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Final Abstract Number: 43.206
Session: Poster Session III
Date: Saturday, March 5, 2016
Time: 12:45-14:15
Room: Hall 3 (Posters & Exhibition)

Identification of human papillomavirus types causing lesions in penile canerous, pre-cancerous and benign lesions using laser microdissection

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Background: Almost half of penile cancers and the majority of penile warts are associated with the two HR types (HPV 16 and HPV 18) and two LR HPV types (HPV 6 and HPV 11), respectively. It is therefore important to document the burden HPV associated diseases of the penis and identify the HPV types associated with the diseases. HPV E6 and E7 mRNA detection is the best indicator of HPV status that is clinically relevant as it indicate transcriptionally active HR HPV infection in lesions. In HR HPV infection an increase in E6 and E7 mRNA expression causes an overexpression of p16INK4A and thus used as a cellular correlate of the increased expression of HR HPV E6 and E7 mRNA in cervical samples. The aim of the study was to identify HPV type responsible for the development of the penile lesions.

Methods & Materials: To do that we genotyped and quantified 66 (18 benign lesions, 4 pre-cancerous and 44 cancerous lesions) penile tissue biopsies and performed LMD on the selected penile samples (7). RNA in situ hybridization (ISH) was performed using HPV16 alone, for HPV HR18 cocktail: HPV types 16,18,26,31,33,35,39,45,51,52,53,56,58,59,66,68,73,82) and HPV11 probes.

Results: HPV 11 (50.9%) and HPV 16 (49.1%) showed almost similar incidence in the study patients. Multiple infections were observed in 18/55 (32.7%) of the positive samples, majority were in condyloma and verrucous carcinoma cases and HPV 11 showed higher viral loads compared to the other HPV types. After lesion dissection with LMD and HPV 11 and/or HPV 16 were the only types detected, compared to multiple HPV types (HPV 11, HPV 16, HPV 18, HPV 31, HPV 33, HPV 35, and HPV 39) initially detected in whole tissue sections. Almost all the SCC lesions were positive for HPV 16 and showed p16INK4a overexpression in contrast there was no expression of p16INK4a in verrucous carcinoma and condyloma acuminatum lesions irrespective of the HR HPV types present.

Conclusion: In conclusion p16INK4a overexpression and mRNA expression correlated with HPV type associated with the lesion.

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Viral aetiologies of acute encephalitis in a hospital-based population in Sri Lanka

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Background: The aetiological spectrum of acute encephalitis in Sri Lanka remains unknown. We aimed to identify the viruses which are known to be a major cause of infectious encephalitis

Methods & Materials: A cross-sectional study was conducted among 99 patients with encephalitis/meningoencephalitis admitted to two tertiary care hospitals in Colombo. CSF and serum were tested for conventional viruses and emerging viruses that can cause encephalitis. Specific nucleic acid amplification assays and antibody assays were used to identify viruses. Plaque reduction neutralization test (PRNT) was done to confirm the diagnosis of West Nile virus (WNV).

Results: Patients' age ranged from 1 month to 73 years (mean=24.91; SD=21.33) with male: female ratio of 1.75:1. A viral aetiology was identified in only 27.3%. These included *Dengue virus* (40.7%), *Japanese encephalitis virus* (25.9%), *Varicella zoster virus*, *Epstein Barr virus* and WNV (11.1% each). None of the patients were positive for Herpes simplex virus 1 or 2, Cytomegalovirus, Nipah or Chandipura viruses. Screening for bacterial aetiologies was negative for all patients. There were no distinguishable clinical or routine laboratory features between the different viral aetiologies.

Conclusion: A viral aetiology was identified in only about a quarter of patients with encephalitis. Dengue virus accounted for the majority. HSV accounted for none. This is the first identification of human WNV in Sri Lanka.

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