

Herpesvirus saimiri U RNA sequence variation

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Herpesvirus saimiri, a tumorigenic, lymphotropic virus of New World primates, expresses a set of five viral U RNAs (HSURs) in tumor tissue (1, 2, 3). HSURs can be immunoprecipitated by anti-Sm and anti-m₃G antibodies and contain stem-loop structures (2). HSURs are expressed from U RNA specific control regions (enhancer, snRNA TATA box, and 3' end formation signals) similar to consensus human U RNA control regions (2). The HSUR genes are located in the leftmost variable region of unique viral DNA (L-DNA) which is associated with the oncogenic potential of h. saimiri (4). Using polymerase chain reaction (PCR), HSUR genes were identified in nine h. saimiri strains. Some PCR amplified HSUR DNAs were cloned and sequenced and then compared to the previously published HSUR sequences of strains 11 and 488 (2, 3, 4, 5). Nucleotide substitutions relative to the strain 11 sequence are shown in the figure below. Dashes indicate deletions. Important features of the sequence are underlined and labeled. The primer sequences

used for amplification from the ends are also indicated. The Sm binding site (AT₃G), stem loop structures, and polyA signal complement (HSUR1) are conserved. These new HSUR sequences are likely to be representative of group A isolates since the primers used were based on strain 11. The new HSUR sequences are clearly more closely related to the group A strain 11 HSUR sequences than to those recently published for the group C strain 488 (5).

REFERENCES

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HSUR 1

strain	snRNA TATA box/primer	30	40	50	60	5' end RNA	poly A signal complements	110	120
11	<u>ITACCTAACTAAAACAGT</u> TTGCCTTTTGAAGACTAGTCAATAGAGCTGCTAAAGTACACTACATAIIIIIIIIIIIICTTAGTAACTTTACTGGAACTTAAATCTGTGATA								
24-76		T		G C					
488-77P		T	C	A					

strain	130	140	150	Sm binding stem	190	stem	5' end RNA	3' end signal/primer
11	ACCTAACTAAAAGTCTCAACACAC-CCGTTACTTGCTGACCA <u>ATIIIIIGTAGGACTGGGTGTAATATGA</u> --TGACCGGTACCATCTAAGTAA <u>GTTAAAAGTAGA</u>							
24-76	T--			A			AA A A G C	
488-77P	C	T		A G G			AC A A G C	

HSUR 3

strain	snRNA TATA box/primer	30	40	50	60	5' end RNA	80	90	Sm binding stem
11	<u>CTTACCTAACTAAATATAGATAGTGTATATGTTAT-<u>AAACAATAGCATGATATATTAAGACTTGCTATAGGAGATTACACCCAGGATATATIIIIIGTAGGCTCTGG</u></u>								
24-76				T	CA		AA		
488-77P		AG		T	CA		A C		
ONI				T	CA		AA		

strain	120	stem	5' end RNA	3' end formation signal/primer
11	GTCTTAGGTCCAAC <u>CCAGTGCCACCTT</u> AGAG <u>TTAAAACAGA</u>			
24-76			T	
488-77P		C	T	
ONI			T	

HSUR 4

strain	snRNA TATA box/primer	30	40	50	60	m ₃ G cap	80	90	100
11	<u>ACTTACTATACTTAAAGGAGGATTATTTTTACTTAAAGTAACAACTTGAACAGAGACTGCCAGAGCCAGAGGTTACTCTTCAGGTT-CATACAGTTGGAGC</u>								
24-76				TG	GT	----		T	A
ONI				TG	AGT	----		T	A

strain	110	120	130	Sm binding stem	160	stem	5' end RNA	3' end formation signal/primer
11	TTCTCAGTTTCAGAGCCTCAGCA <u>ATIIIIIGTAGGCTCTGGG</u> TAGTCCAA <u>CCAGTGCCACTTAGTAA</u> <u>GTTAAAACAGA</u>							
24-76			T	T			TT	
ONI				T		C	TT	