

HPV16

HPV16 mRNAs isolated from transfected cells and a variety of tumor cell lines and lesions containing both extrachromosomal and integrated HPV-16 genomes have been analyzed in multiple laboratories (2,3,5-8). Viral/host chimeric mRNAs have been purposely omitted. All nucleotide positions correspond to the revised HPV16 sequence published in Part I of the 1995 compendium. Most mRNA species were determined by RT-PCR, so the identity of the 5' and 3' ends are not known. However, at least two promoters have now been identified for HPV-16. One promoter (P₉₇) is active in cervical cancers and cervical cancer-derived cell lines as well as in monolayer and organotypic raft cultures containing extrachromosomal HPV-16 DNA (3,9). Species A–K are most likely transcribed from this promoter. A differentiation inducible promoter (P₆₇₀) has been identified by analysis of RNA obtained from organotypic raft cultures containing extrachromosomal HPV-16 DNA (3). This promoter has a major start site mapped by primer extension analysis to around nt 670 and minor start sites at nt 693, 706, 713, and 766. It is likely that the E1^{E4} mRNA (transcript L) is transcribed from this promoter. In addition, *in situ* hybridization analyses have suggested that the most abundant transcripts in intraepithelial neoplasias and invasive cancers are transcribed from this promoter (1). An additional differentiation inducible promoter may also exist with a start site around nt 480 (3). The promoter responsible for the transcription of the late mRNAs (species O–P) is not known. The early and late polyadenylation signals are located at nt 4215 and nt 7321, respectively (4,5).

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Extracted from:

Maps of Papillomavirus mRNA Transcripts

1995, 1996 and 1997 LANL Human Papillomavirus Database

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