acetylcysteine. *Staphylococcus aureus* isolates exhibited 7.9% of resistance to oxacillin/cefotaxin disc (MRSA), while remaining isolates were susceptible. *Streptococcus pneumoniae* isolates showed 33% of resistance to penicillin. Other important isolated bacteria were *Escherichia coli* (n=14; 6.3%), and none of the isolates was an extended spectrum beta lactamase (ESBL) producer, in contrast to 10% in *Klebsiella pneumoniae* isolates (n=10; 4.5%). *All Pseudomonas aeruginosa* isolates (n=6; 2.7%) were susceptible to ceftazidime. Acute gastroenteritis (80.0%) was the main presentation of NTS bacteraemia, while skin and soft tissue infections with lower respiratory tract infections (31.6%) were common in bacteraemia caused by *Staphylococcus aureus*. *Streptococcus pneumoniae* bacteraemia presented mainly as pneumonia (60.8%).

**Conclusion:** Hence, NTS was the most common aetiological agent isolated in bacteraemia and mainly manifested as acute gastroenteritis.

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**Five-year review of non-typhoidal salmonella meningitis in Cape Town, 2010 - 2015**

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**Background:** *Salmonella* species are gram negative bacilli with over 2600 serotypes and a worldwide distribution. Non-typhoidal *Salmonella* (NTS) typically causes self-limiting gastroenteritis, but may become invasive. In sub-Saharan Africa invasive NTS disease is associated with a high mortality, associated with malnutrition, malaria and human immunodeficiency virus (HIV) co-infection. Meningitis due to NTS is a rare complication, with mortality rates over 40% in children. We report three cases of NTS meningitis in paediatric patients in Cape Town (Note: two more cases have been identified).

**Methods & Materials:** A five-year review of NTS cultured from cerebrospinal fluid (CSF) at the Division of Medical Microbiology, Groote Schuur Hospital was performed. This is a tertiary academic microbiology laboratory. The National Health Laboratory Service (NHLS) laboratory information system was searched from 1 July 2010 to 30 June 2015. Retrospective clinical reviews were conducted for these cases including patient history, clinical features, risk factors, treatment and outcomes.

**Results:** From all CSF cultures sent to GSH Microbiology laboratory (n=41865), three cases of NTS meningitis were identified. All three *Salmonella* meningitis cases were in infants less than one year old. One infant was Zimbabwean with a travel history. All cases were HIV-uninfected: one child was HIV exposed. NTS was isolated from both CSF and blood culture in 2 cases, no blood culture was done on the third. *Salmonella enterica* serotype Enteritidis (Salmononella Enteritidis) was cultured from two cases and *Salmonella* Heidelberg from the third. All isolates were susceptible to all antimicrobials tested. One patient died within 72 hours of admission; the remaining two developed neurological complications, including hydrocephalus, hemiplegia and cerebral infarcts.

**Conclusion:** NTS meningitis should be considered in infants if gram negative bacilli are observed in CSF. The prevalence of NTS meningitis in South Africa appears to be low. A third-generation cephalosporin (Ceftriaxone/Cefotaxime) remains the empiric treatment for meningitis. The duration of treatment for gram negative meningitis is usually 21 days. For NTS meningitis at least 4 weeks of therapy may be indicated to prevent relapses. In view of the poor prognosis and high risk of relapse the use of combination therapy with a cephalosporin and fluoroquinolone, which has enhanced intracellular activity, may be required.

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**Increased isolation of Enterococcus faecium from neonates with sepsis: An attempt to investigate the suspected outbreak**

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**Background:** Neonatal sepsis accounts for 30-50% of total neonatal deaths in developing countries and there are several reported nosocomial outbreaks of neonatal sepsis. We have noted an increase in the isolation of *Enterococcus faecium* from blood of neonates admitted in intensive care unit with sepsis. In the present study we report the clinical, microbiological profile and an attempt to investigate the suspected outbreak by *E. faecium*.

**Methods & Materials:** Neonates admitted in intensive care units with sepsis in the month of March 2009 were included. Blood cultures collected in Trypticase soy broth and sent to the laboratory were processed conventionally. Identification and antibiotic susceptibility of the isolates were performed by conventional methods and Vitek-2. Case sheets were reviewed for clinical features. *E. faecium* isolates were subjected to 16S rRNA gene sequencing with fluorescence-labeled dideoxynucleotide terminators using an ABI 3130 XL automated sequencer. The sequences were analysed and identified using the Megablast search program of the GenBank database. The relatedness of sequences of the isolates was studied for any outbreak.
**Results:** Blood cultures from 40 neonates received during the study period. Blood cultures from 18/40 neonates showed bacterial growth. Nine of 18 (50%) neonates showed the growth of *E. faecium*. All the *E. faecium* isolates were susceptible to Vancomycin and Linezolid. Susceptibility to other antibiotics :uniformly susceptible to Quinupristin/Dalfopristin and Chloramphenicol. Resistant to macrolides,fluoroquinolones, Gentamicin(high-level).

