Jednostránkový souhrn v angličtině

Crohn's disease (CD) has been shown associated with the variants in *NOD2, ATG16L1* and *IL23R* genes, in the IBD5 locus as well as in other genes involved in the immune response. The frequencies of the variants profoundly differ among populations and so does the associated risk. Moreover, the role of the IBD5 locus and *CTLA4* gene in development of Crohn's disease has not been clarified.

We examined the associations of variants in the *NOD2*, *ATG16L1*, *IL23R*, *TNFA* and *PTPN22* genes and variants in IBD5 and *CTLA4* chromosomal regions with pediatric-onset and adult-onset CD in the Czech population. The genotype, phenotype, and allelic frequencies were compared between 469 unrelated patients with CD and 470 unrelated healthy controls. The strongest association with CD was found in *NOD2* gene (three variants), followed by two variants in IBD5 locus (IGR2063b_1, rs6596075), weaker association with variant in *IL23R* and *ATG16L1* genes, while no independent association was found for the p.R620W variant in the *PTPN22* gene or for the g.2308G>A variant in the *TNFA* gene. We have reported a high frequency of the minor allele of the *NOD2* 1007fs polymorphism in the Czech population and a strong effect of this allele on the age at diagnosis and ileal form of disease. Our study confirms the importance of IBD5 in determining CD susceptibility, and demonstrates that two independent genetic factors may be responsible for the association observed within this locus. A protective effect of a *CTLA4* haplotype was unmasked after stratification for the risk variants in the *NOD2* and *IL23R* genes, and may point towards the biological relevance of the molecule in the pathogenesis of the disease. No genetic predictors of infliximab dependency have been found.

We described association of main genetic factors that contribute to development of CD in the Czech population. We also documented an association of two independent variants on IBD5 locus and found possible interaction of *NOD2* and *IL23R* genes with *CTLA4*.