**610. Barriers and Facilitators to Uptake of Male Partner Attendance for HIV VCT During Prenatal Care in Brazil**

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***Background.*** Male partner involvement in sub-Saharan Africa has been investigated and shown to improve outcomes for the entire family. However, little research is available in other regions. In Porto Alegre, Brazil, partners of pregnant women are encouraged to attend prenatal care for HIV voluntary counseling and testing (VCT) to decrease acute HIV serconversion during pregnancy. Uptake of this intervention has been sub-optimal.

***Methods.*** From November 2016 to July 2017, 202 men who attended prenatal care at Hospital Conceicao and 201 men who did not attend prenatal care were interviewed using computer-assisted telephone interviews regarding individual, relationship and system-wide facilitators and barriers to attending prenatal care. Multivariate regression was performed to identify factors associated with male involvement in prenatal care.

***Results.*** Of 403 men interviewed, 91% stated they had been invited to prenatal care, 94% of men stated they would accept HIV testing if offered, but only 50% attended. Men identified making their partner happy as the most important facilitator for prenatal care attendance, and having to miss work as the most significant barrier. Frequency of commonly identified barriers and facilities are indicated by Figure 1. Individual factors that predicted prenatal care attendance included over-estimating the risk of mother-to-child transmission (AOR 2.1 95% CI 1.3–3.3), and endorsing that HIV-infected individuals can live satisfying lives (AOR 7.8, 95% CI 2.1–50.8). Partnership factors associated with attendance included being invited by partner (AOR 5.6, 95% CI 2.4–15.6), whereas admitting jealous behavior was negatively associated with attendance (AOR 0.82 95% CI 0.7–0.97). Systemic factors negatively associated with prenatal care attendance included a history of not affording medical care (AOR 0.28, 95% CI 0.15–0.55) and identifying work as a barrier (AOR 0.19 95% CI 0.11–0.31).

***Conclusion.*** Involvement of male partners during pregnancy may be enhanced by providing free care during flexible hours. Partners should be actively invited to prenatal care as once involved, almost all would accept HIV VCT and other interventions to protect partners and infants from HIV and other sexually transmitted diseases during this vulnerable period.

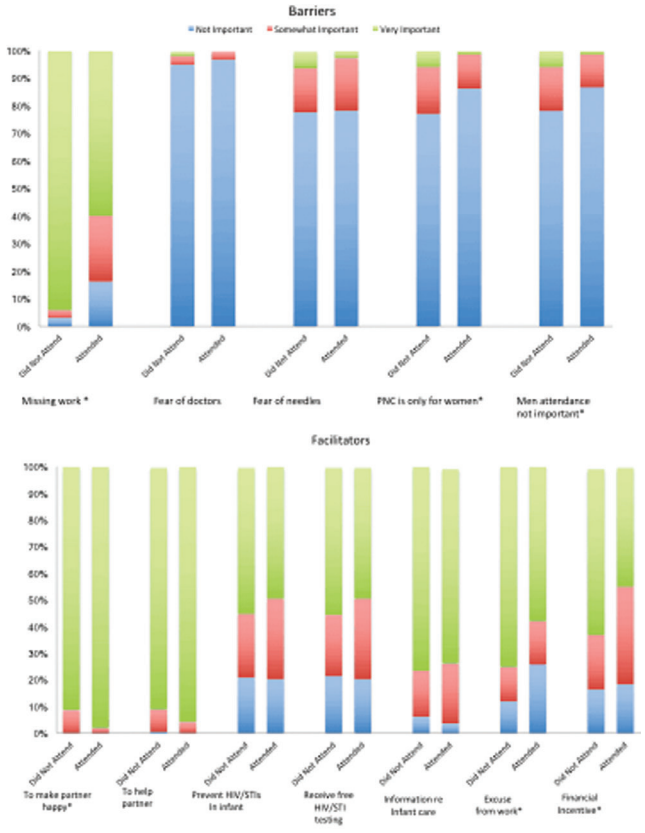


Figure 1: Barriers (top) and Facilitators (bottom) identified as very important (green), somewhat important (red) and not important (blue) to male involvement in prenatal care.
* Denotes significant differences in responses between those who did and did not attend prenatal care , PNC (prenatal care), STI (sexually transmitted disease)

