P1.011 WHOLE GENOME SEQUENCE OF THE TREPONEMA PALLIDUM SSP. ENDEMICUM, STRAIN BOSNIA A

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

Methods To define genetic differences between TEN Bosnia A and other pathogenic treponemes including the agents of syphilis (*T. pallidum* ssp. *pallidum*, TPA) and yaws (*T. pallidum* ssp. *pertenue*, TPE), a high quality sequence of the Bosnia 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 Bosnia A (1,137,653 bp) was smaller in size (~2 kb) but structurally almost identical to other TPA and TPE strains. The Bosnia 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 Bosnia A-specific nt changes (i.e. sequences different from TPA and TEN genomes) were found as the result of our analysis.

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

P1.012 URINARY CYTOKINE PROFILES IN NON-SPECIFIC, MYCOPLASMA GENITALIUM AND CHLAMYDIA TRACHOMATIS URETHRITIS

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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 = 13). Cytokines 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 = 0.030), VEGF (p = 0.049) and IFNa (p = 0.008). When compared with uninfected 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 = 0.032). 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

P1.013 EMERGENCE OF *NEISSERIA GONORRHOEAE* ISOLATES WITH *IN VITRO* DECREASED SUSCEPTIBILITY TO CEFTRIAXONE IN ARGENTINA

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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^{LS}) appear in 2011.

Materials and Methods: We studied 5649 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*, *pen*A, *por*B) by sequencing and carry out the molecular typing by Ng multi-antigen sequence typing (NG-MAST).

Results We detected 10 CRO^{LS} 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 (Penicilin 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 ST925 (n = 3) and ST1407 (n = 3) being most common. Also found ST225, ST3620 and two new STs: ST8508 and ST8509.

The *pen*A 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 G120 and A121 positions in *por*B1b allele and one isolate revealed A121G substitution in allele *por*B1a, both previously described. All isolates carried a nucleotide (A) deletion in the inverted region of *mtr*R 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 emphasise surveillance studies to ESC and know the distribution of ST1407 in our Region and its associated resistance.

P1.014 HERPES SIMPLEX VIRUS TYPE 2 UL23 THYMIDINE KINASE: MOLECULAR DETECTION OF POLYMORPHISM AND MUTATIONS ASSOCIATED WITH ACYCLOVIR RESISTANCE IN SOUTH AFRICA

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