negative microscopy and NAAT 2 months after stopping dequalinium.

Conclusion Prolonged dequalinium may offer an alternative treatment option for recalcitrant TV, particularly where high dose systemic antibiotics have been unsuccessful.

Disclosure No significant relationships.

CCS02.2 PENILE INTRAEPITHELIAL NEOPLASIA: MYRIAD PRESENTATIONS AND INTRACTABLE COURSE

Somesh Gupta*. *All India Institute of Medical Sciences, Dermatology and Venereology, New Delhi, India*

10.1136/sextrans-2019-sti.101

Disclosure No significant relationships.

CCS02.3 PERSISTING URETHRITIS IN AN IMMUNOCOMPROMISED PATIENT

William Geisler*. *University of Alabama at Birmingham, Birmingham, USA*

10.1136/sextrans-2019-sti.102

CCS03 – CASES FROM THE CLINIC

Wednesday, July 17, 2019

7:00 AM – 8:00 AM

CCS03.2 NEONATAL HSV: COULD THIS TRANSMISSION HAVE BEEN PREVENTED?

Elizabeth Foley*. *Solent NHS Trust, Genitourinary Medicine, Southampton, UK*

CCS03.3 ZOON BALANITIS IN HIV-INFECTED PATIENT

RC Melo*, M Ramos. *Ambulatório de Dermatologia Sanitária, Porto Alegre, Brazil*

10.1136/sextrans-2019-sti.103

Background Genital lesions lead patients to seek care in sexually transmitted diseases (STD) clinics. The old axiom “all genital lesions must be considered sexually acquired until proved to the contrary” is true today. A high level of suspicion of an STD must accompany examination of patients with genital lesions. Although other causes are also seen, we present a case of Zoon’s balanitis in a patient with HIV infection.

Methods A 40-year old, white male, sought attention for a genital lesion evolving over six months. He was on treatment with antiretrovirals, and underwent treatment with topic and systemic antifungal without improvement. He had multiple, well-delimited, moist red-orange lesions on the glans and foreskin. Some lesions had a face-to-face (kissing) disposition. Treponemal and non-treponemal serology was negative. With the hypothesis of plasmacytic balanitis, a biopsy was performed. Histopathologic examination demonstrated a lichenoid inflammation with an inflammatory infiltrate with plasmacytes, lymphocytes and neutrophils. No vascular alteration was found. There was spongiosis and erosion of the epithelium.

Results Zoon balanitis is a chronic, idiopathic, reactive balanoposthitis. It is believed to be associated with irritation in the context of a dysfunctional foreskin. It presents as well-circumscribed orange-redish moist lesions in the glands and foreskin, usually asymptomatic. HIV infection is an acknowledged risk factor for other STDs. Infectious causes such as candidiasis and syphilis are much more common and must be considered. Syphilitic lesions and Zoon balanitis share clinical and histopathological features including a slight thickening of the epidermis, parakeratosis, and patchy lichenoid infiltrates of lymphocytes and plasma cells, making their differential diagnosis complex, hence the need of always performing syphilis serology in such cases.

Conclusion In spite of STD generally being the first hypothesis in patients with genital lesions, many causes must be considered, especially when atypical lesions are present or there is poor response to therapeutic measures.

Disclosure No significant relationships.

Oral Presentations

O01 – DEVELOPMENT OF VACCINES FOR BACTERIAL STIS

Monday, July 15, 2019

10:45 AM – 12:15 PM

O01.1 GENETIC SIMILARITY OF GONOCOCCAL HOMOLOGS TO MENINGOCOCCAL OUTER MEMBRANE PROTEINS OF SEROGROUP B VACCINE

Henju Marjuki*, Nadav Topaz, Sandeep Joseph, Kim Gernert, Ellen Kersh, Antimicrobial Resistant *Neisseria gonorrhoeae* Working Group, Xin Wang. *Centers for Disease Control and Prevention, Atlanta, USA*

10.1136/sextrans-2019-sti.104

Background Human pathogens, *Neisseria gonorrhoeae* (Ng) and *N. meningitidis* (Nm), share high genome similarity. Retrospective analysis of surveillance data in New Zealand suggests cross-protection against Ng infections conferred by serogroup B meningococcal (MenB) outer membrane vesicle (OMV)-based vaccine. We explored the possible cross-protective mechanisms against gonorrhea conferred by the licensed multicomponent 4CMenB (Bexsero™) vaccine containing NZ98/254 OMVs.

Methods A dataset of 970 Ng genomes of isolates collected from the Gonococcal Isolate Surveillance Project sites across the United States was analyzed to identify common proteins present in both Ng and NmB, and assess the sequence diversity of vaccine antigens and OMV components between the two bacteria, and within the Ng strains. Bioinformatics tools were applied to predict the subcellular localization of each identified common protein.

Results We found 1525 common proteins shared by both *Neisseria* species, of which 59 were predicted as outer membrane proteins (OMPs). The 4CMenB vaccine antigen Nhba showed moderate sequence identity (73%) to the respective gonococcal homologs, and was highly conserved within Ng.

