Association of 8 SNPs with metabolic changes in type 2 diabetes mellitus in the Kazakh population

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Introduction: The steady growth of patients with type 2 diabetes mellitus (T2D) in the Republic of Kazakhstan over the past decade indicates the need to develop a program for the prevention of T2D. A change in the expression of candidate genes can lead to impaired insulin synthesis, a decrease in the number of insulin receptors, β-cell dysfunction, and obesity. The purpose of this study is to analyze the association of the SNPs with biochemical and anthropometric parameters of T2D in representatives of the Kazakh population.

Materials and methods: In total, 139 patients with T2D and 100 randomly selected patients with no signs of disease were registered in the current study. Cases of T2D are diagnosed based on World Health Organization criteria. The samples were ethnically homogeneous and included only the Kazakhs. The biochemical (total cholesterol, LDL, HDL, glucose and HOMA-IR index) and anthropometric indicators were evaluated.

Statistical processing of the results was carried out using the software package: MS Office Excel 2013, STATISTICA v. 6.0. Differences were considered significant when $p \leq 0.05$.

Results: Two of the tested loci (rs7901695 and rs7903146 in the TCF7L2 gene) showed statistically significant associations with T2D. The TCF7L2 gene is involved in the processes of adipogenesis, differentiation of adipose tissue, and in the regulation of pancreatic β-cells development and functioning. A statistically significant relationship was found between rs7901695 and rs7903146 in the TCF7L2 gene and indicators of glucose metabolism, lipid spectrum and BMI. Insulin resistance is a major factor in the development of T2D. The study found associations of hyperglycemia, high levels of LDL, hypertriglyceridemia and a decrease in HDL with genetic markers rs2237892 in the KCNQ1, rs7756992 and rs7754840 gene in the CDKAL1 gene in patients with T2D. The fact that these genes are active in β-cells confirms the notion that β-cell dysfunction is fundamental in the pathogenesis of T2D.

These results suggest that in the Kazakh population, these polymorphisms are associated with an increased risk of developing T2D through β-cell dysfunction, regardless of obesity. Thus, based on the results, it can be concluded that in the Kazakh population, the leading role is played by polymorphisms that affect the level of synthesis and secretion of insulin in pancreatic β-cells.

Biography

Almagul Nagimtaeva has the experience as a doctor - genetics, improved her skills in conducting differential syndromic diagnostics, methods of medical and genetic counseling for pregnant women and families at risk of hereditary and congenital pathologies. Along with clinical activities, research work was carried out. The study of a genetic predisposition is important, as it provides an understanding of the potential mechanisms related to the early stages in the pathogenesis of multifactorial diseases. The implementation of the scientific research results will ensure a decrease in mortality rates and growth in survival rates by increasing the effectiveness of early diagnosis and personalization of treatment and will make a significant contribution to the development of healthcare in the Republic of Kazakhstan.

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