# Epigenetic change of genome in pulmonary tuberculosis

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The aim of this study was to evaluate genetic and epigenetic variation of the genome in patients with sensitive Pulmonary Mycobacterium tuberculosis (PT) before and after treatment, under the effect of peptide bioregulator–Ala-Glu-Asp-Gly .

In lymphocyte cultures from patients with sensitive primary PT were studied: total heterochromatin with differential scanning calorimeter - (DSC); facultative heterochromatin (sister chromatid exchanges - SCE) with 5-bromdeoxyuridin (BrdU) and mutation (chromosome aberrations).

We determined:

There was an epigenetic alteration of functional parameters of the genome in PT before treatment. The level of heterochromatin decreased in the telomeric regions of chromosome groups - $A_1$, $A_2$, B, C, D, F and G (in control it was high) and increased in the middle regions of chromosome groups - $A_1$, B, C, E, F, and G (in control it was reduced);

There was a high level of somatic recombination;

Revealed an increase of the frequency of cells with chromosome aberrations.

We found that instability of the genome existed to a lesser extent, but persisted after treatment of patients with PT. The bioregulator (Ala-Glu-Asp-Gly) could be used as an aid in the prevention and treatment of tuberculosis.

The results of our study of epigenetic alterations in PT (redistribution of heterochromatin from the telomeric to middle chromosome arms) make it possible to define a sensitive form of PT, and then monitor the results of treatment and develop a new therapy.

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