 

# Nucleotide sequence of HSUR 6 and HSUR 7, two small RNAs of herpesvirus saimiri

J.-C.Albrecht and B.Fleckenstein
Institut für Klinische und Molekulare Virologie, Friedrich-Alexander Universität Erlangen-Nürnberg, Loschgestraße 7, 8520 Erlangen, Germany

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Herpesvirus saimiri is a common virus of the squirrel monkey (*Saimiri scuireus*); it induces fatal lymphoma and leukemia in various other species of New World primates and transforms human and monkey T-lymphocytes to continuous growth in cell culture (1). The leftmost 5.5 kbp of genomic L-DNA have been shown to encode a set of five small RNAs, the first viral U-RNAs (HSURs) described to date (2–4). They are related to each other, but different from small RNAs of other viruses, and they are distinct from any previously characterized cellular U RNAs. We determined the nucleotide sequence of the region adjacent to that encoding HSUR 1–5 and found two additional genes for viral U RNAs, HSUR 6 and HSUR 7. The genes have characteristic, U RNA specific transcription control regions including enhancer octamer motifs, snRNA TATA boxes, and 3′-end formation signals, which are comparable to those found in cellular U RNA genes.

Total RNA from the marmoset T cell line 1670, which had been transformed by herpesvirus saimiri, was analysed by primer extension experiments for expression of predicted U RNAs. The conserved 3′-end regions of the transcripts have been used to design oligonucleotides as primers specific for HSUR 6 and HSUR 7 (Figure 2). Complementary DNA molecules synthesized were found to be 81 nucleotides (nt) and 75 nt, respectively, in length (Figure 1). This is in agreement with the expected size derived from sequence analysis. Computer assisted searches did not reveal any other HSUR sequences within the genome of herpesvirus saimiri which has been completely sequenced recently.

The function of the HSURs is not known. It has been supposed that they may contribute to T cell transformation. HSURs are encoded in the genomic region required for oncogenicity and they are the most abundant transcripts detected in transformed cells. The 5′-ends of HSUR 1, 2, and 5 have sequences identical to the AUUUA motif which directs mRNAs of several proto-oncogenes, cytokines, and lymphokines for prompt degradation. This suggests that some of the HSURs may alter the degradation process of certain cellular mRNAs, thereby assisting viral transformation (5).

## REFERENCES

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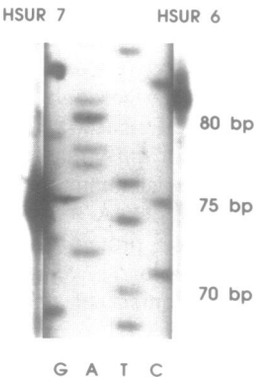


**Figure 1.** Expression of HSUR 6 and HSUR 7 in 1670 cells. Primer extension samples were run on 6%-polyacrylamide gels. A sequencing reaction run in parallel has been taken as marker.

| | | sm-site | | stem | | loop | stem | |
|---|---|---|---|---|---|---|---|---|
| HSUR 1 (143 nt) | ... | AUUUUUG | UA | GGUACUGG | | .GU.GU.....AAAUA..UGAUGA | CCGGUACC | A |
| HSUR 2 (115 nt) | ... | AUUUUUG | AA | AGCGCUGG | | .GU.GU.....ACAUAUUUAAAAA | CCAGCGCU | G |
| HSUR 3 ( 76 nt) | ... | AUUUUUG | AA | GGCUCUGG | | .GUCUU....UAGGU....CCAAA | CCAGUGCC | A |
| HSUR 4 (106 nt) | ... | AUUUUUG | AA | GGCUCUGG | | GGUAGU.............CCAAA | CCAGUGCC | A |
| HSUR 5 (114 nt) | ... | AUUUUUG | GA | GGCAAUGG | | UGU.GUGAC.........UAACAA | CCAGAGCC | G |
| HSUR 6 ( 81 nt) | ... | AUUUUUG | GA | GGCUCUGG | | .GA.AUG...UAAG....UAUAAC | CUAGAGCC | A |
| HSUR 7 ( 75 nt) | ... | AUUUUUG | GA | GGCACUAG | | .GUACUUAGGCAAACUUAGGGAAA | CUAGUGCC | A |

**Figure 2.** Alignment of 3′ termini of herpesvirus saimiri U RNAs (HSURs). The 3′ end of HSUR 6 and HSUR 7 was deduced from the 3′-end consensus sequence of HSUR 1–5. Oligonucleotides complementary to the underlined sequences were used for transcript specific priming during cDNA synthesis. The length of HSUR transcripts is indicated in brackets and only sequences downstream the sm-binding site are shown. The sm-binding site and the stem-loop structure building inverted repeats are boxed.