



Novel transcripts of human cytomegalovirus clinical strain found by cDNA library screening

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ABSTRACT. Human cytomegalovirus (HCMV) is a double-stranded DNA virus with the largest genome (~235 kb) of the known human herpes viruses. The coding potential and transcript structures of most HCMV predicted genes have not been identified. New or unknown genes could exist in clinical strains. The SMART (switching mechanism at 5' end of RNA template of reverse transcriptase) technique was used to construct a full-length cDNA library of an HCMV clinical strain in the late expression phase. Randomly selected clones were sequenced. The sequenced expressed sequence tags were used to identify the expression and transcript structures of some predicted and unpredicted genes of HCMV. The transcripts of the UL99, TRIL5/IRL5, UL73 to UL75, UL4, and UL115 genes, which were previously detected, were obtained with full-length structures from this library. Some novel transcripts, including several transcripts of UL/b' genes and three antisense transcripts of UL83, UL87 and UL31 were found. The novel transcripts that were found, particularly the antisense transcripts of UL83, UL87 and UL31, showed that the transcription of HCMV genes is more complex than previously predicted. Our study highlights the

usefulness of the full-length cDNA library for discovering new genes and transcripts of HCMV.

Key words: Human cytomegalovirus; Full-length cDNA library; Novel transcripts; Antisense transcripts