related to resistance and epidemiological characteristics was performed. We analysed 143 isolates (69 resistant and 74 susceptible); 81% was from men who have sex with men (MSM). Azithromycin resistant isolates had significantly more often C2611T mutations of 23S rRNA (n=62, 89.9%, p<0.001), an NG-MAST genogroup G2992 (p<0.001), G5108 (p<0.001), or G359 (p=0.02), and were more often part of NG-MLVA clusters (p<0.001). Two resistant isolates (2.9%) had A2059G mutations, and five (7.3%) were wild-type 23SrRNA. Four of the five NG-MLVA clusters contained resistant and susceptible isolates, and isolates from HIV-positive and HIV-negative patients. Two of the clusters consisted mainly of resistant isolates and were strains from MSM, heterosexual men and women. Co-occurrence of resistant and susceptible strains in NG-MLVA clusters and frequent occurrence of resistant strains outside of clusters suggests that azithromycin resistance develops independently from the 'background genome'.

O13.3 VACCINE DEVELOPMENT TO COMBAT ANTIMICROBIAL RESISTANT GONORRHOEA

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Introduction *Neisseria gonorrhoeae*, the causative agent gonorrhoea, is a major public health problem worldwide with an estimated global incidence of 106 million cases/yr. If left undiagnosed or untreated, infection can lead to severe sequelae that include pelvic inflammatory disease, infertility, neonatal complications, and an increased risk of HIV. It recognised by WHO and CDC as an urgent threat to global health due to the emergence of multi-drug resistant gonococcal strains. There is currently no vaccine, and no new antibiotics or new vaccine candidates in late-stage development.
Methods To facilitate gonococcal vaccine development, we performed mathematical modelling to predict the impact of different vaccine scenarios. We have also identified and characterised a series of potential vaccine candidates.
Results Mathematical modelling of different vaccine scenarios indicates that even a modestly efficacious vaccine could have a substantial impact on gonorrhoea prevalence and sequelae. We have also characterised 2 highly conserved and immunogenic candidate vaccine antigens. *In vitro* assays, using wild type, knock-out and complemented strains, have shown that NGO1958 (gonococcal homologue of the Neisseria heparin binding antigen (NHBA) present in the serogroup B meningococcal vaccine) is involved in serum resistance and adherence to cervical epithelial cells. Similar assays show that NGO2139 (methionine uptake receptor) is involved in resistance to killing by human serum, monocytes and macrophages, as well as adherence and invasion of cervical epithelial cells. Antibodies to these proteins are bactericidal and can block gonococcal infection of cervical epithelial cells. Additional studies are underway to determine if antibodies to these proteins can protect again infection in a mouse model.
Conclusion We present two antigens that elicit both bactericidal and functional blocking antibodies, which are valid candidate antigens for possible inclusion in an urgently needed vaccine for the prevention of gonorrhoea.

O13.4 MULTIPLE CYTOKINE GENE EXPRESSION DETECTED AFTER HPV VACCINATION

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Introduction Human papillomavirus (HPV) infection does minimal damage and does not induce the production of immune mediators by host epithelial cells. The induction of a pro-inflammatory immune response is necessary to break the tolerance induced by HPV. Therapeutic interventions with vaccines to induce an effective immune response have the potential to treat latent infection as well as clinically apparent lesions. The aim of this study was to evaluate the influence of the human papillomavirus (HPV) vaccination on peripheral blood mononuclear cell (PBMC) proliferation and cytokine gene transcription.
Methods PBMCs isolated after immunisation were incubated with HPV vaccine, phytohemagglutinin (PHA) or buffer. Cell proliferation was assessed by MTT reduction assay. RNA was extracted from PBMCs, and the relative concentration of cytokine messenger RNA (mRNA) transcripts (IFN-b, IFN-c, IL-12, TNF-a, IL-6, IL-17, or IL-10) relative to transcription of the b-actin gene was determined by real-time polymerase chain reaction.
Results PBMC proliferation in response to HPV vaccine and PHA were greater than that observed in unstimulated cells (p<0.001). Cytokine mRNAs were upregulated in stimulated PBMC cultures. The median increase in vaccine-stimulated cultures was: IFN-b=334.4 fold; IL-12=46.33 fold; IFN-c=12.64 fold; IL-6=9.07 fold; IL-17=7.33 fold; IL-10=6.47 fold; and TNF-a=2.36 fold.
Conclusion The IFN-b expression was significantly higher (p<0.05). Proliferative PBMC responses and multiple cytokine gene expression were detected in women who received the HPV vaccine.

O13.5 CORE GROUPS OF INDIVIDUALS WITH CHLAMYDIA AND/OR GONORRHOEA REINFECTIONS HAVE INCREASED ODDS OF DIAGNOSIS WITH INFECTIOUS SYPHILIS: A POPULATION-BASED RETROSPECTIVE COHORT STUDY IN BRITISH COLUMBIA, CANADA, 2006–2015

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Introduction The incidence of infectious syphilis (primary, secondary, or early latent) has increased in British Columbia (BC). Identifying core groups at risk for syphilis can inform public health programming. We assessed the odds of syphilis infection among individuals with repeat *Chlamydia trachomatis* (CT) and/or *Neisseria gonorrhoeae* (GC) infections in this population-based analysis.
Methods Surveillance records for all BC residents diagnosed with ≥2 CT (CT reinfection) or ≥2 GC (GC reinfection) or ≥2 infections including CT and GC (CT/GC reinfection) from 1/1/2006 to 12/31/2015 were linked with all infectious syphilis cases from the same time period. Logistic regression models