GENETIC FACTORS OF DEVELOPING BRONCHIAL ASTHMA

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Bronchial asthma is a chronic inflammatory disease associated with variable airway obstruction and bronchial hyperresponsiveness, which manifests itself in the form of repeated episodes of wheezing, coughing, a feeling of lack of air and a feeling of tightness in the chest [1]. This is a multifactorial disease: it develops under the influence of environmental factors in the presence of a person's genetic predisposition [2, 3].

Bronchial asthma is recognized as a classic example of a multifactorial disease. This means that it develops under the influence of external environmental factors in the presence of a person's genetic predisposition. The hereditary conditionality of bronchial asthma has been known for over a hundred years. More than 500,000 genetic variants have been studied to determine the association with asthma. The role of many genes in the pathogenesis of this disease has been ascertained. However, during the recent years more and more researches are devoted to epigenetics (studying the influence of external environmental factors on the activity of genes). The article presents literature review on the issue of genetics and epigenetics of bronchial asthma. The data on the influence of nutrition, fasting, consumption of vitamins, smoking, air and water pollution on the risk of asthma and its severity are also given.

The fact that asthma is hereditary. The word has been known for a century - since 1916, when Cooke and Vander presented the results of an epidemiological study. It involved 621 probands with atopy, 76 without it (control group) and their family members. A hereditary history of atopy was identified in 48.4% of probands with atopy and in 14.5% without it. 100 years later, in 2016, Ulemar et al. in a study involving 25,306 twins aged 9-12 years, revealed a hereditary cause of bronchial asthma in 82% of cases. It has been shown that asthma is diagnosed more often in monozygotic twins than in dizygotic twins. According to a number of authors, the genetic component is observed in 60-80% of cases of asthma development. Numerous studies have proven that genetic factors greatly enhance the effect of environmental factors in patients with bronchial asthma. Genomic association studies have recently been published that examined more than 500,000 genetic variants to determine association with asthma [4].

Genes involved in the pathogenesis of bronchial asthma. The first studies of the role of genetics in the pathogenesis of asthma conducted among children were based on biology or location in the genome. Thus, the causally significant role of a number of genes and loci was proven: DPP10, PCDH1, HLAG, NPSR1, PHF11, PLAUR, ADAM33, IL10, CD14, IL4, IL13, ADRB2, HLA-DRB1, HLA- DQB1, TNFA, FCER1B, INPP4A, STAT6 and IL4RA. Sequencing has provided significant breakthroughs in understanding the genetics of asthma. It should be emphasized that the identified causally significant genes in the pathogenesis of asthma are consistent with the hypothesis that the disease in question develops as a result of initial dysfunction of the epithelial barrier and disorders of the primary or adaptive immune response.

It is known that there are genes, the answer is genes that are responsible only for predisposition to asthma, and vice versa, there are genes that are responsible only for the

severity of the disease. For example, in the work of F. Miriam et al. (2010), it was found that there is little difference between the loci regulating the level of total serum IgE (with the exception of IL-13 and the HLA region) and the loci responsible for susceptibility to asthma. general. Therefore, elevated IgE may be an intermittent manifestation of asthma rather than its underlying cause, consistent with the lack of association between sensitization and asthma in many populations. Conversely, the SERPINE1 gene is not a susceptibility gene for asthma, but is responsible for the severity, progression and response to long-term use of inhaled corticosteroids. Patients with the 5G allele are characterized by a higher level of serum IgE, more severe respiratory dysfunction and a more severe course of the disease. It has been demonstrated that greater gene expression in the allele is associated with a better effect of inhaled corticosteroids [9].

However, the data obtained are sometimes contradictory, which, according to the authors themselves, requires more research. Much effort is being directed towards the development of this area in the hope that epigenetics will make it possible to cope with the most difficult moments in the treatment of many diseases, including bronchial asthma.

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