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

**611. Placental Pathology and Neonatal Outcomes in Pregnancies of Perinatally vs. Nonperinatally HIV-Infected Women**

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***Background.*** Perinatally HIV-infected (PHIV) women are reaching childbearing age, but little is known about the impact of long-term exposure to HIV and antiretroviral therapy on pregnancy outcomes of PHIV women, including the impact on neonatal health and placental pathology.

***Methods.*** We performed a retrospective cohort analysis over a 10-year period (2007–2017) of PHIV women, matched by age and date of delivery in 1:2 ratio, to behaviorally HIV-infected women (BHIV). The primary maternal outcome variable included virologic suppression (viral load ≤ 400 copies/mL) at delivery. Secondary outcome variables included hospital length of stay (LOS), mode of delivery, infectious (chorioamnionitis, funisitis) and vascular (vasculitis) placental complications based on histopathological analysis of placental specimen (composite variable). The primary neonatal outcome was preterm birth (<37 weeks); secondary neonatal outcomes included APGAR scores and infant HIV status. Primary and secondary maternal and neonatal outcomes were compared between PHIV and BHIV women. Logistic regression models measured the association between primary maternal and neonatal outcomes and perinatal status, adjusting for age and race.

***Results.*** A total of 60 deliveries were evaluated during the study period (20 from women with PHIV and 40 from BHIV). Women with PHIV were significantly younger (20 vs. 29, $P < 0.05$) and less likely to be suppressed at delivery (55% vs. 90%, $P < 0.05$) compared with women with BHIV. A total of 19 women experienced placental pathologies but no differences were found by perinatal status (31% vs. 36%, $P = 0.7$, among PHIV and BHIV, respectively). Other than viral suppression, there were no significant differences among maternal and neonatal outcomes of interest by mode of HIV acquisition. In the multivariable regression, women with PHIV were significantly less likely to be suppressed after adjusting for age and race (AOR 0.07, 95% CI 0.01–0.80). There was no significant difference for preterm birth.

***Conclusion.*** Women with PHIV were significantly less likely to be suppressed at delivery but did not experience other complications at birth. Neonatal outcomes were similar among women with PHIV and BHIV.

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

**612. Increase in Perinatal HIV Infection in North Florida: Missed Opportunities to Prevent Maternal-to-Child Transmission in Rural Areas**

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***Background.*** The rate of mother-to-child transmission of human immunodeficiency virus (HIV) in the United States has significantly declined due to routine opt-out HIV testing of pregnant women and implementation of effective prenatal, intrapartum and postnatal interventions. This includes first trimester HIV testing and retesting in the third trimester in areas with high HIV prevalence or in high-risk social situations. The University of Florida Pediatric Infectious Disease division serves a 31 county area for pediatric HIV care that includes Gainesville, Tallahassee and the entire Florida panhandle encompassing mostly rural counties. There are two HIV perinatal coordinators for pregnant women serving 19 of the counties.

***Methods.*** HIV-positive mother–infant pair chart review 2008–2018.

***Results.*** Between 2008 and 2012 there was one HIV-infected infant in the entire catchment area. From 2013 to 2017, there were 10 HIV-infected infants and two thus far in 2018. Statewide from 2013 to 2017 there were 41 HIV-infected infants. In the past 2 years, the North Florida region had 31% of the total number of HIV-infected infants. Eight of 12 mothers transmitting infection were known to be HIV infected and were prescribed antiretroviral (ARV) therapy with noncompliance documented in all 8. Two were teenagers; four received no prenatal care and insurance problems were reported in 3 as reasons for ARV noncompliance. Mental illness and/or substance abuse was documented in 6. Three were presumed infected during the third trimester—two tested negative in the first trimester, one was retested early in the third trimester and one was tested only at delivery due to lack of prenatal care.

