

The role of xenobiotic enzyme genes in predicting fetal loss syndrome in Uzbekistan

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Introduction: Fetal loss syndrome is a multifactorial disease characterized by a universal integrated response of the female body to any ill health in the pregnant woman, the fetus and the environment, the result of the action of functionally weakened variants (alleles) of many genes against the background of adverse external and internal factors. Glutathione-S-transferase (GST) metabolizes foreign substances or controls the entry of carcinogens into cells.

Aim: The goal of our research was to establish the role of the polymorphic variants of the xenobiotic enzymes genes *GSTM1* and *GSTT1* and *Ile 105Val* of the gene *GSTP1* in the mechanism of formation and development of fetal loss syndrome.

Material & Methods: Molecular genetic studies were conducted in 114 pregnant women aged from 20 to 45 years old. Molecular genetic examination of biomaterials (DNA) was performed at Department of Molecular Medicine and Cellular Technologies of the Research Institute of Hematology and Blood Transfusion of the Ministry of Health of the Republic of Uzbekistan. Statistical analysis of the results was carried out using the statistical software package "OpenEpi 2009, Version 2.3".

Results: The results of molecular genetic studies in pregnant women with Fetal Loss Syndrome (PPS) showed an increased detection rate of combined functionally defective genotypes *GSTM10/0+GSTT10/0* - 25.4%, against the control group 4.1% ($\chi^2=12.4$; $P=0.0004$; $OR=7.8$; 95% CI 2.146-28.65). Whereas, with the combined variants - the null and functional genotypes of the polymorphism of the *GSTM1* and *GSTT1* genes between the studied groups did not reveal statistically significant differences ($\chi^2=0.1$; $P=0.3$; $OR=1.4$; 95% CI 0.697-282; $p>0.05$). Whereas, the distribution of genotypes *Ile 105 Val* of the *GSTP1* xenobiotic enzyme in pregnant women revealed a high detectability of A/G genotype polymorphism in the pregnant group compared to the control group 56.1% versus 19.4%, which was 2.9 times higher than the control groups. Thus, an analysis of the association of genic combinations of zero polymorphisms of the *GSTM1* and *GSTT1* genes revealed that in the group of pregnant women with fetal loss syndrome, combinations of the homozygous del/del genotype responsible for the lower level of protein product synthesis are significantly more common. The chance of developing pathology in the presence of this combination of the genotypic version of the del/del genes *GSTM1* and *GSTT1* increases significantly: Up to 7.8 times more than other genotypes ($\chi^2=12.4$; $P=0.0004$; $OR=7.8$; 95% CI 2.146-28.65). Whereas, the functionally unfavorable *GSTP1* G allele 2.7 times was statistically significantly predominant in the studied chromosomes of pregnant women with PPS compared with pregnant women without PBS ($\chi^2=4.6$; $P=0.03$; $OR=4.5$; 95% CI 1.061-19.5).

Conclusion: Analysis of the results showed that the polymorphism variants of the *GSTM10/0+GSTT10/0* genotypes of the *GSTM1* and *GSTT1* genes, as well as the G/A *Ile 105 Val* genotypes of the *GSTP1* gene are significant predictors of the risk of developing fetal loss syndrome, resulting in disorders of the detoxification process in the body in women during pregnancy.

Biography

Nigora Mavlyanova is the Scientific Leader of the Youth Applied Grant from the Republican Specialized Scientific and Practical Medical Center of Obstetrics and Gynecology, Ministry of Health of the Republic of Uzbekistan. She is a Member of the Association of Obstetricians and Gynecologists of the Republic of Uzbekistan. She has published over 20 articles in famous magazines.

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