Background Treponema pallidum ss. endemicum (TEN) is the causative agent of endemic syphilis (bejel). The TEN Bosnian A strain was isolated in 1950 from a patient’s penile lesion in northeastern Bosnia.

Methods To define genetic differences between TEN Bosnian A and other pathogenic treponemes including the agents of syphilis (T. pallidum ss. pallidum, TPA) and yaws (T. pallidum ss. pertenue, TPE), a high quality sequence of the Bosnian A genome was determined using 454-pyrosequencing, Illumina, SOLiD and traditional Sanger sequencing. Combined average coverage of these sequencing methods was greater than 340x.

Results Compared to other TPA and TPE treponemes, the genome of Bosnian A (1,137,653 bp) was smaller in size (~2 kb) but structurally almost identical to other TPA and TPE strains. The Bosnian A genome clustered with TPE strains (nucleotide identity excluding indels ranged between 99.91 – 99.94%) while TPA strains were more distantly related (99.79 – 99.82%). More than 400 Bosnian A-specific nt changes (i.e. sequences different from TPA and TEN genomes) were found as the result of our analysis.

Conclusions The Bosnian A genome showed similar genetic characteristics as other TPA and TPE strains. Genetic differences found between TPA strains and Bosnian A genome could be used for identification of potential virulence factors of syphilis treponemes. Moreover, genetic changes specific for Bosnian A genome could help develop molecular diagnostic tests for endemic syphilis.

Background Previously, we demonstrated that urinary white cell count increases in proportion to pathogen load in cases of urethritis caused by Mycoplasma genitalium but not Chlamydia trachomatis. We further investigated urethritis pathogenesis caused by these organisms by comparing concentrations of 23 cytokines present within first void urine (FVU) specimens of male urethritis cases. Methods FVUs from 52 symptomatic male patients (all underwent Gram stain urethral smear) were collected and patients stratified into those with non-specific urethritis (n = 12), M. genitalium urethritis (n = 13), C. trachomatis urethritis (n = 14) and non-urethritis controls (n = 15). Cytokine measurements from FVUs specimens were obtained using a Human 30-Plex Luminex assay. Concentrations were obtained for 23 of the 30 cytokines analysed and compared between the four groups using multivariate ANOVA.

Results Overall, there was a significant difference in urinary cytokine profile between groups (p = 0.042). For individual cytokines, clinical group was associated with differences in concentrations of IL-1β (p = 0.007), GCSF (p = 0.042), CCL11 (p = 0.012), MIP-1α (p = 0.029), TNF-α (p = 0.026), IL-7 (p = 0.029), EGF (p = 0.050), VEGF (p = 0.049) and IFNa (p = 0.008). When compared with infected non-urethritis controls, cytokine concentrations in: M. genitalium samples, were increased for IL-1β (p = 0.017), GCSF (p = 0.010) but decreased for EGF (p = 0.017); C. trachomatis samples, were decreased for EGF (p = 0.049); and in non-specific urethritis samples, were increased for CCL5 (p = 0.049), IL-1β (p = 0.05), IL-1RA (p = 0.033) and decreased for EGF (p = 0.052). No significant differences were demonstrated in cytokine concentrations between C. trachomatis and M. genitalium groups.

Conclusion The increased levels of pro-inflammatory cytokines present in the urethritis groups when compared to non-urethritis controls reflect the acute inflammatory state. The data suggests that M. genitalium genital infection may be associated with a discrete mucosal immunological profile potentially explaining the link between cellular inflammatory response and bacterial load, previously observed.

Background N. gonorrhoeae (Ng) has developed resistance to most antimicrobial used for treatment. The report of the first resistant isolates of Ceftriaxone (CRO) in Japan, France and Spain, highlighted the lack of alternatives for syndromic treatment of Ng. In Argentina, although no resistance has been reported, the first isolates with decreased susceptibility to CRO (CRO<sub>DS</sub>) appear in 2011.