***Conclusion.*** Improved access to prenatal case management and access to mental health and substance abuse services are seriously needed in rural areas. Improving pregnancy compliance with ARV therapy is crucial in preventing vertical transmission. The number of perinatal coordinators needs to be significantly increased to support compliance and provides services. HIV testing in the first and third trimesters should become routine and testing of all (but especially high-risk women such as teenagers and those with mental illness or substance abuse) should be strongly considered at the time of delivery.

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

**613. Transmission of Influenza Virus in Mother and Infant Transmission Events in Nepal**

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***Background.*** Influenza immunization of pregnant women provides protection of the infant against influenza disease. A potential mechanism of protection is prevention of maternal illness that may result in secondary transmission to infants. We aim to characterize influenza transmission in mother–infant pairs.

***Methods.*** Pregnant mothers were enrolled in a randomized controlled trial of influenza immunization in rural Nepal from April 2011 to April 2013. Mothers and infants were surveyed weekly until 180 days post-partum for respiratory illness and mid-nasal swabs were collected at time of illness and tested for influenza virus by reverse-transcriptase polymerase chain reaction (RT-PCR). We defined a transmission episode as a mother–infant pair with an influenza-positive illness within 14 days of each other. Influenza viruses were strain-typed by RT-PCR and/or mass spectrometry.

***Results.*** Seventeen mother–infant transmission episodes occurred with maternal illness preceding infant illness in 12 (70.6%). Of transmission pairs, 12 (70.6%) were influenza B, three (17.6%) H3N2 influenza A, one (5.9%) H1N1 influenza A, and one (5.9%) unspecified influenza A. Five (29.4%) mothers received the influenza vaccine. Successful strain-typing with RT-PCR/mass spectrometry of 11 pairs revealed that 10 (90.9%) were synonymous strains. Figure 1 shows the start of respiratory symptoms and virus type associated with influenza illness in the 17 mother–infant pairs.

***Conclusion.*** Mothers are an important source of infant influenza infection. Transmission was confirmed with nearly all paired transmissions demonstrating a similar strain. The majority of transmission events occurred in nonvaccinated mother–infant pairs.

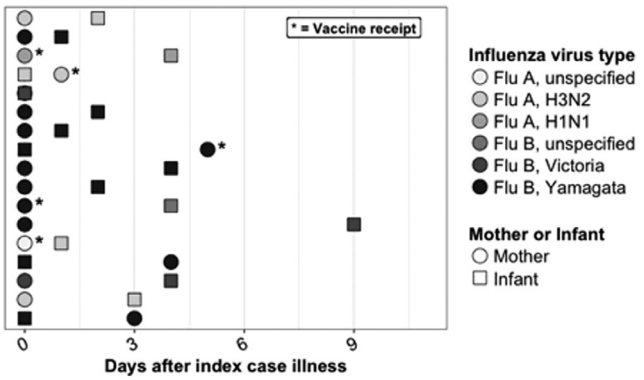


**Figure 1:** Influenza transmission events in mother–infant pairs. Symbols represent first day of respiratory symptoms associated with influenza-positive illness.

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**614. Modeling Changes in Gastrointestinal and Respiratory Tract Bacterial Community Diversity Attributable to Common Antibiotic Exposures During Long-Term Acute Care**

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***Background.*** Reduced gastrointestinal tract bacterial community diversity has been associated with increased risk for healthcare-associated infections, including *Clostridium difficile* infection. We sought to develop a model for concomitant change in bacterial community diversity at gastrointestinal and respiratory tract sites, drawing upon a recently completed cohort study of 92 subjects recruited from a long-term acute care hospital (LTACH) for dense longitudinal oral, endotracheal aspirate (ET), and stool specimen collection.

***Methods.*** We evaluated the first 30 subjects enrolled from the LTACH cohort, for whom complete antibiotic administration data and 16S rRNA gene (V1–V2 amplicon) sequencing data were available. Sequencing was performed via the Illumina HiSeq platform; operational taxonomic units (OTUs) were formed and taxonomy assigned (GreenGenes 13.8) via the QIIME 1.9.1 pipeline. Generalized linear mixed effects models were fit using R (3.5.0), Stan (2.1.7), via the "rstan" and "rethinking" packages.

