SEXUALLY TRANSMITTED INFECTIONS, HIV/AIDS

RESEARCH INTO PRACTICE-NEW INSIGHTS INTO HSV INFECTIONS

Rajul Patel (1)

University of Southampton, Sexual Halth and HIV Medicine, Southampton, United Kingdom (1)

The herpesviruses are a large group of enveloped double-stranded DNA viruses, 8 of which cause human disease. The alpha group comprises of 3 important human pathogens, Varicella Zoster virus (VZV), Herpes simplex virus 1 (HSV-1) and Herpes simplex virus 2 (HSV-2). All three are characterized by their ability to establish lifelong reversible neuronal latency. HSV-1 is mostly associated with orofacial infections but is increasingly implicated in acquisition episodes of genital herpes, while HSV-2 is still generally associated with genital herpes. For HSV studies utilising multiple daily swabbing and Nucleic Acid Amplification technology as well as biopsy of the affected epithelium looking at gene products, immune responses(both during symptoms, and asymptomatic periods) has revolutionised our understanding of the natural history of these infections. There is a complex relationship between the pathogen and host immune system that modifies the extent of clinical disease and indirectly facilitates subclinical transmission of the virus - the most frequent means of spread for HSV. In addition we recognise that viral reactivation from latency is a much more frequent event then previously appreciated. Both HSVs cause significant human disease, so knowledge of the structure of their DNA genomes and the extent of their genetic variation is very important.

HSV-1 and HSV-2 have been studied extensively in vivo and in vitro, including studies of genetic variation at the level of individual genes and in patterns of restriction-length polymorphisms. The full genome sequence for HSV-1 and for HSV-2 have been estabishedfor over 20 years. Early studies looking at genome sequences were limited by the need for large quantities of virus (requiring initial culture and harvest of virions) –which may have favored those viral strains able to multiply quickly in laboratory conditions. A high overall GC content and the presence of highly reiterated repeat regions in both noncoding and coding portions of the genome complicated sequence determination. In addition the technology was cumbersome and the costs prohibitive. The field has in recent years rapidly developed and modern techniques allow genomic sequencing from direct patient specimens and to generate whole sequences within 72 hours. The number of published genomic sequences has grown and much has been learned about genetic variation. Recent work has started using these technologies and applying them to clinical problems, as well as attempting to identify genetic associations with disease and vaccine efficacy