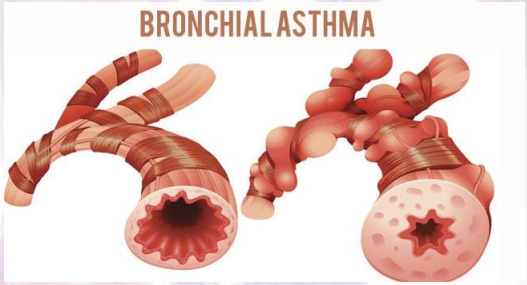
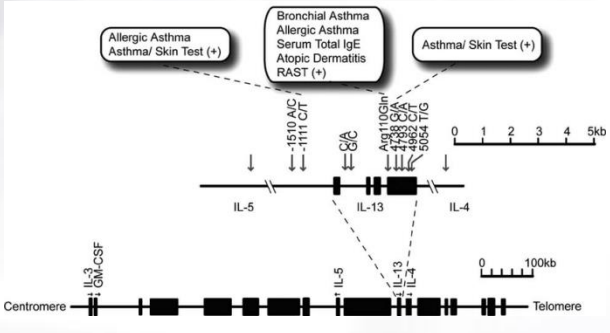
Gene polymorphism *IL13* in moderate-to-severe asthmatic Siberian children with different diseases control

Marina Smolnikova, Nina Gorbacheva, Marina Malinchik, Sergey Tereshchenko
Scientific Research Institute of Medical Problems of the North FRC KSC SB RAS

Bronchial asthma (BA) is a global multifactorial disease, since both environmental factors and the person's genetic predisposition contribute to the development of the disease. A number of associative relationships of cytokine gene polymorphism produced by Th2 cells with the development of bronchial asthma have been obtained.





Interleukin-13 (IL-13) is the central mediator involved in the pathogenesis of bronchial asthma. The IL13 gene has a number of polymorphisms associated with the clinical manifestations of BA. Of particular interest is the study of **rs1800925 polymorphism** due to its location in the promoter region of the IL13 gene, as well as the revealed association between this SNP and BA in both adult and children populations. Carriers of the homozygous variant for the minor allele of this polymorphism developed an association with increased IL-13 production, airway hyperreactivity, and a positive skin test for allergen, and heterozygotes and homozygotes for the minor allele are sure to be associated with an elevated concentration of IgE.

The purpose of the study was to evaluate the associations between rs1800925 polymorphism of the *IL13* gene and bronchial asthma with different control levels and disease severity in children of Caucasian origin in Eastern Siberia.

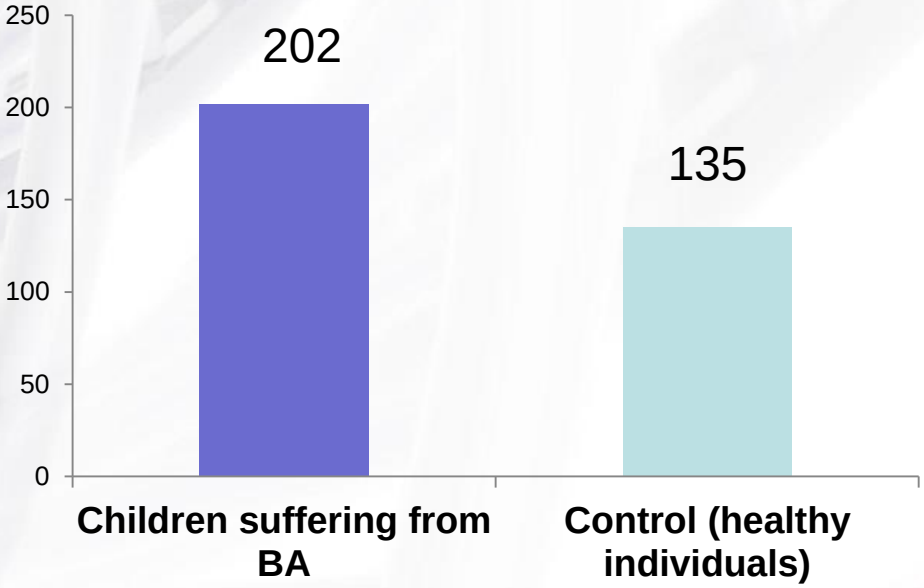


Fig. 1. The number of examined individuals in the control group and the group of patients with BA

