
Analiza uwarunkowań genetycznych wrodzonej naczyńniakowatości krwotocznej choroby Rendu-Oslera-Webera - doniesienia wstępne

Analysis of molecular background of hereditary haemorrhagic telangiectasia - Rendu-Osler-Weber disease - preliminary results

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Introduction. Hereditary haemorrhagic telangiectasia (HHT) known also as Rendu-Osler-Weber syndrome is an autosomal dominant disorder characterized by localized angiodysplasia due to mutations in *ENG* (endoglin, 9q34.1) or *ALK-1* gene (the activin receptor-like kinase 1, 12q13). *ENG* and *ALK-1* are found associated with two disease subtypes designated as HHT1 and HHT2, respectively. Subtype HHT1 remains in the frame of interest of laryngology because of frequent bleeding in head and neck region. **Material and method.** The study was designed to identify a genetic background in a large family (29 individuals) with diagnosed HHT. Pedigree analysis showed autosomal dominant pattern of inheritance. Study design comprised segregation analysis to determine locus with subsequent direct sequencing of the gene. Four microsatellite markers (d9s61, d9s65, d12s368, d12s347) with high frequency of heterozygosity in population study were used. **Results.** The results concerning heterozygosity ranged from 15% to 53%. The established differences were not sufficient enough to indicate co-segregation of the studied loci. DNA sequence analysis in exon 11 of *ENG* gene did not reveal mutations. The latter result could be explained by an occurrence of mutations in other exons of *ENG*. **Conclusions.** The study requires continuation for gene identification and precise genotype-phenotype correlation aiming for an improvement of HHT1 therapy.