Conclusion. PEP with a combination of oral ribavirin and lopinavir/ritonavir appears to be effective and generally safe for preventing MERS-CoV infection after high-risk exposure in healthcare workers.

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

2492. Clinical, Virologic, and Immunologic Characteristics of Zika Virus Infection in a Cohort of US Patients

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Background. The clinical, virologic and immunologic characteristics of Zika virus (ZIKV) infections in US patients are poorly defined.

Methods. US patients with suspected Zika virus (ZIKV) infection were enrolled and clinical data and specimens were prospectively collected. Body fluids were tested for ZIKV RNA by PCR and blood was tested using serologic and cellular immune assays. Findings from those with confirmed ZIKV infections (cases) and ZIKV-negative controls were compared.

Results. We enrolled 45 cases and 14 controls. The most commonly reported symptoms among cases and controls were maculopapular rash (97.8% and 81.8%), fatigue (86.7% and 81.8%) and arthralgia (82.2% and 54.5%), respectively. The sensitivity and duration of detection by PCR were highest in whole blood samples (94% of 35 cases who had samples collected up to day 79 post illness onset were positive); strikingly, 84% of those were still positive at 65–79 days post illness onset (Figure 1). ZIKV neutralizing antibodies were detected in all cases and none of the controls, and titers were significantly higher in dengue virus (DENV)-experienced subjects than in DENV-naïve ones (Figure 2). Among cases, anti-ZIKV IgG antibodies were also significantly higher in DENV-experienced patients, while anti-ZIKV IgM antibodies were no higher in DENV-experienced compared with naïve ones. Using intracellular cytokine staining, the highest frequencies of T cells producing IFN-γ, IL-2 and/or TNF-α were against the NS1, NS3, and NS5 proteins for CD4+ T cells, and against the E, NS3, and NS5 proteins for CD8+ T cells (Figure 3).

Conclusion. Detection of ZIKV RNA was more frequent and much more prolonged in whole blood samples compared with other body fluids. Diagnostic molecular assays on this easily obtained fluid should be prioritized for point-of-care development. Robust cellular responses to E, NS3 and NS5 proteins could have implications for vaccine development.

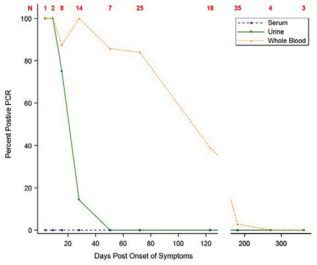

Figure 1. Percent of Zika virus infected patients with a positive PCR in whole blood, urine and serum by day post onset of symptoms. N represents the number of subjects with the specified body fluid at the specified time point.

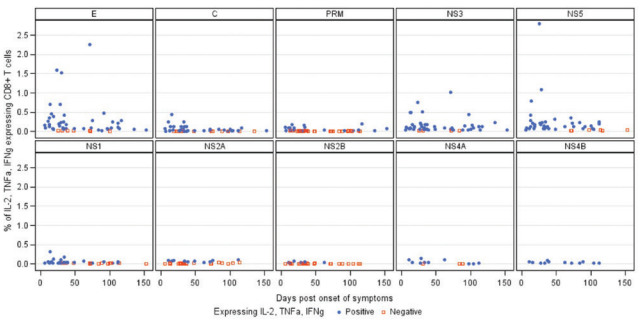

Figure 2. Percent of CD8+ T cells expressing IL-2, TNF-a and IFN-g following stimulation with the specified proteins in cases (positive) and controls (negative).

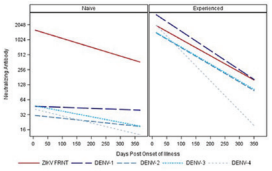

Figure 3. Neutralizing antibody titers by days post onset of illness in Dengue virus-naïve and experienced patients with confirmed Zika virus infection. FRNT=focus reduction neutralizing test.

Disclosures. **R. L. Atmar**, Takeda Vaccines, Inc.: Investigator, Research grant.

2493. Marburg Virus Disease: Virulence of Angola vs. Musoke Strain in Cynomolgus Macaques

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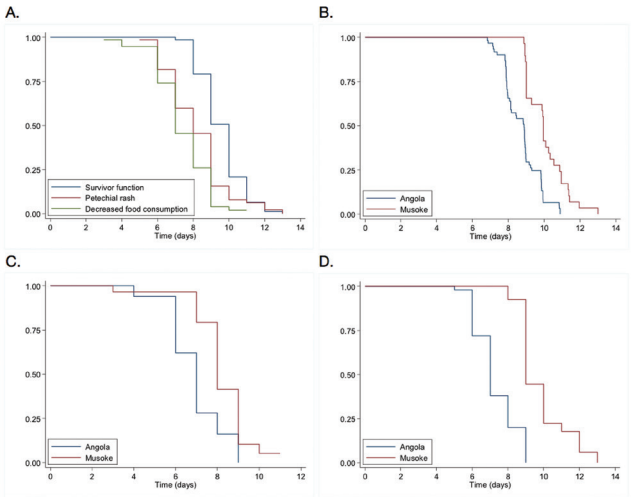
Background. From 2004 to 2005, an outbreak of Marburg virus, a filovirus, in Angola led to a case-fatality rate of 90 percent. However, little information is available regarding the virulence of the Angola strain from this outbreak compared with the virulence of other strains. Therefore, we sought to assess time to selected outcomes in non-human primates (NHPs) experimentally infected with either Angola or Musoke Marburg strains.

