urinary tract infection, a localization study should be performed.

Pathogens usually recognized as causing a chronic prostate infection are the same as the traditional uropathogens (TP), mainly *E. coli*, other *Enterobacteriaceae*, *Pseudomonas aeruginosa*, and enterococci. But also non traditional pathogens (NTP) including Gram-positive bacteria, such as staphylococci and streptococci, and also ureaplasmas, mycoplasmas and especially *Chlamydia trachomatis* (Skerk 2008). A gonococcal prostatitis may be fairly rare and can be acute and chronic.

The fluoroquinolones are recommended as drugs of choice in chronic infection of the prostate, if the pathogens are susceptible, because of their favourable prostate pharmacokinetics, which are however different between the analogues. Clinical studies with levofloxacin have shown, that our conventional dosage regimens may have to be reconsidered in favour of higher dosages and probably shorter treatment durations. In case of STI in addition macrolides and tetracyclines may be included into the therapeutic armamentarium.

In chronic pelvic pain syndrome (CPPS) where infection cannot be found, phenotyping of the symptoms and a multimodal therapy may be considered since such a complex syndrome may have several underlying pathologies.

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Type: Invited Presentation

Final Abstract Number: 40.003
Session: Sexually Transmitted Infections: Global Challenges
Date: Saturday, March 5, 2016
Time: 15:45-17:45
Room: G.01-03

Global challenges of implementing human papillomavirus vaccines

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Abstract: Every year cervical cancer affects around 528000 women and causes 266000 deaths worldwide with 80% of deaths occurring in less developed countries with a concomitant 18-fold difference in mortality occurring between developed and developing countries. Cervical cancers is caused by the Human Papilloma Virus (HPV) with the oncogenic types 16 and 18 accounting for 70% of invasive disease. Other cancers associated with HPV infection include vaginal, vulvar, penile, oropharyngeal and anal cancers. In addition, HPV types 6 and 11 cause anogenital warts and recurrent respiratory papillomatosis. In 2009, the World Health Organisation issued the first position paper on HPV vaccines, revised in 2014, in which it supported HPV vaccine introduction into national immunization programmes where: 'i) prevention of cervical cancer and/or other HPV-related disease is a public health priority ii) the introduction is programmatically feasible and economically sustainable, and where iii) cost-effectiveness aspects have been duly considered. They recommended that the primary target population should be girls aged 9-13 years but that HPV vaccination of males is not recommended as a priority, especially in resource-constrained settings, as the available evidence indicates that the first priority should be for cervical cancer reduction by timely vaccination of young females and high coverage with each dose. In 2014 the

In 2011 the Global Alliance on Vaccines and immunisation (GAVI), tasked with supporting the introduction of new vaccines into the world's poorest countries, approved support of HPV vaccines introduction into GAVI eligible countries with the low negotiated price of US$ 4.50 per dose compared to US$ 100 in high-income countries. By 2015 GAVI plans to support the immunisation of approximately one million girls with HPV vaccines and by 2015 more than 30 million girls in less developed countries.

This presentation will explore the reach, successes and epidemiological impact of HPV vaccine introduction worldwide and will consider some of the challenges such as the introduction of school immunisation programmes, the immunisation of boys, and the controversy around HPV vaccine introduction in India.

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Type: Invited Presentation

Final Abstract Number: 40.004
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Room: G.01-03

Prospects of untreatable gonorrhea and ways forward

T. Tbd

Abstract: (no abstract received from presenter)

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Type: Poster Presentation

Final Abstract Number: 41.001
Session: Poster Session I
Date: Thursday, March 3, 2016
Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

Antimicrobial resistance, phylogenetic distribution and molecular docking of integrons in multidrug resistant diarrheagenic E.coli isolates from children under five in Delhi, India.

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Background: Integrons are versatile gene acquisition systems commonly found in bacterial genomes. They are ancient elements that are a hot spot for genomic complexity, generating phenotypic diversity and shaping adaptive responses. Mobile gene cassettes captured within integron arrays encompass a vast and diverse pool of genetic novelty. These elements are able to capture and express gene cassettes encoding antibiotic resistance. The main aim of this study was to investigate the distribution of integrons in multidrug resistant diarrheagenic *E.coli* isolates, to analyze the possible relationship between the antimicrobial resistances profiles,

phylogenetic grouping with presence of integrons and to perform molecular docking of integron proteins.

