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Associations of single nucleotide variants of the *FTO* gene with metabolic disorders in children with obesity

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Abstract

Background: Single nucleotide variants (SNV) of the gene associated with fat mass and obesity (*FTO*) make a significant contribution to the violation of energy metabolism and the development of obesity. **Aim:** study of associations of SNV of the *FTO* gene with the development of metabolic disorders in children with obesity.
Materials and methods. 252 obese children aged 6-18 years were examined. The main group (n=152) was represented by children with metabolically unhealthy obesity (MUO). The control group (n=100) consolidated of children with metabolically healthy obesity (MHO). Whole genome sequencing (CeGat, Germany) was performed in 31 children of the main and 21 children of the control group.
Results: The association with the development of obesity is higher for the A allele rs2287142 (t=2.29) and the T allele SNV rs17823223 (t=6.34) than in healthy individuals. Serum IL-6 level in MHO depends on SNV rs2287142 (r=0.73). Allele A of SNV rs1080312 is associated with basal hyperglycemia (r=0.43) and impaired carbohydrate tolerance (r=0.33). The T allele of SNV rs778691805 is associated with a high level of low-density lipoprotein cholesterol in blood serum (r=0.33). The T allele of SNV rs17823223 directly correlates with high-density lipoprotein cholesterol (r=0.33), $p<0.05$.
Conclusions. In obese children, SNV rs2287142 is associated with pro-inflammatory status, and SNV rs1080312, rs17823223, rs778691805 of the *FTO* gene is associated with metabolic markers.
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Keywords: single nucleotide variants, gene associated with fat mass and obesity, obesity, children.