Methods. Between 2012 and 2017, nine therapeutic trials at the US Army Medical Research Institute of Infectious Diseases were conducted in *Macaca fascicularis* monkeys challenged with 1 to 10,000 plaque forming units of Marburg virus administered intramuscularly. The current study population was comprised of 90 control NHPs, of which, 61 were administered Angola strain in four separate trials and 29 with Musoke strain in five trials. Clinical responses including development of rash and oral intake were collected following infection. The primary outcome of interest was time to death or euthanasia post-inoculation between strains evaluated using Cox proportional hazards regression. Secondary endpoints included time to development of a petechial rash and time to decreased appetite.

Results. Following Marburg virus challenge, all NHPs died and most NHPs experienced decreased food consumption (97%), and petechial rash (96%). The median time to death for Angola-infected NHPs was 8.9 days (25th, 75th percentiles: 7.9, 9.3), whereas Musoke-infected NHPs survived for a median of 10.0 days (25th, 75th percentiles: 9.0, 10.9) (Figure 1). Irrespective of strain, petechial rash was preceded by decreased food consumption by 0.7 days (SD 1.5) on average. Angola strain was associated with statistically significant earlier death (adjusted HR = 21.8; 95% CI: 8.9, 53.2), earlier development of petechiae (adjusted HR = 17.6; 95% CI: 7.0, 44.5) and earlier loss of appetite (adjusted HR = 5.8; 95% CI: 2.9,11.7).

Conclusion. This was the first study to compare survival and clinical characteristics in NHPs between these strains. Despite sharing the similar genetic lineage, our data strongly supports increased virulence of Angola strain compared with Musoke strain. Pathophysiological mechanisms involved in increased virulence require further study.

Figure 1. Kaplan Meier survival curves in Cynomolgus macaques for A) overall time to death, petechial rash, and decreased food consumption (n=77); B) time to death by strain (n=90); C) time to decreased food consumption by strain (n=79); D) time to petechial rash by strain (n=77).



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

2494. Influenza B Hospitalizations Are Associated With Mortality in Children, FluSurv-NET, 2011–2017

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Background. Influenza B viruses (B) co-circulate with influenza A viruses (A) and contribute to influenza-associated hospitalizations each season. We used data from the Influenza Hospitalization Surveillance Network (FluSurv-NET) to determine the association between B virus hospitalizations and mortality among children.

Methods. We included data from children aged 0–17 years, residing in a FluSurv-NET catchment area, and hospitalized with laboratory-confirmed influenza during 2011–2012 through 2016–2017. We abstracted data on underlying conditions, clinical course and outcomes from medical charts. After excluding cases with unknown influenza type or with A/B coinfection, we compared characteristics of children hospitalized with A vs. B using univariate analyses and multivariable logistic regression, to determine the independent association between virus type and in-hospital mortality.

Results. Among 7671 children hospitalized with influenza, 5607 (73%) had A and 2064 (27%) had B. The proportion of B hospitalizations varied by season from 11% during 2013–2014 to 42% during 2012–2013. Among children with B, median age was 4 years (interquartile range 1–8 years), 58% were male and 36% were non-Hispanic white. In univariate analysis, children with B were more likely to be older, have cardiovascular and neurologic disease, to be vaccinated (38 vs. 32%), and to be hospitalized ≥2 days after illness onset, and were less likely to have asthma and receive antivirals (71 vs. 79%) compared with those with A ($P < 0.05$). There were no differences in the proportion with ≥1 underlying condition (59% both groups). Patients with B vs. A were no more likely to require intensive care (19 vs. 20%; p 0.34) or receive mechanical ventilation (6 vs. 5%; p 0.13); however, patients with B were more likely to die in-hospital (1 vs. 0.4%; $P < 0.01$). The unadjusted odds of in-hospital mortality for children with B vs. A was 2.3 (95% confidence interval (CI) 1.3–4.1), which remained elevated at 2.0 (95% CI 1.1–3.7) after adjusting for age, season and underlying conditions.

Conclusion. Influenza B virus infections were associated with severe outcomes among hospitalized children. Although death was uncommon, children with B had twice the odds of dying in-hospital compared with those with A virus infection.

Disclosures. **E. J. Anderson**, NovaVax: Grant Investigator, Research grant. Pfizer: Grant Investigator, Research grant. AbbVie: Consultant, Consulting fee. MedImmune: Investigator, Research support. PaxVax: Investigator, Research support. Micron: Investigator, Research support. **H. K. Talbot**, Sanofi Pasteur: Investigator, Research grant. Gilead: Investigator, Research grant. MedImmune: Investigator, Research grant. Vaxinnate: Safety Board, none. Seqirus: Safety Board, none.

