 2.21 (95% CI 1.36–3.56, P = 0.001), lung disease RR 1.91 (95% CI 1.17–3.14, P = 0.01), and co-detection of respiratory pathogens (TEM PCR/sputum culture/serology) RR 2.65 (95% CI 1.60–4.38, P = 0.0001), but none with age ≤65 RR 1.46 (95% 0.83–2.56, P = 0.18), flu type RR 1.59 (95% CI 0.85–2.98, P = 0.14), active smoking RR 1.40 (95% CI 0.79–2.47, P = 0.24) or vaccination RR 1.21 (95% CI 0.70–2.12, P = 0.48). Fatality rate was 6% with significant association with arrival from facility RR 4.56 (95% CI 1.55–13.46, P = 0.006).

Conclusion. 2017–2018 Influenza season among hospitalized patients involved more elderly and earlier in January. Sensitivity of flu swab was 36% calling for better utilization of TEM PCR in hospitalized patients. Severe flu had significant association with arrival from facility, lung disease and co-detection of respiratory pathogens. Fatality had significant association with arrival from facility. Confounders not accounted.
2521. The Potential Rise in the Incidence of Rotavirus G3P[8] in Kuwait
Widad Widad Al-Nakib, FRCPat., FIDSA1 and Wassim Chehadeh, PhD2;
1Microbiology, Faculty of Medicine, Kuwait University, Kuwait, Kuwait; 2Virology
Unit, Faculty of Medicine, Kuwait, Kuwait

Session: 255. Virology Potpourri
Saturday, October 6, 2018: 12:30 PM

**Background.** The group A rotavirus infections are associated with severe gastroenteritis in children. G1P[8] was the most prevalent genotype found in Kuwait in a study conducted between 2005 and 2006. The demographic change in Kuwait, and the recent decision to include the Rotateq vaccine in the Kuwait national immunization program, prompted us to investigate a potential change in the prevalence of rotavirus genotypes circulating in Kuwait, and to identify the VP4 and VP7 subgenomic lineages.

**Methods.** Viral RNA was isolated from the stool samples of 101 children under 5 years of age, hospitalized for severe diarrhea. Rotavirus dsRNA was detected by RT-PCR in 24.7% of children with median age of 1 year.

**Results.** The genotype G3P[8] accounted for 47% of cases, followed by G1P[8] (26%), G9P[8] (10.5%), G4P[8] (10.5%), and G9P[4] (5%). Only VP7 nucleotide sequences of rotavirus G3 or G4 type clustered in the same lineage as RotaTeq, while most VP4 nucleotide sequences of rotavirus P[8] type clustered in a different lineage than Rotarix and RotaTeq vaccines.

**Conclusion.** Our findings highlight the potential rise in the incidence of rotavirus G3P[8] in Kuwait, and invites future investigations to know whether the recent introduction of RotaTeq vaccine selects for certain genotypes and subgenomic lineages.

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