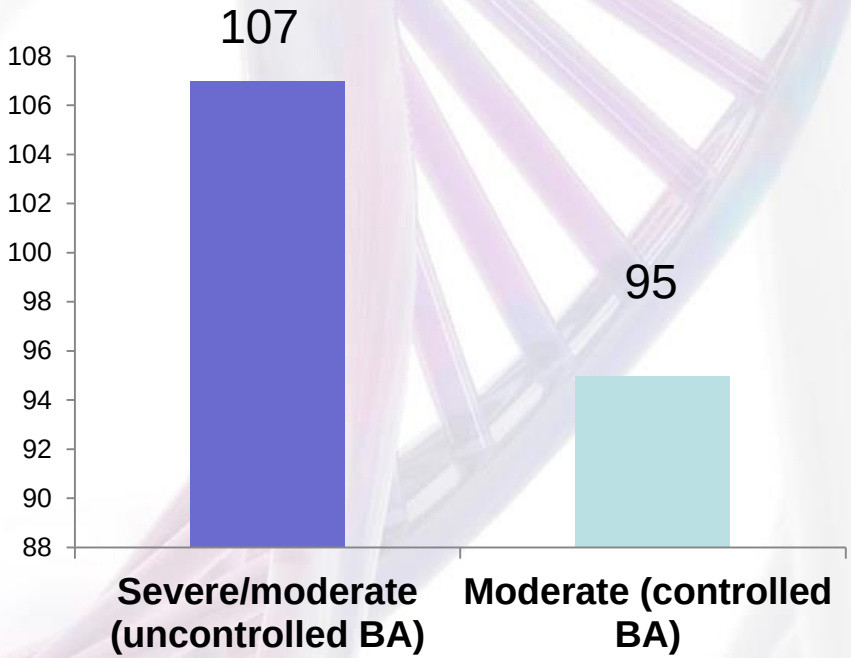


Fig. 2. The number of examined BA patients depending on the severity and the level of control of the disease

Methods. DNA from peripheral blood was isolated using salting out method. Genotype test of IL13 (rs1800925) was carried out using the RT-PCR method. Comparison of the allele frequency and genotypes between groups was provided using an online calculator, χ-square test.

Results. The research resulted in obtaining the data on cytokine polymorphism distribution in the patients with asthma in the Europeans origin (Eastern Siberia, Russia): rare allele variants were represented by T**IL13*, G**IL31* and C**IL33* allele, which goes in conformity with world databases.
The frequency of the CT genotype in patients with controlled asthma was significantly higher in comparison with control (46,2%/36,6%, OR 1,51 [1,03-2,19], p=0,033). We also obtained statistically significant differences in the frequency of the TT genotype between the population sample (6,7%) and the group with uncontrolled asthma (15,5%, OR 1,65 [1,06-2,56], p=0,027) (Fig. 3).

Conclusion. We have shown genetic markers of the risks of asthma development: both CT and TT ***IL13* (rs1800925)** genotypes associated with asthma.
Li J. et al. (2014) previously shown that the homozygous variant of the allele T* *IL13* (rs1800925) is associated with increased production of IL-13 and respiratory tract hyperresponsiveness, which occurs in severe asthma.
The obtained in present study results have contributed to the data on the role of polymorphisms of IL-13 into the development of asthma in children as exemplified by a European population of East Siberia, Russia.

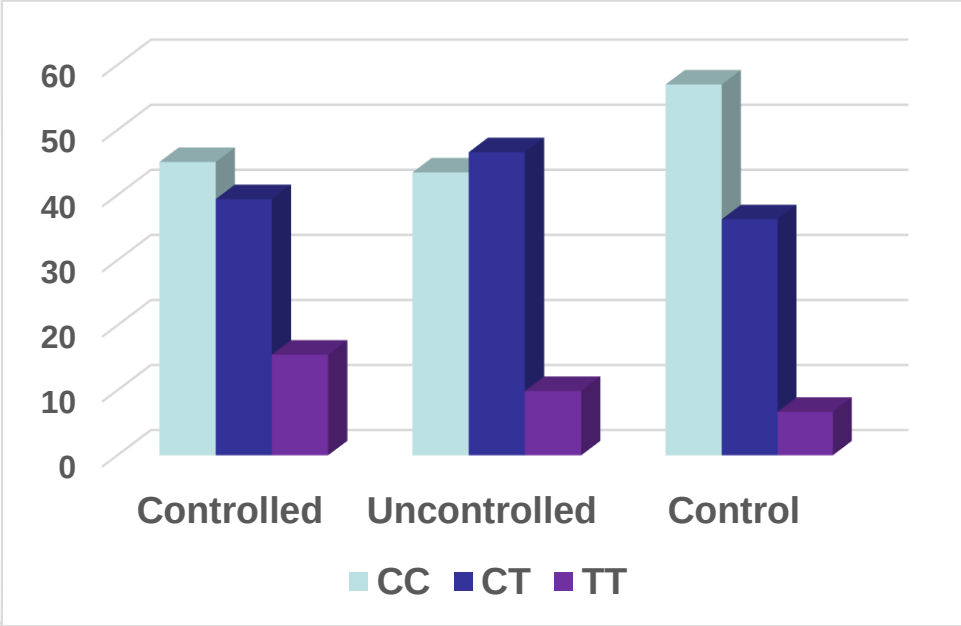


Fig. 3. Frequencies of genotypes of the *IL13* (rs1800925) in patients with bronchial asthma with different levels of control of disease

Address for correspondence: Marina Smolnikova, E-mail: smarinv@yandex.ru