***Results.*** We evaluated 472 subject-days of study enrollment across the 30 subjects (median 15 days/subject). ET specimens were available for all subject-days; oral and stool for 357 and 177 subject-days, respectively. We modeled daily change in Shannon diversity across oral, ET, and stool specimens, parameterized with daily exposure to cefepime, piperacillin–tazobactam, meropenem, IV vancomycin, and oral vancomycin. All parameters fit with Rhat value lower than 1.1. Absent antibiotic exposure on the previous day, the daily change in Shannon diversity at all sites was near zero. The largest observed effect was oral vancomycin on stool (daily delta Shannon: −0.6, 95% CI: −1.38 to 0.09). All estimated effects for intravenous antibiotics on the stool, and for all antibiotics at other sites were smaller.

***Conclusion.*** Small daily changes in bacterial community diversity were attributable to individual antibiotics, but all 95% certainty intervals crossed zero in this pilot study. Further work will focus on modeling specific taxonomic changes attributable to individual antibiotics and antibiotic interactions.

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

**615. Can We Restore the Lung Microbiome with Fecal Microbiota Transplant (FMT)?**

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***Background.*** Unabated use of antibiotics for human diseases, in livestock and aquaculture has resulted in natural selection of multi-drug-resistant organisms (MDROs). The emergence of pan-resistant strains of *Pseudomonas* spp. pose a major threat to patients appropriately exposed to antibiotics (e.g., cystic fibrosis, lung transplant recipients). This organism evades antibiotics by a combination of efflux pumps, harboring multiple-resistant genes and acquiring low permeability of the outer membrane. Altering the gut microbiome could potentially modify the lung microbiome of patients colonized or infected with MDROs.

***Methods.*** A 17-year-old patient with CF developed recurrent exacerbations with an extreme drug-resistant *Pseudomonas aeruginosa*; due to the lack of effective antibiotics to treat her while awaiting a decision to proceed with lung transplantation, sputum cultures were collected as part of clinical care. We modeled patient-derived isolate of predominantly MDR *Pseudomonas* in C57Bl6/j mice, where we engrafted the isolate into humanized murine lungs and studied host cytokine responses and microbial composition of the gut and lungs to the engraftment.

***Results.*** Our data shows that there is a dominant IL6- and IL17-mediated immune response to the engraftment, accompanied by measurable changes to the lung and gut microbiota. We also show that some of these changes can be reversed by fecal microbial transplant (FMT) of 'normal' microbiota into the gut and lungs.

***Conclusion.*** This murine model results suggest a potential role and effectiveness of gut FMT as a therapeutic measure for MDR bacterial infection in the lungs. Further studies are required to assess response in humans.

***Disclosures.*** **L. M. Abbo**, Roche Diagnostics: Scientific Advisor, Consulting fee.

**616. Vancomycin Is Frequently Administered to Hematopoietic Cell Transplant Recipients Without a Provider Documented Indication and Correlates with Microbiome Disruption and Adverse Events**

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***Background.*** The gut microbiome of hematopoietic cell transplant (HCT) recipients correlates with the risk of acute graft- vs.-host disease (aGVHD). IV vancomycin is the most commonly used nonprophylactic antibiotic in HCT recipients at our center. We evaluated indications for vancomycin use and impact of vancomycin exposure on the microbiome.

***Methods.*** Antibiotic exposures and provider-documented indications for vancomycin use were assessed through chart review. We assessed adherence to guideline-based recommendations for vancomycin use for courses during neutropenic fever. Weekly stool samples collected from HCT patients before and up to 100 days post-transplant in a previously described cohort had bacterial composition determined from 16S rRNA amplicons analyzed with a phylogeny classifier and was correlated with vancomycin exposure using mixed effects modeling to correct for overlapping and repeated antibiotic exposures.