HPV11

HPV11 mRNAs, isolated from genital condyloma acuminata and experimental condylomatous cysts implanted under the renal capsules of nude mice, have been analyzed by several laboratories (1,2,4,6,7). HPV11 mRNAs expressed in cultured cells derived from laryngeal papillomas and expressed from transiently replicating HPV11 genomes in SCC-4 cells have also been analyzed (3,5). The types of analyses include cDNA cloning (species A), electron microscopy analysis of R-loops (species A–D, G, I, Q–S), and RT-PCR analysis (species C–G, I–P, R). The deduced mRNA structures are presented in the HPV-11 map. The 5' ends of most mRNAs have not been mapped at the nucleotide level. However, three promoters have been mapped by Smotkin et al. (8) using nuclease S1 analysis: the E6 promoter initiates at nt 90, the E7 promoter at nt 264, and the E1 promoter at nts 674–714. Dilorenzo and Steinberg (3) used an RNAse protection assay to confirm the locations of the E6 and E7 promoters, but mapped a slightly broader distribution of 5' ends from the E1 promoter to nt 677–726. In addition, they showed that the E1 promoter is differentiation specific. Renaud and Cowsert (5)used a modified RACE procedure to map a 5' end slightly further downstream to nt 743. The 5' end of the cDNA representing species A is located at nt 716 (4), so this mRNA is presumably transcribed from the E1 promoter. Renaud and Cowsert (5) also used 5' RACE to map additional 5' ends to the vicinity of nt 1374 (species E, K, O), suggesting that there may be an additional promoter in this region. The early poly(A) site has been identified from analysis of species A cDNAs; poly(A) addition sites were found at nt 4388, 4390, and 4392 (4). The late poly(A) site has not been identified experimentally, but the L1 and L2 mRNAs are presumably polyadenylated utilizing the poly(A) signal at nt 7457.

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Extracted from:

Maps of Papillomavirus mRNA Transcripts

1995, 1996 and 1997 LANL Human Papillomavirus Database

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