2495. Real-World Burden of Transmission and Care Seeking Among Family Members With a Primary Influenza Infection

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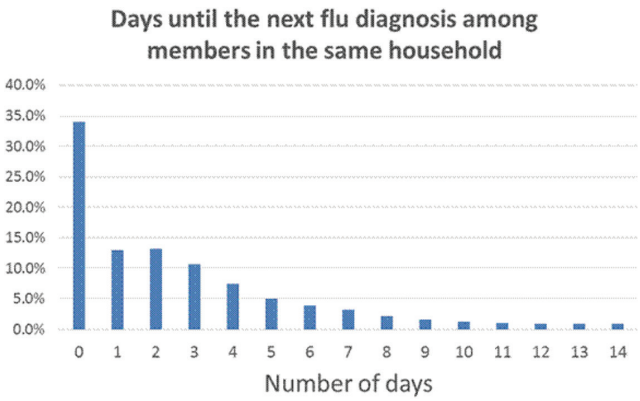
Background. Seasonal influenza is known to be a significant burden to patients and the healthcare system. Understanding how this highly contagious infection is spread, particularly among family members, is important for quantifying the burden of flu and potential impact of upcoming therapeutic agents that limit transmission. This study used real-world US claims data to understand families' medical care seeking behavior for flu infection and the relationship between family size and days families are burdened with flu within their household.

Methods. This was a retrospective analysis of US commercial claims data from the 2014–2016 flu seasons. Patients with enrolled family members and a diagnosis code for flu were identified and required to have continuous coverage during each influenza episode (defined as 14 days from the first flu case in a family).

Results. We identified 1,224,808 primary cases of flu among families of 2 or more members. The median family size was 4 members (25th, 75th percentiles = 3, 4). Of these families with at least one case of flu, 119,883 (9.8%) had additional member(s) who sought care for flu within the same flu episode. 70.8% (84,903) of these cases occurred within 3 days after the first member's claim for influenza (Figure 1).

Increased family size was associated with a higher percentage of families where flu spread to other members of the family beyond the first member diagnosed (6.4% of families of size 2 or 3 vs. 12.6% of families of size 4 or greater, $P < 0.001$). Family size was also positively correlated with the number of days between the first and last flu-related office visit within a family (Spearman coefficient = 0.09, $P < 0.001$). The majority of family members who sought care for flu were children (n = 810,867; 59.5%), followed by employees (n = 323,277; 23.7%) and their spouses (n = 228,775; 16.8%).

Conclusion. In data for the last 3 available flu seasons, we identified a significant number of secondary cases of flu among families with a primary case. Larger families had higher likelihood for subsequent flu infections and more number of days for dealing with flu. Transmission of flu between family members represents a large burden on the healthcare system and reveals an unmet need for treatment options that limit transmission.



Disclosures. **All Authors:** Roche: Employee, Salary.

2496. A Comparative Evaluation of the Burden of Disease Caused by Influenza A and Influenza B During the 2011–2012, 2012–2013, and 2013–2014 Influenza Seasons in Canada

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Background. When assessing burden of influenza disease, influenza B has typically been associated with infection in children and young adults, and is considered less prevalent and/or severe in older adults. We sought to assess the burden of influenza type A disease compared with influenza type B disease in Canadian adults admitted to hospital with laboratory-confirmed influenza.

Methods. The Serious Outcomes Surveillance (SOS) Network of the Canadian Immunization Research Network (CIRN) conducted active surveillance for laboratory-confirmed influenza in adults (≥16 years) hospitalized across Canada during the 2011–2014 influenza seasons. Eligible patients who were admitted to hospital with any acute respiratory illness or symptom had a nasopharyngeal swab collected and tested for influenza virus using reverse transcriptase polymerase chain reaction (PCR). Demographic/clinical information, as well as in-hospital outcomes were collected. Frailty Index scores were also recorded at baseline and 30-days after discharge, when possible, in patients ≥65 years. Patients with influenza A and B were compared using descriptive statistics; discrete outcomes were compared using Chi-squared (χ^2) tests; continuous outcomes were compared using student's t-tests.

Results. Overall, there were 3484 influenza A cases and 1375 influenza B cases enrolled in the SOS Network from 2011 to 2014. Mean age was significantly different between influenza A and influenza B cases (mean age of influenza A: 65.8, mean age of influenza B: 71.2, $P < 0.01$). A significantly larger proportion of influenza B patients were admitted from long-term care (A: 5.5%, B: 12.1%, $P < 0.01$). There was no significant difference with respect to length of hospitalization (influenza A: 11.1 days, influenza B: 10.27 days, $P = 0.07$) or mortality (A: 9.01%, B: 9.45%, $P = 0.63$) between influenza A and B. Patients with influenza B were significantly more frail prior to the onset of illness (A: 0.21, B: 0.22, $P < 0.01$).

Conclusion. Current attitudes consider influenza A to be the more significant virus in terms of morbidity and mortality in adults. However, influenza B is responsible for similar duration of hospitalization and similar mortality rates. In addition, influenza B predominantly affected the frail elderly and thus optimizing influenza B protection is important in this population.

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