1664. Maternal Hookworm Infection and Its Effect on Maternal/Child Health: A Systematic Review and Meta-Analysis
Tara Ness, MD, MPH1; Kathryn R. Bedard, MD2; Peter J. Hotez, MD, PhD2; Jill Weatherhead, MD, MS1; Baylor College of Medicine/Texas Children's Hospital, Houston, Texas; Baylor College of Medicine, Houston, Texas
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Background. Hookworm is an intestinal parasite that infects 500 million people, with about 80% of the global burden at risk, especially in poverty-stricken, tropical and subtropical regions. In 2005, an estimated 6.9 million pregnant women living in Sub-Saharan Africa were infected with hookworm, despite efforts for mass drug administration (MDA) being recommended. This study aimed to investigate the health impact of hookworm infection in pregnant women in order to guide public health interventions.

Methods. A systematic review and meta-analysis were conducted using Medline and PubMed for the MeSH terms, with subsequent translation to EMBASE and Cochrane Library. We performed a meta-analysis on the association between maternal hookworm and maternal anemia, as well as maternal hookworm co-infection with malaria. Other effects on maternal/child health were investigated and summarized without a meta-analysis due to the limited study numbers.

Results. Our search resulted in 471 studies for the meta-analysis, of which 23 met inclusion criteria. The prevalence of hookworm ranged from 1% to 67% in pregnant women, with prevalence ranging from 11% to 81% Pregnant women with anemia were more likely to have concurrent hookworm infection (combined odds ratio [COR] 2.21 [1.94, 2.51], P < 0.001). Additionally, pregnant woman with malaria were more likely to have hookworm infection (COR 1.71 [1.43, 2.03], P < 0.001). Our investigation also showed an association between maternal hookworm and infant anemia, maternal malaria co-infection, and other areas, such as infant cognitive outcomes. Some of the studies did show a weak correlation between hookworm infection and infants who failed one or more tests.

Conclusion. Hookworm infection in pregnant women is an important global health issue associated with significant maternal anemia and concurrent parasitic infections, such as malaria. Despite current MDA strategies in pregnant women, heavy hookworm burden, co-infection with malaria, and subsequent anemia persists. Further investigation on maternal-child outcomes of hookworm infection on maternal anemia, maternal malaria co-infection, and other areas, such as infant cognitive outcomes, will provide potential public health interventional targets to reduce morbidity.

Disclosures. All authors: No reported disclosures.

1665. The Cascade of Care for the Strong Hearts Chagas Disease Screening and Treatment Program in East Boston, Massachusetts
1666. Community Beliefs about Ebola and Implications for Disease Control in Eastern Democratic Republic of the Congo
Qasim Mian, MD, MBA1; Kasera Masumbuko Claude, MBCCh2; Michael Hawkes, MD, PhD,3 University of Alberta, Edmonton, AB, Canada; Université Catholique de Graben, Butembo, Nord-Kivu, Congo, (Congo A– Kinshasa)
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Background. The current Ebola epidemic in Eastern Democratic Republic of the Congo (DRC) has surpassed 1,300 cases and 800 deaths. Social resistance is a major barrier to control efforts, and invites an exploration of community beliefs around Ebola and its origins.

Methods. Mixed-methods study, using focus group discussions (FGDs) with key community informants and a 19-item survey questionnaire broadly sampling the outbreak zone.

Results. Between 4 to 17 August, 2018, we conducted 4 FGDs (20 participants) and 1666 community members across Eastern DRC. FGDs revealed a widespread rumor in Mangina early in the epidemic of two babies bewitched by their aunt after eating her cat, who developed bleeding symptoms and triggered the epidemic. However, this myth appeared to dissipate as the epidemic progressed and biomedical transmission became generally accepted (medical knowledge). In our survey, 66% of respondents endorsed supernatural origins of Ebola. This subgroup did not differ from other respondents in terms of knowledge of biomedical modes of transmission or resistant attitudes toward infection control measures, but was more likely to believe that traditional healers could cure Ebola. Wild animals of the forest were recognized as sources of the Ebola virus by 53% of survey respondents. Our findings suggest that skepticism and/or denial of the biomedical model, coupled with mistrust and fear of ETUs may fuel “underground” transmission of Ebola outside western-style medical facilities, as patients seek care from traditional healers, who are ill-equipped to deal with the contagious biohazard.

Conclusion. A deeper understanding of beliefs around Ebola origins may illuminate strategies to engage communities in control efforts.

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1667. Influenza A and B Co-Circulation and Burden: A 2018–2019 Influenza Season Analysis Using the National Active Surveillance Database in Mexico
Adriana Guzman Holst, MPH1; Luis Gilberto Gomez, BSc2; Maria Yolanda Cervantes Apolinar, MD2; Gloria Huerta, MD1; GSK, Panama City, Cocle, Panama; GSK, Mexico City, Distrito Federal, Mexico
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Background. Seasonal influenza is a prevalent respiratory infection for children and adults in Mexico. Influenza A and B viruses co-circulate and there is a need to better understand local epidemiology to inform vaccination recommendations (tri- vs. quadrivalent vaccines). We describe the 2018-2019 influenza season to estimate influenza burden, virus co-circulation and understand the vaccine match in Mexico.

Methods. We reviewed preliminary sentinel surveillance data for the influenza season (October 2018-May 2019) from the Mexican Health Secretariat and World Health Organization’s (WHO) Flunet databases. We performed a descriptive analysis of cases and deaths due to influenza-like illness (ILI), severe acute respiratory infections (SARI) and lab-confirmed influenza to estimate the prevalence of influenza A and B circulating strains, per state and age group and, determine B strain vaccine match.

Results. During the 2018–2019 season in Mexico, there were 52,525 reported cases of ILI/SARI with 6,997 lab-confirmed influenza cases (28% positivity rate among ILI/SARI) and 787 (11%) deaths (Figures 1 and 2). The states with 36% of cases were Mexico City, State of Mexico, Hidalgo, Tlaxcala, and Guanajuato. More than half of the Mexican states had a high (10–14.9%) to intense (25%) accumulated case positivity rate of confirmed influenza in relation to ILI/SARI cases (Figure 3). Most cases were reported among the 1–9 and 60–69-year-old groups. 45% of deaths occurred in State of Mexico, Hidalgo, Mexico City, Puebla, and Guanajuato. The seasonal profile was dominated by A/H1N1 (68%), followed by B (16%) and A/H3N2 (12%), with 90%