DNA NUCLEOTIDE SEQUENCE DIVERGENCY IN CLINICAL ISOLATES OF HUMAH CYTOMEGALOVIRUS

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The analysis of epidemiological aspects of virus infections requires a reliable and convenient methods for genetic comparison of clinical isolates. Being used for amplification of virus DNA sequences from clinical samples, the method of polymerase chain reaction (PCR) appears to be ideal for molecular detection of different virus strains. We have compared several clinical isolates of cytomegalovirus (CMV) using of PCR. With this aim the same amplicon from different sources has been sequenced [1].

The amplicon contains both a conservative structural part and a 3'-untranslated one of MIE (Major Immediate Early) gene of CMV. Being compared with well known laboratory strains, Towne and AD169, all seven independent samples contain 2–3 substitutions within the 119 bp fragment of structural part and 1–2 substitutions or deletions or insertions within 98 bp fragment of 3'-untranslated part of MIF gene.

On one side the data show a great divergency of virus DNA. On the other side the divergency seems to be suitable for epidemiological analysis. The possibility of infection of one person by several virus strains has been demonstrated. Taking together, all the data describe the scheme of genesis for molecular markers of human CMV.

REFERENCES

1. *Vinogradskaya G.R. et al.* Reports of Academy of Sciences (Russia), 1992. V.325. N°6. P.1234–1237.