Methods & Materials: 80 diarrheagenic *E.coli* strains were isolated from children with diarrhea and processed by known conventional methods. All isolates were tested for antimicrobial susceptibility using CLSI guidelines followed by identification of their phylogroups by Clermont et al, 2013 method after extraction of genomic DNA. Presence of class 1, 2 and 3 integrons was seen by Real Time PCR. Docking was performed using various softwares like Marvin sketch, viewerlite, pymol, pardock. Statistical analysis was used for the comparison of the categorical data

Results: Class 1 integron was identified in 58.75% isolates while 18.75% isolates harbored class 2 integron and no class 3 integrons were detected in any of the isolate. 11.25% isolates showed co existence of class 1 and class 2 integrons. Integrons were significantly associated with resistance to certain antibiotics, including; Cefotaxime (P = 0.01), Ceftazidime (P=0.006), Azetronam (P=0.046), Nalidixic acid (P=0.01), Gentamycin (P=0.001), Amikacin (P=0.01) and Piperacillin+tazobactam (P=0.037). Docking of integron protein was performed with Cefotaxime and Ciprofloxacin.

Conclusion: Our study demonstrates the importance of integrons for the occurrence and transmission of multidrug resistance. Identical predominant class 1 and 2 integrons in *E.coli* servers' indicate horizontal transfer. This study emphasizes the alarming role of integrons in antibiotic resistance within diarrheagenic *E. coli* strains. Modeling and docking studies may provide useful insights for developing new antibiotic drugs to minimize multidrug resistance.

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Type: Poster Presentation

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Date: Thursday, March 3, 2016
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Room: Hall 3 (Posters & Exhibition)

Correlation of β-lactam resistance with over expression of efflux pumps among neonatal septicaemic isolates of Acinetobacter baumannii from India

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Background: The emergence of multidrug-resistant *Acinetobacter baumannii* has created severe challenges for neonates hospitalized in NICU. *A. baumannii* strains have the propensity for developing antimicrobial resistances extremely rapidly. Neonatal sepsis is a common diseases caused by *A. baumannii* in a developing country like India. Emergence of β-lactam resistance makes the scenario more critical for neonates for whom treatment options are limited. Now-a-days efflux pumps are getting importance because of their wide substrate profile. Although their presence were scarcely reported but often work in concert to produce high antibiotic resistance. Our aim was to assess the role of efflux pumps in β-lactam resistance among neonatal septicaemic *A. baumannii* isolates.

Methods & Materials: MIC values of carbapenems (meropenem, imipenem) and cephalosporins (cefotaxime, ceftazidime) for neonatal septicaemic *A. baumannii* isolates were determined using broth dilution method with and without efflux pump inhibitor PAβN. Efflux pump genes of RND families (AdeABC, AdeIJK, AbeXYZ), and SMR family (AbeS) were confirmed by PCR followed by sequencing. Over expression of the genes was carried out by real time PCR. The regulatory components (*adeR* and *adeS*) of AdeABC pump was investigated for the isolates, over expressing *adeB* gene.

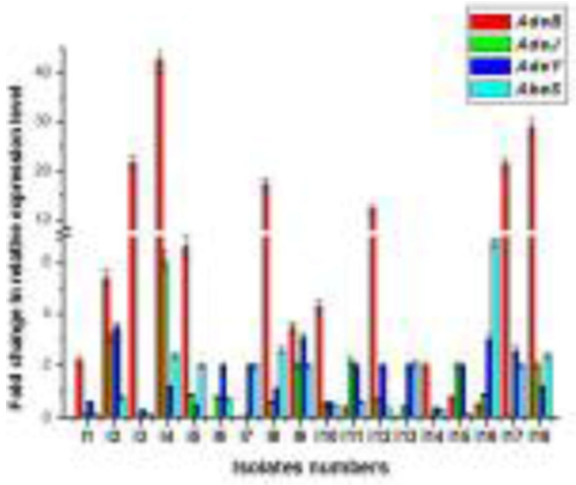

Figure 1. The relative expression level for RND families (AdeABC, AdeIJK, AbeXYZ) and SMR family (AbeS) efflux pump genes among neonatal septicaemic A. baumannii isolates (Isolate 1 to Isolate 18).

Results: Carbapenems and cephalosporins resistance was found among 61% and 90% of total *A. baumannii* isolates (n=49). Exposure of the isolates to PAβN resulted in ≥4-fold MIC decreases for carbapenem and cephalosporins among 25% and 35% of the isolates which indicated the existence of multidrug efflux pumps. Overall, 55% of these isolates had shown over expression of *adeB* gene followed by *adeY*, *abeS*, and *adeJ* (Figure 1). The relative expression level for *adeB* was highest in comparison to the other pump genes. The presence and over expression of AdeXYZ efflux pump had never previously been reported among *A. baumannii* isolates. Specific mutations had been detected within *adeR* (V136A) and *adeS* (K121E) which might have positive effect on over expression of the pump.

Conclusion: This is probably the first study that showed the active efflux pumps appeared to play important roles in the β-lactam resistance of *A. baumannii* isolated from neonates. Therefore, efflux pump inhibitors may be useful as adjunct therapy for treatment of these multidrug-resistant strains.

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