COMPARISON OF THE CLINICAL AND DEMOGRAPHIC CHARACTERISTICS OF NEONATAL HERPES INFECTIONS CAUSED BY HERPES SIMPLEX VIRUS TYPE 1 AND TYPE 2: FINDINGS FROM A POPULATION-BASED SURVEILLANCE SYSTEM, 2006–2012

Methods To compare the clinical and demographic characteristics of nHSV due to HSV-1 and herpes simplex virus type 2 (HSV-2), we used standard case investigation forms to abstract infant inpatient/outpatient medical records, and maternal labour and delivery records for babies ≤60 days of age diagnosed with laboratory-confirmed herpes infection and reported in NYC, dating 2006–2012. Disease syndromes were grouped as invasive (disseminated/central nervous system infection/death) versus localised (skin/eye/mucous membrane infection). Cases lacking liver function test results, or lumbar puncture were excluded from analyses of disease syndrome. Bivariate analyses compared clinical and demographic characteristics by viral type.

Results There were 91 cases reported (HSV-1, 40; HSV-2, 36; untyped, 15). Among 76 cases with viral typing, the majority (55%; 40/76) were HSV-1. There were no statistically significant differences by viral type for any variables examined: age ≤7 days at presentation (HSV-1, 59% versus HSV-2, 41%), fever (HSV-1, 58% versus HSV-2, 46%), vesicles (HSV-1, 46% versus HSV-2, 53%), invasive disease (HSV-1, 53% versus HSV-2, 70%), case fatality rate (HSV-1, 18% versus HSV-2, 19%), maternal history of genital herpes (HSV-1, 20% versus HSV-2, 20%), maternal genital lesions at delivery (HSV-1, 8% versus HSV-2, 3%), vaginal delivery (HSV-1, 69% versus HSV-2, 61%), white non-Hispanic maternal race/ethnicity (HSV-1, 26% versus HSV-2, 12%), maternal age <20 (HSV-1, 15% versus HSV-2, 27%).

Conclusions Neonatal herpes infections due to HSV-1 and HSV-2 have a similar presentation, and death rate. To prevent nHSV, candidate HSV vaccines will need to protect against HSV-1, as well as HSV-2 infection in women.

0.05 - Molecular analysis of STI pathogens and their environments

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. HPV 16 was found in 14/29 (48%), HPV 18 in 3 and HPV 58 in 3. The remaining HPV types that could be linked to a lesional area were HPV 36, 31, 35, 58, 53, 54, 89, 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.

MEASURING SYPHILIS: QUANTITATIVE PCR CAN BE USED TO MONITOR TREATMENT RESPONSE

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