NOTES

Human Papillomavirus Type 27: Detection of a Novel Human Papillomavirus in Common Warts of a Renal Transplant Recipient

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The cloning and partial characterization of the genome of human papillomavirus type 27 (HPV-27) is described. Hybridization analyses reveal that this is a new HPV type, with the strongest homology to HPV-2.

While screening a common hand wart from a renal transplant patient for human papillomavirus (HPV) DNA under low-stringency conditions, a novel type of HPV was identified and molecularly cloned into a bacteriophage Charon 27A vector by partial cleavage of the cellular DNA with *Bam*HI.

found within the subcloned small *Bam*HI fragment [Fig. 1]), and hybridization of subgenomic fragments with other HPV DNAs (Fig. 1). Some filter hybridization under stringent conditions was observed with most of the HPV-2 genome and also with a fragment of HPV-6 DNA from the L1 open

FIG. 1. Restriction endonuclease map of HPV-27. A series of restriction endonucleases was mapped on HPV-27 as indicated. Below the map are the open reading frames of HPV-5 which have been aligned with those of HPV-27 by hybridization under low-stringency conditions with HPV-5 and by sequence analysis of the indicated *Hpa*II fragment. Restriction endonuclease fragments are labeled alphabetically according to size, with the approximate number of nucleotides indicated.

By S1 nuclease analysis, this new HPV species, HPV type 27 (HPV-27), was found to hybridize less than 50% to all previously characterized HPV DNAs, but it was most closely related (20%) to HPV-2. We further characterized this species by restriction endonuclease analysis, partial nucleotide sequence analysis (647 bases of a *Hpa*II fragment

reading frame. This latter observation was probably due to the highly conserved nature of the sequences in this region. On the basis of this analysis, the genome was aligned as shown (Fig. 1) with the open reading frames of the complete HPV-5 genome for reference.

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