## Nucleotide sequence of HSUR 5 RNA from herpesvirus saimiri

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Herpesvirus saimiri, a lymphotropic virus of New World primates, encodes a set of U snRNAs that can be precipitated from transformed T cell extracts by anti-Sm and anti-m<sub>3</sub>G antibodies. These RNAs have been named HSURs for herpesvirus saimiri U RNAs. HSURs 1-4 have recently been characterized (1). Here we present the nucleotide sequence of another herpesvirus saimiri U RNA called HSUR 5. Northern blots probed with the sequences containing the viral gene, located on the BgIII (nucleotide 2851) to HindIII (nucleotide 3490) fragment of the herepesvirus saimiri strain 11 L DNA (2), identify three forms of HSUR 5 that are 111, 113, and 114 nucleotides in length. All three HSUR 5 RNAs can be immunoprecipitated by monoclonal antibodies against the Sm protein determinant as well as by antibodies specific for the m<sub>3</sub>G cap structure found on the 5' end of most U RNAs. The sequence of HSUR 5 was determined, as for HSURs 1-4 (1), by analyzing the terminal nucleotide sequences and aligning them with the known herpesvirus saimiri genomic sequence (Murthy, Trimble and Desrosiers, manuscript in preparation). The 5' ends were found to be heterogeneous by Maxam-Gilbert sequencing of the three reverse transcription products from a deoxyoligonucleotide primer that hybridizes approximately 20 nucleotides away from the 5' end of HSUR 5. The 3' end of one of the HSUR 5 RNAs was determined by enzymatic RNA sequencing of hybrid selected RNA. The final 3' nucleotide was identified by thin layer chromatography of a complete T<sub>2</sub> RNase digest of <sup>32</sup>pCp-labeled RNA. The heterogeneity at the 5' end can account for the size difference in the HSUR 5 RNAs determined by northern blots. It is not known whether the 5' heterogeneity is due to transcription of different HSUR 5 genes or different transcription initiation sites within a single HSUR 5 gene.



Figure 1. Sequence and Genomic Location of HSUR 5

HSUR 5 is depicted in a possible secondary structure with the putative Sm binding site boxed. Nucleotides shared with HSURs 1-4 near the 3' end are indicated by capitals; sequences shared with HSUR 1 and HSUR 2 at the 5' end are designated by the stippled bar. Arrows indicate the 5' terminal nucleotides of the HSUR 5 RNAs. The shortest RNA (marked by the bold arrow) is the most abundant HSUR 5 RNA according to northern blot and primer extension analyses. The location the the HSUR genes on the herpesvirus saimiri genome (2) is shown below.

## **References**

 Lee, S. I., Murthy, S. C. S., Trimble, J. J., Desrosiers, R. C., and Steitz, J. A. (1988). Cell 54, 599-607.
Murthy, S., Kamine, J., and Desrosiers, R. C. (1986). EMBO J. 5, 1625-1632.