The gonococcal FHbp was predicted as not being surface-expressed, while NadA was absent in all the Ng isolates. The immunodominant OMV protein PorA was present in nearly all Ng isolates, but harbored deletions in the promoter regions, preventing its transcription. Noteworthy, OMPs including FetA, PilQ, Omp85, RmpM, LbpA and TonB-dependent receptors, previously identified and abundantly expressed in the NZ98/254 OMV, displayed $\geq 93\%$ sequence identity between Nm and Ng, and were highly conserved within Ng.

Conclusion Our results provide a better understanding of the OMPs present in the OMV of the 4CMenB vaccine. These OMPs may contribute to the observed cross-protection, and can serve as potential antigen targets for guiding the next steps of gonorrhea vaccine development.

Disclosure No significant relationships.

001.2 GENETIC, STRUCTURAL, AND SURFACE ANTIGENIC VARIATION OF *TREPONEMA PALLIDUM*'S OMPEOME: STEPS TOWARDS A GLOBAL SYPHILIS VACCINE

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10.1136/sextrans-2019-sti.105

Background The failure of current prevention strategies to curtail the spread of syphilis, including mother-to-child transmission, underscores the need for a vaccine with worldwide efficacy. Characterization of variation within *T. pallidum* (TPA) outer membrane proteins (OMPs) is critical for this goal.

Methods ClustalW identified polymorphisms within 21 β -barrel forming OMPs (TPA's OMPeome) of 15 unique TPA strains. Structural models and conformational B-cell epitopes (BCEs) were predicted. Clade assignments were made using *tp0548* and *tp0558* sequences.

Results TPA OMPeomes contain four paralogous families (Tpr, FadL, OmpW, and efflux pump OMPs) and orthologs for BamA and LptD. The Tprs group into Subfamilies I (C/D/I), II (E/G/J) and III (B/H/L); Tpr β -barrel domains contain 10 β -strands and five extracellular loops (ECLs) harboring BCEs. TprI is invariant, while TprC and TprD have variability located predominantly in ECLs. The closely related TprE and TprJ β -barrels exhibit extremely low variability. TprG β -barrels variants contain a 23 aa insertion derived from TprE or TprJ. The TprB and TprH β -barrels are fully conserved; there are two TprL β -barrels variants. The FadL orthologs (TP0548, TP0856, TP0858, TP0859, TP0865) consist of 14-stranded β -barrels with seven ECLs harboring predicted BCEs. Variability among FadLs range between fully conserved (TP0856) to highly variable (TP0548). Both OmpWs are fully conserved and consist of 8-stranded β -barrels with four ECLs containing BCEs. The highly conserved efflux pump OMPs (OprJ/TP0966, OprN/TP0967, TolC/TP0969) likely form homotrimeric 12-stranded β -barrels. The 18-stranded BamA/TP0326 β -barrel contains a single aa substitution in ECL4. The LptD/TP0515 β -barrel contains 24 β -strands, 12 ECLs and

numerous BCEs, which cluster primarily into two variants. Most OMPs do not align with clade designations.

Conclusion 1.) TPA OMPs display variable degrees of sequence and surface antigenic variation. 2.) TPA OMPeomes are mosaics likely resulting from recombination among circulating strains. 3.) Our analysis enables selection of variable and non-variable OMPs for assessment of protective capacity.

Disclosure No significant relationships.

001.3 ENGINEERING HYBRID BACTERIAL TRANSFERRIN RECEPTOR-BASED VACCINES TO CONFER BROAD PROTECTION AGAINST *NEISSERIA GONORRHOEA*

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10.1136/sextrans-2019-sti.106

Background The bacterial transferrin receptor has long been considered an outstanding vaccine target against pathogenic *Neisseria* species as it is surface-exposed and essential for bacterial survival and virulence *in vivo*. Required for iron uptake from the human protein transferrin (hTf), this receptor is composed of two proteins, an integral membrane channel (transferrin binding protein A; TbpA), and a surface anchored lipoprotein (TbpB). Vaccine development has predominantly focused on TbpB as it is a soluble, stable antigen that is highly immunogenic and easy to produce in large quantities. However, TbpB is also highly variable and so achieving broad cross-protection in a vaccine has been considered challenging. In comparison, TbpA is highly conserved but the production of this integral membrane protein is technically challenging and not considered practicable for large-scale development.

Methods We performed protein structure-based engineering to remove variable unstructured surface loops on TbpB to provide a soluble, stable and immunologically cross-protective scaffold upon which surface-exposed loops of TbpA have been displayed. These chimeric immunogens have been used to immunize rabbits and mice, including 'humanized' transgenic mice that express human hTf. Immunological cross-reactivity against a broad panel of *N. gonorrhoeae* isolates and the presence of functional antibodies targeting the gonococcal transferrin receptor were monitored by ELISA, hTf-binding and growth-based analyses, and immunized mice were challenged with genital *N. gonorrhoeae* infection.

Results The chimeric immunogens elicit antibodies against both TbpA and TbpB. The antisera is broadly cross-reactive against the gonococcal strain panel, is bactericidal, blocks transferrin-based iron acquisition and growth, and protects mice against gonococcal infection. While wild type TbpB-based immunogens have reduced functional antibody in hTf-expressing mice, the binding-defective Tbp-based immunogens are equally efficacious in both wild type and hTf-transgenic animals.

Conclusion Our rationally-designed hybrid immunogens simultaneously target two components of an essential iron acquisition pathway, eliciting broad cross-protection against gonococcal colonization and disease.

Disclosure No significant relationships.