Sequences of seven of the nine isolates were deposited in GenBank (GenBank accession numbers HM222631 to HM222637). The sequence of the each isolate was different from the other. The neonates were either preterm or low birth weight. Babies presented with respiratory distress(6/9), with seizures (2/9) and refusal to feed (1/9).

**Conclusion:** Among the neonates from whom *Enterococcus faecium* was isolated in blood, no specific clinical feature could be noticed. The isolates were found to be different from each other in our attempt to establish the relatedness of the strains.

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Room: Hall 3 (Posters & Exhibition)

**Vaginal colonization by microbes during early pregnancy and their association with adverse pregnancy outcomes**

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**Background:** Role of maternal intrauterine infections/inflammation (IUI) in the causation of adverse pregnancy outcomes (APOs) such as preterm birth (PTB), low birth weight (LBW) and preterm premature rupture of membranes (pPROM) is well acknowledged. In many instances, ascent of colonizing microbes from lower genital tract (LGT) during pregnancy and more importantly their influence on the pregnancy outcomes.

**Methods & Materials:** A hospital based cohort study was undertaken comprising of 790 pregnant women with in the age of 18-35 years and gestational age of 8-24 weeks at a secondary care hospital in south India. Upon recruitment, high- vaginal (HV) and endocervical swabs (EC) from all study participants were collected. All HV swabs were subjected to microbiological culture techniques. PCR based detection of genital mycoplasmas and *C.trachomatis* DNA was performed from HV and EC swabs respectively. Data was analysed using SPSS software. Detection rates of individual bacteria and in combinations was analysed using descriptive statistic tools and 2x2 tables. Association of microbes with APOs was estimated using chi square test and univariate analysis

**Results:** Majoriy (43%) of the study participants were within 12-16 weeks of gestation at the time of sampling. Vaginal colonization of *Candida* spp (15.7%) followed by anaerobic GNB (98, 12.4%) and *Trichomonas vaginalis* (94, 11.9%) were predominately observed among the study participants. Presence of any one of the genital mycoplasmas was observed among 9% of the women. None of the study subjects were positive for *C.trachomatis*. PTB, LBW and pPROM was observed among 7, 11.4 and 1.4% women respectively. Colonization of *G.vaginalis*, anaerobic GNB and *M.hominis* were significant risk factors for PTB, while anaerobic GNB and *M.hominis* were for LBW and presence of *T.vaginalis* and *U.urealyticum* were significant risk factors for pPROM in the study population.

**Conclusion:** Our study findings underscore the need for routine microbiological screening of pregnant women for LGTIs and vaginal dysbiosis during early pregnancy.

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**Is the QuantiFERON-TB Gold test (QFT) better than the Tuberculin Skin Test (TST) in diagnosing active and latent tuberculosis in BCG-vaccinated children?**

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**Background:** Interferon-gamma release assays like the QuantiFERON-TB Gold test(QFT) have advantages in diagnosing tuberculosis(TB) over the Tuberculin Skin Test(TST) that gives false-positive results in BCG-vaccinated children due to common antigens in BCG and tuberculosis. This study was done to compare the QFT and TST in the diagnosis of active and latent TB in predominantly BCG-vaccinated children.

**Methods & Materials:** Retrospective cohort study of children aged 1 to 15 years evaluated for tuberculosis with TST and QFT testing in the Department of Pediatrics, Christian Medical College, Vellore from January 2007 to December 2010. The Department of Clinical Microbiology’s QFT database was accessed and records of study-eligible children reviewed for demographic data, TST results and final diagnosis.

**Results:** 175 children underwent both TST and QFT testing, of whom 173 (99%) were BCG-vaccinated. 30 children were diagnosed with tuberculosis based on WHO criteria. TST was positive >10 mm in 43 while QFT was positive in 27 children. TST and QFT concordance in 168 evaluable children was 83.2% in culture-confirmed TB and 87.1% in those with negative AFB cultures; 78% in 27 children with clinical TB (kappa 0.526) and 85% in 141 without tuberculosis. Sensitivity of TST and QFT in culture-confirmed TB was 66.7% and 71% respectively, with specificity of 84.2% and 79% and negative predictive value of 97.8% for both. Sensitivity of TST and QFT in clinical TB was 48.8% and 55.6% respectively with specificity of