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Human Papillomavirus Type 29 (HPV-29), an HPV Type Cross-Hybridizing with HPV-2 and with HPV-3-Related Types

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The cloning and partial characterization of human papillomavirus (HPV) type 29 is presented. By hybridization analyses, this virus appears to be related to HPV types associated with common warts and HPV types associated with flat warts.

A human papillomavirus (HPV) DNA with a unique restriction endonuclease cleavage pattern was identified by agarose gel electrophoresis and ethidium bromide staining in the DNA preparation obtained from a skin wart. The genome of this HPV, named HPV type 29 (HPV-29), was cloned in *Escherichia coli* after insertion in plasmid pBR322, using its unique *Bam*HI cleavage site. Blot hybridization experiments, performed under stringent conditions, revealed significant cross-hybridization only between the genome of HPV-29 and the DNAs of HPV-2 and of three related types, HPV-3, HPV-10, and HPV-28. The extent of DNA sequence homology between HPV-29 and types 2, 3, 10, and 28 was determined to be 8, 15, 18, and 17%, respectively, by hybridization in liquid phase at saturation, followed by nuclease S1 analysis (2). Under these conditions, HPV-3, HPV-10, and HPV-28 DNAs showed only a 3% cross-hybridization with HPV-2 DNA. The physical map of HPV-29 was aligned with those of HPV-2 (1) and HPV-3 (2) (Fig. 1), by electron microscopic analysis of heteroduplex molecules formed at T_m − 19°C. From the mapping of duplex segments shown in Fig. 1, it appears unlikely that HPV-29 derives from the genetic recombination of HPV-2 and HPV-3. HPV-29 was not found in cutaneous wart specimens from 119 patients, including 43 butchers and 20 immunosuppressed patients. In conclusion, HPV-29 appears to be an uncommon HPV, phylogenetically related both to HPVs inducing common warts (HPV-2) (3) and to those inducing flat warts (HPV-3, HPV-10, and HPV-28) (2).

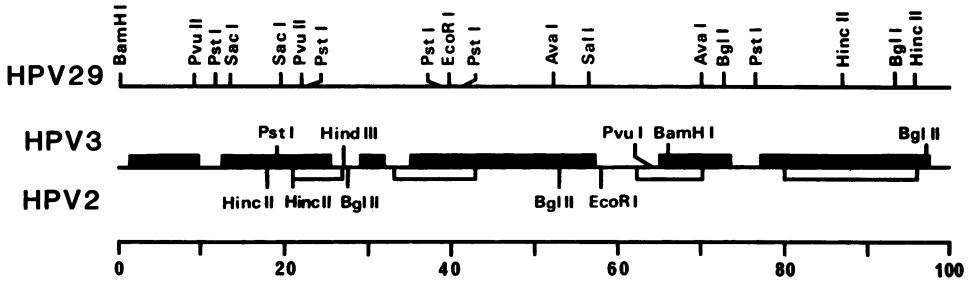

FIG. 1. Physical map of HPV-29 DNA and alignment of the HPV-29 map with HPV-2 and HPV-3 maps. The unique *Bam*HI site has been taken as the origin of the HPV-29 DNA map. The endonucleases that do not cleave HPV-29 DNA are *Bgl*II, *Hin*dIII, *Hpa*I, *Pvu*I, and *Sma*I. The mapping of duplex segments formed at T_m − 19°C between HPV-29 and HPV-2 DNAs (□) and between HPV-29 and HPV-3 DNAs (■) is indicated on the simplified maps of HPV-2 and HPV-3 (1, 2), as aligned with the HPV-29 map.

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LITERATURE CITED

1. **Heilman, C. A., M. F. Law, M. A. Israel, and P. M. Howley.** 1980. Cloning of human papilloma virus genomic DNAs and analysis of homologous polynucleotide sequences. J. Virol. **36**:395–407.
2. **Kremsdorf, D., S. Jablonska, M. Favre, and G. Orth.** 1983. Human papillomaviruses associated with epidermodysplasia verruciformis. II. Molecular cloning and biochemical characterization of human papillomavirus 3a, 8, 10, and 12 genomes. J. Virol. **48**:340–351.
3. **Orth, G., M. Favre, and O. Croissant.** 1977. Characterization of a new type of human papillomavirus that causes skin warts. J. Virol. **24**:108–120.