ABSTRACT

TITLE:	Determination of the HTLV-1 Pro-Pol Frameshift Site Secondary Structure
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ABSTRACT: Human t-cell leukemia virus type 1 (HTLV-1) is a retrovirus that targets CD4+ T-cells in humans. Expression of human t-cell leukemia virus type I (HTLV-I) enzymes requires two -1 programmed ribosomal frameshifts (PRFs). These events occur between the gag-pro and pro-pol open reading frames. Each frameshift site includes a heptanucleotide slippery sequence followed by a downstream structure, which act in cis to produce specific frameshift efficiencies. While the -1 PRF and slippery sequences of these frameshift sites have been established in HTLV-I, the secondary structures have not been determined. In the pro-pol frameshift site, an RNA pseudoknot is predicted to fold downstream of the UUUAAAC slippery sequence. However, no structural data exists for this RNA. Here, we report a preliminary structure of the HTLV-1 pro-pol frameshift site RNA. Nucleotide reactivity data acquired from selective 2'-hydroxyl acylation experiments analyzed by primer extension (SHAPE) is consistent with a pseudoknot secondary structure. These results suggest the existence of a pseudoknot structure in the HTLV-1 pro-pol frameshift site.