

MEETING ABSTRACTS

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Human herpesvirus type 8 variants in Kaposi's sarcoma before and after AIDS era

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Background

Human herpesvirus 8 (HHV- 8) variants have been found heterogeneously distributed among human populations living in diverse geographic regions, but their differential pathogenicity in Kaposi's sarcoma (KS) development remains controversial. The aim of the present study was to analyze variations of HHV-8 genomes in tumor biopsies collected before and in the course of HIV epidemic (1971 - 2008), from patients with classic, iatrogenic, endemic as well as epidemic KS living in Africa, Europe, and North America.

Materials and methods

DNA samples have been extracted from cutaneous KS lesions of 68 patients living in Africa (n=23, Cameroon, Kenya and Uganda), Europe (n=34, Greece and Italy), and North America (n=11). The identification and characterization of HHV-8 variants has been based on PCR amplification followed by direct nucleotide sequencing and phylogenetic analysis of the highly conserved ORF 26 and T0.7, the hypervariable ORF K1, as well as on the analysis of P and M alleles of the K14.1/15 locus.

Results

Among the 23 African samples, the majority of HHV-8 ORF 26 variants clustered with the subtype R (n=12) and B (n=5). Conversely, the viral sequences obtained from 45 European and North European tumors belonged mainly to subtype A/C (n=36). In general HHV-8 and K1 variant clustering paralleled that of ORF

26 and T0.7. Genotyping of the K14.1/15 loci revealed a large predominance of P subtype in all tumors.

Conclusions

Although the virus has genetic regions of high variability, approaching that of HIV-1 env gene, the HHV-8 subtypes remained stably distributed before and after the AIDS epidemic. These results suggest that the increased incidence of epidemic KS in low-incidence countries was not related to the spreading of high pathogenic HHV-8 variants, furthermore, suggest the presence of other cofactors in high risk KS countries pre-existing in pre-AIDS era [1].

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