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Structure characterization of human cytomegalovirus UL131A, UL130 and UL128 genes in clinical strains in China

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ABSTRACT. Human cytomegalovirus (HCMV) genetic determinants of endothelial cell tropism, leukocytes and dendritic cells have been identified in the genes UL131A, UL130, and UL128. We examined the structure of these three genes in HCMV. Eighteen low-passage clinical isolates and five non-passage strains from congenitally HCMV-infected infants in China were used to assess the structures of the UL131A, UL130, and UL128 genes and to find possible relationships between sequence polymorphism and different signs of HCMV disease. Comparisons were made between the UL131A, UL130, and UL128 genes of clinical strains and published sequences of Towne and Merlin strains. The UL131A coding region in the clinical strains was similar to that of Towne and Merlin strains, while UL130, and UL128 coding regions in the clinical strains were parallel with those of Towne and Merlin, respectively. Sequence comparison indicated that the UL130, and UL128 genes encode chemokine-like proteins in the clinical strain; the transmembrane regions of UL131A, and UL130 were conserved in all clinical and reference strains. The three genes of clinical strains from infants with different signs of HCMV disease had similar structure characterization. We conclude that the UL131A, UL130, and UL128 genes are highly conserved in these clinical strains. No correlation was found between the

structure of the three genes and variations in HCMV disease. The finding of chemokine-like domains in UL130, and UL128 putative proteins suggests that the predicted products play a role in HCMV infectivity.

Key words: Human cytomegalovirus; Structure characterization; UL131A, UL130, and UL128 genes

