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.

### 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

10.1136/sextrans-2019-sti.102

### CCS03.3 ZOON BALANITIS IN HIV-INFECTED PATIENT

RC Meio*, 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 smegmasis complex, hence the need of always performing syphilis serology in such cases.

**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.

**Disclosure** 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

**001 – DEVELOPMENT OF VACCINES FOR BACTERIAL STIS**

**Monday, July 15, 2019**

10:45 AM – 12:15 PM

#### 001.1 GENETIC SIMILARITY OF GONOCOCCAL HOMOLOGS TO MENINGOCOCCAL OUTER MEMBRANE PROTEINS OF SEROGRUP B VACCINE

Henju Marjuki*, Nadav Topaz, Sandeep Joseph, Kim Gemert, 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.

**Disclosure** No significant relationships.