Results. Participants’ median age was 23 (interquartile range [IQR] 20–28). Most women reported no or <7 years of education (84.1%), were farmers (61.3%), and were WHO stage 1 (81.9%). They had a median PHQ-9 score of 3 (IQR 0–5) and 47 (43.6%) had moderately severe or severe depressive symptoms, with 19.6% missing PHQ-9 scores. Among 867 pregnant partners with PHQ-9s, demographic and clinical covariates were not meaningful predictors of PHQ-9 score. Male partner’s PHQ-9 score, however, was associated with (covariate-adjusted Spearman’s $r$ 0.58, 95% Confidence Interval [CI]: 0.51-0.65) and strongly predictive of a pregnant partner’s score (Figure). An increase in a male partner’s PHQ-9 score from 9 to 10 was associated with a 4.7 times increased odds (95% CI 1.37-1.58) of a ≥2 point increase in a woman’s PHQ-9 score.

Figure: Female Partner’s Depressive Symptoms

Conclusion. Depressive symptoms are highly correlated among pregnant people and their partners, which may have implications for pregnancy care. Interventions aimed to reduce depressive symptoms and improve HIV-related outcomes during pregnancy may have greater success when focused on addressing both partners’ depressive symptoms.

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728. Genomic Characterization of Burkholderia pseudomallei Isolates in Colombia
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Results.

Background. Melioidosis is a serious infection caused by Burkholderia pseudomallei (Bps), an opportunistic organism, highly adaptable and with a wide array of intrinsic virulence factors and antimicrobial resistance determinants. Bps is underdiagnosed due to its slow growth on routine laboratory media and the lack of robust diagnostic infrastructure in rural areas of low/middle income countries. Recent data indicates that Bps infections are increasing in Colombia (COL). However, the understanding of the genomic epidemiology and population structure of the emerging Bps isolates in COL is unknown. Here we characterize the genomic features of Bps isolates from infected patients in COL.

Methods. We identified 13 Bps clinical isolates recovered in 5 Colombian cities between 2018 and 2020. We performed WGS and phylogenomic analyses using Bayesian methods. For comparisons, we included 82 publicly available genomes from Bps recovered worldwide (including 10 additional isolates from COL). Additionally, we characterized the resistome, virulome and MLST of all isolates.

Results. 12 out of the 13 isolates were confirmed as Bps and 1 belonged to the B. cepacia complex. The Bps population structure was divided in two main clades: clade 1 with isolates from Asia and Australia, and clade 2 with isolates from Africa, America, and the Caribbean (Figure 1). We found two groups of Colombian isolates, the first was related to ST518 and the second, highly diverse including 11 different STs (1742, 1748, 92, among others). Genomic characterization showed the presence of β-lactamases PenA (n=11) and OXA-57 (n=1). We also identified a TSP44A substitution in PBP3 (n=11). All genomes contained virulence determinants of motility (BimA), invasion (Flagella), signaling (CdpA) and adherence (Type IV pil). Type III and VI secretion systems, were also found in all isolates resembling Bps from other parts of the world.

Figure 1. Maximum clade credibility tree of 82 genomes of Bps. The inner ring shows the ST for each genome, while the outer ring shows the geographical region associated with any available data.

Conclusion. Bps is an emerging pathogen in COL and its population structure seems highly diverse, predominantly of the American lineage and absence of Australasians strains. A high prevalence (~90%) of resistance determinants, particularly related to β-lactams, suggest that active surveillance of these emergent pathogens is needed in countries like COL.

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729. Lassa Fever Associated Hearing Loss
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Background. Hearing loss (HL) is the second leading cause of disability affecting approximately 19% of the world’s population. Despite well known social, economic, and neurologic consequences this condition receives little attention. Lassa Fever (LF) was noted to be associated with HL shortly after its discovery in the 1970s. However, the true burden of this sequelae is likely underestimated due to a lack of standardized measurement and reporting.

Methods. We performed a cross-sectional study of LF survivors and household controls in Kenema, Sierra Leone. Upon recruitment, survivors and controls were screened for HL by determining Pure Tone Averages (PTA) of air conduction thresholds using an AMBCO audiometer, according to WHO standards. Individuals found to have elevated PTAs were referred to confirmatory testing measuring both air and bone thresholds using a SHOBOX audiometer to differentiate sensorineural and conductive HL. All subjects completed symptom questionnaires and physical exams to understand the full spectrum of viral sequelae.

Results. 94 LF survivors and 281 controls were recruited. The average age of LF survivors was higher than controls (32.9 vs 28.7, p=0.008). Of these 94 LF survivors, 40 (43%) were found to have HL in comparison to 40 (14%) of controls (p<0.001). Lassa fever survivors were also found to have significantly worse HL with 16 (40%) found to have profound HL compared to only 2 (5%) of controls (p=0.001). Logistic regression of this cohort found that LF infection (OR = 1.30, p<0.001), any inner or middle ear symptoms (OR = 1.20, p=0.041), or pharyngeal symptoms (OR = 1.23, p=0.012) were significant risk factors of developing HL (p< 0.05). Animal model studies suggested that LF infection may result in the development of an ANCA