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THE STUDY OF GLUTATHIONE-TRANSFERASE M AND T POLYMORPHISM IN PATIENTS WITH LUNG TUBERCULOSIS IN ODESSA REGION.

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Background. In Ukraine tuberculosis (TB) notification rates are constantly increasing since 1991 with incidence and mortality rates in 2004 being 80.9/100,000 and 22.6/100,000 respectively. In Odessa region in 2004 TB incidence and mortality rates were reported at 73.6/100,000 and 19.0/100,000 respectively. The south part of Ukraine and Odessa region in particular are hot-spots of TB and HIV epidemics in the Ukraine.

The glutathione-S-transferases M and T (GSTM and GSTT) are the major phase II detoxification enzymes in humans. Recent reports have demonstrated that GSTM-null and GSTT-null-genotypes are risk factors for the development of pulmonary diseases, particularly pulmonary TB.

Objectives: to study the association between allelic variants of the GSTM and GSTT genes in humans and progression of TB infection and the outcomes of pulmonary TB.

Materials and Methods: Blood samples were collected from 70 patients (all native Ukrainian and Russians) with newly diagnosed TB randomly selected from those attending Odessa Regional TB Center in 2005. GST-polymorphism was detected in blood samples using the multiplex PCR with two pairs of primers. The resulting DNA fragments were separated using agarose electrophoresis. The analysis of the TB infection progression was done after 2 months of treatment. The criteria of the positive dynamic of the pulmonary TB used: the bacterioexcretion termination, the resorption of the infiltration zones, the cavities closing, and forming of the posttuberculosis pneumosclerotic changes. The rest of cases were considered of being negative.

Results: GSTM-null-genotype was found in 39/70 samples (55.7%), GSTT-null-genotype – in 13/70 samples (18,5%), which is similar to the proportions reported earlier for the Eastern European population. The deletion of both genes was observed in 6 cases.

GSTM positive genotype was found in 31/70 samples (44,3%), GSTT positive genotype – in 57/70 (81,5%). The positive dynamic of the TB infection progression in patients with null-genotypes was observed in 19 cases (15 with the GSTM-null genotype, 4 with GSTT-null-genotype), with positive genotype detected in 60 cases (21 with the GSTM+, 39 with GSTT+). The lack of the positive dynamic was found in 33 cases with null-genotype (24 with the GSTM-null genotype, 9 with GSTT-null-genotype) and 28 cases with plus-genotype (10 with the GSTM+, 18 with GSTT+). Univariate statistical analysis demonstrated association between GST-null-genotype and the negative dynamic of TB infection progression (for GSTM-null-genotype OR – 3.36 (95% CI 1.25-9.06), GSTT-null-genotype OR – 4.88 (95% CI 1.32-17.95). Preliminary analysis demonstrates that detection of GST genotype in TB infected persons may be useful in prognosis, optimization of TB patients management and treatment.