

GENETIC MARKERS FOR PREDICTION OF ASTHMA SEVERITY IN CHILDREN

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Abstract

The prevalence of asthma among children in Ukraine ranges within 5–22 %. Asthma mortality increases annually. Asthma is a multifactorial disease which is caused by genetic and environmental factors.

Aim. To develop a method for predicting of asthma severity in children by determining phase II xenobiotic detoxification enzyme genotypes and cardiovascular tone genes and their interactions.

Materials and methods. 107 children with varying severity of asthma were examined: 29,9% — severe, 51,4% — moderate, and 18,7% — mild. All children underwent complete examination and were treated according to official national and international standards. Genetic testing was also performed.

Results. The polymorphisms of GSTM1, GSTP1, AT2R1, ACE genes and characteristics of their interaction were determined. It was revealed that combinations AT2R1-1166CC and ACE-DD / or AT2R1-1166CC and GSTM1 deletion / or AT2R1-1166CC, ACE- DD and GSTM1 deletion predicted severe asthma; while GSTP1-AG and ACE-ID combination — moderate asthma.

Conclusions. Current method allows to predict quickly a severe asthma in children. Its results become available in 12 hours and help to provide quality and timely care to children, improving asthma outcomes and reducing disability and mortality of the disease.

Key words: asthma, children, severity, prognosis, gene polymorphism.

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