Materials and Methods: We studied 3649 Ng isolates since 1993 derived from Argentine Gonococcal Antimicrobial-Susceptibility Network. MIC was determined by agar dilution according to CLSI recommendations. We studied extended spectrum cephalosporins (ESCs) resistance determinant (mtr, penA, porB) by sequencing and carry out the molecular typing by Ng multi-antigen sequence typing (NG-MAST).

Results We detected 10 CRO<sub>DS</sub> isolates, 4 showed a CRO MICs of 0.064 μg/ml and 6 of them of 0.125 μg/ml. All isolates were also resistant to two or more antimicrobial agents (Penicillin and Tetracycline and/or Ciprofloxacin) and showed decreased susceptibility to Cefixime with MICs between 0.125 and 0.5 μg/ml.

Six NG-MAST sequence types (STs) were detected, with ST295 (n = 3) and ST1407 (n = 5) being most common. Also found ST225, ST3260 and two new STs: ST8508 and ST8509.

The penA gene analysis revealed three different no mosaic alleles patterns: V (n = 1), IX (n = 1) and XII (n = 1) and two mosaic alleles patterns: XXXIV (n = 4) and X (n = 3). Nine isolates showed mutations in C120 and A121 positions in porB1b allele and one isolate revealed A121G substitution in allele porB1a, both previously described. All isolates carried a nucleotide (A) deletion in the inverted region of mtrA gene.

Conclusion The evidence of the first isolates with decreased susceptibility to ESC in Argentina and the presence of ST1407 involved in the extensively drug resistant Ng raise the need for emphasis surveillance studies to ESC and know the distribution of ST1407 in our Region and its associated resistance.
Background Acyclovir (ACV) is the first-line treatment for symptomatic primary and recurrent genital herpes in South Africa. Resistance to ACV is mainly due to mutations in the HSV-2 viral UL23 gene that codes for thymidine kinase (TK), resulting in an inability for the drug to inhibit viral replication. The objectives of this study were to obtain genotypic data on the frequency of HSV-2 TK resistance mutations and natural polymorphism as well as to assess the prevalence of ACV-resistant HSV-2 among participants in the genital ulcer aetiology studies conducted between 2007 and 2011.

Methods We amplified and fully sequenced the UL23 gene of 254 HSV-2 positive specimens obtained from participants in genital ulcer aetiological studies conducted between 2007 and 2011 in Gauteng Province, South Africa. Additionally, intratypic differences between the HSV-2 were determined based on the number of reiterated sequences located in the non-coding regions of the US1 and US12 genes of HSV-2.

Results We identified 63 single and/or double nucleotide mutations in the UL23 genes analysed, that resulted in 30 silent mutations and 32 amino acid changes. 41% of these amino acid changes were due to natural polymorphism. In addition, we identified 19 unknown amino acid changes in 30 samples that have not been described before. All unknown mutations detected were outside the TK resistance “hotspots”, which are renowned sites for ACV resistance mutations to occur. No frameshift mutations or mutations causing stop codons were identified in the UL23 genes of the samples analysed.

Conclusions No evidence was found of known ACV resistance mutations in HSV-2 following the addition of ACV as first-line therapy for genital ulceration in South Africa. Genotyping of HSV-2, based on the length of reiterated sequences in the US1 and US12 genes of HSV-2, revealed a high degree of HSV-2 heterogeneity in this population.

