**Methods**

The epidemiology of neonatal herpes infection (nHSV) is changing as herpes simplex virus type 1 (HSV-1) is an increasingly common cause of genital herpes. Few sources of population-based data for nHSV exist; nHSV has been a notifiable disease in New York City (NYC) since 2006.

**Results**

Among the 125 women diagnosed with acute PID, twenty two percent (n = 27) tested positive for *M. genitalium*, while CT and bacterial vaginosis were present in 14%, 7% and 54%, respectively. Forty six women (37%) had histologic endometritis. Histologic endometritis was more common among those having cervical infections with GC, CT or MG than uninfected women (66% vs. 24%, p < 0.001). Among women with endometritis, GC, CT and MG were present in 17%, 30% and 36%, respectively. Endometritis was present in 71% (20/28) of women with endometrial GC, CT or MG. Endometrial identification of GC (100% vs. 54%, p < 0.05), CT (77% vs. 32%, p < 0.01) and MG (64% vs. 33%, p < 0.05) were each independently associated with endometritis.

**Conclusion**

*Mycoplasma genitalium* is identified in 22% of women diagnosed with acute PID. Similar to CT and GC, the presence of MG in the endometrium is highly associated with endometritis among women diagnosed with PID. This study suggests that *M. genitalium* may play an important role in the pathogenesis of PID.

**0.05 - Molecular analysis of STI pathogens and their environments**

**006.1 HIGH GRADE ANAL INTRAEPITHELIAL NEOPLASIA: ONE VIRUS, ONE LESION**

**Background**

Prevention and treatment of anal intraepithelial neoplasia (AIN) in HIV+ men who have sex with men (MSM) is subject of discussion. Knowledge on causative HPV types is crucial in understanding AIN and in vaccination studies. However, data on AIN-specific HPV are limited and whole tissue sections (WTS) often show multiple HPV infections.

In this study, we analysed whether WTS and subsequent laser capture micro-dissection (LCM) with HPV PCR genotyping accurately detects type-specific HPV DNA in individual areas of high grade (HG)AIN.

**Methods**

31 WTS with HGAIN of 21 HIV+ MSM were analysed by the SPF10 PCR/Lipa25 (version 1) HPV genotyping system. In case of multiple HPV types, PCR was repeated in selected areas of AIN, isolated by LCM.

**Results**

WTS PCR showed a single HPV type in 17 (55%). In the remaining 14 WTS sections with multiple HPV types, PCR was repeated in LCM-isolated dysplastic areas (median: 4 per WTS). In 12 of 14 these samples, the number of HPV types could be reduced to single HPV types within discrete areas of a lesion, resulting in a total of 29 (17+12), in which (components of) HGAIN show a single HPV type. In 12 of 14 these samples, the number of HPV types could be reduced to single HPV types within discrete areas of a lesion, resulting in a total of 29 (17+12), in which (components of) HGAIN show a single HPV type. HPV 16 was found in 14/29 (48%), HPV 18 in 3 and HPV 58 in 5. The remaining HPV types that could be linked to a lesional area were HPV 26, 31, 35, 39, 52, 53, 54, 59, 67, 68/73, 74, 91 and one indeterminate HPV type.

**Conclusion**

WTS PCR and subsequent LCM PCR is accurate in detecting lesion specific HPV types in AIN and it seems that 94% of the AIN-lesions (on macroscopic or microscopic level) are caused by a single HPV type. Apart from HPV 16, the predominant type, a wide range of other HPV types are responsible for HGAIN, which has consequences for vaccination development.