Association between polymorphisms of NAT2 gene and lung cancer susceptibility in Yakut population

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ABSTRACT:
Markers of increased risk of lung cancer in Yakuts are the NAT2*857A allele and NAT2*857G/A genotype, the reduced risk is the NAT2*857G allele, NAT2*857G/G genotype.

Introduction
In the structure of cancer incidence among the indigenous people - Yakuts, lung cancer occupies a leading position. Some authors have shown that polymorphic variants of the NAT2 gene contribute to the development of lung cancer.

Methods
A case-control study involving 60 patients (17 women and 43 men) histopathologically diagnosed for lung cancer and cancer-free controls 60 people. For release of DNA was used the phenol–chloroform extraction.

The analysis of polymorphic options 481C>T, 590>T; 857G>A; was carried out by PCR method on the thermocycler T100 (Bio-Rad). RFLP was carried out by KpnI, BamHI, TaqI.

Results
We have not found statistically significant differences in the frequency distribution of alleles and genotypes of the 481C>T, 590G>A polymorphism of the NAT2 gene between the control group and the group of patients with lung cancer.

Significant differences in the frequencies of alleles and genotypes were observed for the polymorphic variant 857G>A. Compared with healthy patients, there was a decrease in the frequency of mutant NAT2*857G allele - 64.2% and 78.3% ($\chi^2 = 42.52; p=0.000...$) and an increase in the frequency of wild NAT2*857A allele 35.8%, 21.7% ($\chi^2 = 42.52; p=0.000...$). In the group of patients, the frequency of the NAT2*857A allele (35.8%; $\chi^2 = 42.52; p=0.000...$) and the heterozygous genotype NAT2*857G/A (71.6%; $\chi^2 = 13.43; p=0.0002$) and the frequency of the homozygous genotype decreased NAT2*857G/G (28.4%; $\chi^2 = 10.95; p=0.0009$) compared to the control 21.7%, 36.6% and 60.1%.

Conclusion
Thus, markers of increased risk of lung cancer in Yakuts are the NAT2*857A allele and NAT2*857G/A genotype, the reduced risk is the NAT2*857G allele, NAT2*857G/G genotype.