

HPV16 mRNAs ending at the late polyadenylation site in differentiated W12 cells

Transcription map of HPV16 late genes deduced from W12 cells (1). The life cycle of human papillomavirus type 16 (HPV16) is intimately linked to differentiation of the epithelium it infects, and late events in the life cycle are restricted to the suprabasal layers. Here we have used 5' RACE of polyadenylated RNA isolated from differentiated W12 cells (cervical epithelial cells containing episomal copies of the HPV16 genome) that express virus late proteins to map virus late mRNAs. Thirteen different transcripts were identified. Extensive alternative splicing and use of two late polyadenylation sites were noted. A novel promoter located in the long control region was detected as well as P97 and Plate. Coding potentials for each RNA species are shown on the right.

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1. Milligan, S.G., Veerapraditsin T., Ahamet, B., Mole, S. and Graham, S.V.

Analysis of novel human papillomavirus type 16 late mRNAs in differentiated W12 cervical epithelial cells. (2007) *Virology* 360:172–181.