BPV1

BPV1 has served as the prototype for the genetic analysis of the papillomaviruses. The mRNAs from BPV1 transformed C127 cells as well as productively infected bovine fibropapillomas have been exhaustively analyzed. The top of the BPV1 map shows the genomic organization of BPV1. The long control region is labeled and, in order to show the position of promoters, is repeated to the left of nt 0. The locations of known promoters (3,5-7,9) are indicated by arrows and labeled P_n where n is the approximate nucleotide position of the RNA start site for that promoter. P_{7185}, P_{89}, P_{890}, P_{2443}, and P_{3080} are also referred to as P_1, P_2, P_3, P_4, and P_5 (5,6) respectively. The late promoter (P_L) is the major promoter active in the fibropapilloma and is the only promoter not active in C127 cells transformed by BPV1 (3). The early and late polyadenylation signals are at nt 4180 and 7156, respectively. The structures of BPV1 mRNAs from BPV1 transformed mouse C127 cells (species A—Q) were determined by cDNA cloning as well as electron microscopy, nuclease protection, PCR, and primer extension. The 5' most ORF containing a translation initiation codon and a significant coding region is indicated at the right of each mRNA. Although an E6/E7 fusion ORF is the 5' most ORF for species I, the cDNA from which this structure was deduced has been shown to encode the E1 M protein (8). Additional very rare mRNA species from cycloheximide treated BPV1 transformed C127 cells have been characterized (5), but are not shown here. The structures of mRNAs unique to the BPV1 fibropapilloma (species R–X) were determined by RT-PCR and cDNA cloning and sequencing (3,4). Although the E2 and E4 ORFs are the first significant ORF for species W and X, these mRNAs may also encode the L2 protein. A more detailed discussion of BPV1 transcription can be found elsewhere, including references for each mRNA (1,2).

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Extracted from:

Maps of Papillomavirus mRNA Transcripts

1995, 1996 and 1997 LANL Human Papillomavirus Database

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