**P1.015 ON THE MECHANISMS OF DRUG RESISTANCE IN HIV-1 RT**


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Human Immunodeficiency Virus Reverse Transcriptase (HIV-1 RT), catalysing synthesis of proviral cDNA has been widely exploited as a most suitable target for attack by anti-AIDS chemotherapeutics. The anti-HIV-1 RT molecules involve dideoxy analogues of dNTP (nucleoside reverse transcriptase inhibitors, NRTIs), which inhibit it competitively by terminating DNA chain extension. The other group of HIV-1 RT inhibitors involves non-nucleoside reverse transcriptase inhibitors (NNRTIs), which bind preferably in the hydrophobic pocket or elsewhere at enzyme surface, inhibit it non-competitively. The AIDS therapy prescribes different combination of various anti-HIV drugs mainly the anti-HIV-1RTs and anti-proteases (in highly active antiretroviral therapy, HAART), which significantly reduces HIV count to undetectable level. Unfortunately, due to drug selection pressure drug resistant variants of HIV-1 emerge and preclude chemotherapy of this pandemic. This paper is an endeavour to illustrate possible mechanisms involved in anti-HIV drugs resistance. Apart from attributes of numerous mutations reported in three key enzymes of HIV (RT, protease and integrase) in making anti-HIV drugs, one plausible mechanism of nucleoside analogue resistance involves ATP/GTP-based excision to unblock chain-terminated primers; thereby allowing viral replication to continue. Such unblocking has also been reported in viro in presence of excess of pyrophosphate concentration; a reaction known as pyrophosphorylation. In addition to viral mutants isolated from the AIDS patients, we have shown some artificial mutants of K154, which exhibited anti-HIV-1 drugs resistance property and the mechanism involved reduction in binding of the drugs to RT because of conformational change. Our recent report on mechanism of resistance of HIV-1RT against rilpivirin due to E188K mutation proposes a new aspect in this context. However, an extensive study exploring some new targets and drug resistance mechanisms is needed for design and development of novel and potential anti-viral agents to combat this challenge.

**P1.016 MOLECULAR ANALYSIS OF ANTIMICROBIAL RESISTANT NEISSERIA GONORROEA ISOLATES FROM DELHI, INDIA: A FUNCTIONAL GENOMICS APPROACH**


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Background In India, knowledge regarding N. gonorrhoeae antimicrobial resistance profiling is limited, and data concerning genetic characteristics of N. gonorrhoeae is also lacking. Herein, we investigated the genetic resistance determinants for various antimicrobials used against N. gonorrhoeae isolated in Delhi, India. Various studies have shown that this resistance towards antimicrobials could be either plasmid or chromosomal mediated involving mutations in various genes.

Methods Molecular basis of plasmid and chromosomal mediated antimicrobial resistance was analysed by amplifying and sequencing the most target genes, penA and porB, of N. gonorrhoeae. Attempts have been made to in-silico model the structure of mutant PenA to understand how mutations in these genes affect the drug binding. A PCR assay was also carried out to analyse the penicillinase producing N. gonorrhoeae (PPNG).

Results Out of the 40 clinical isolates of N. gonorrhoeae studied which were resistant to various antimicrobials, twenty eight isolates showed high resistance to penicillin (3-32µg/ml). These resistant isolates were PPNG positive (70%; 28/40) and predominantly harboured the African type of PPNG plasmid. Only two isolates carried the Asian type of plasmid. Mutations were also observed in penA and porB genes which correlate their effects on drug resistance. Through in silico modelling studies, we were able to even show that a single point mutation at G452S in penA gene changed the susceptibility of N. gonorrhoeae towards penicillin and tetracycline.

Conclusions This study clearly shows a cumulative effect of increasing mutations with subsequent increase in resistance towards various antimicrobials. Presence of both African and Asian type of penicillinase producing plasmid gives an indication of extensive travel of patients affected with Gonorrhea. Our in silico modelling studies of mutant proteins provide new insights to access increasing antimicrobial resistance among Neisseria gonorrhoeae.

**P1.017 UNIQUE ACTIVITY OF SITAFLOXACIN, ONE OF NEWER FLUOROQUINOLONES, AGAINST CIPROFLOXACIN-RESISTANT N. GONORRHOEA**


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Background Fluoroquinolone-resistance in Neisseria gonorrhoeae is spreading in the world and almost 80% of N. gonorrhoeae strains are resistant to fluoroquinolones in Japan. It is known that the resistance to fluoroquinolones is closely related to mutations of quinolone-resistance determining regions (QRDR) on gyrA genes such as gyrA3 or parC. In 2009, the first national surveillance of antimicrobial susceptibilities of N. gonorrhoeae was performed in Japan. In this surveillance, we found that sitafloxacin, one of newer