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Tiivistelmä — Referat — Abstract <p>The sequences of the genomic S, M and L segments encoding the nucleocapsid N protein, the surface glycoproteins G1/G2 and the polymerase L protein of numerous hantaviruses have been determined. Hantavirus phylogenetic relationship based on the comparison of their genomic sequences has shown to be correlated with several factors: 1) host species, 2) geographic locations of hantaviruses isolated, 3) host individuals infected by hantaviruses, etc. Hantaviruses seem to have evolved from a common ancestor because of their genomic homologies. Hantavirus evolution is fast like other RNA viruses. Heterogeneity exists not only between different genotypes and different strains, but also exists between virus particles from the same host individual (quasispecies). Reassortment was found only between closely related hantavirus strains, but not between different genotypes. By analyses of the sequences of S segment, it has been found that the long 5'NCR (genomic sense) is very variable in length and in sequence by comparison of different hantavirus genotypes and far related strains, however, it's rather consensus by comparison of closely related hantavirus strains isolated in the same locations. The function of NCR is still unclear, it was supposed to be that NCR regulates hantavirus transcription and/or replication through some specific sequences of motifs and/or certain secondary structure in viral RNA level. The study of Puumala virus adaption from bank vole to Vero E6 cells shows adapted viruses contain several mutations in NCRs, none in coding region. This finding demonstrates that NCRs are crucial for virus replication and/or transcription.</p>			
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