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

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Methods

• **Aim:** To investigate the possible association between polymorphisms of NAT2 and lung cancer in yakut population.

• A total of 60 patients with lung cancer (43 men and 17 women with lung cancer) and 60 controls was studied. The mean age of two groups was 54 years.

• Molecular analysis of 481C>T, 590G>A and 857G>A substitutions in NAT2 gene was performed by polymerase chain reaction-restriction fragment length polymorphism (PCR-PFLP) technique, from DNA extracted from peripheral blood samples.

• Amplification of genomic DNA was performed using the following primers: 5'-GCTGGGTCTGGAAGCTCCTC-3' and 5'-TTGGGGTGATACATACACAAGGG-3.

• For comparing frequencies of genotypes the standard criterion $\chi^2$ with Yeats’s amendment was used.

Figure 1. Electrophoresis band pattern by KpnI digestion. T/T – a homozygous genotype (4,5,9); T/C – a heterozygotic genotype (3,11,12,13); C/C – a homozygous genotype (1,2,6,7,8,10).

Figure 2. Electrophoresis band pattern by TaqI digestion. G/G – a homozygous genotype (1,6,7,10); A/G – a heterozygotic genotype (2,3,4,9); A/A – a homozygous genotype (5,8).

Figure 3. Electrophoresis band pattern by BamHI digestion. A/A – a homozygous genotype (8); A/G – a heterozygotic genotype (2-7,9); G/G – a homozygous genotype(1).
Results

• Possible 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.

Frequency distribution of genotypes and alleles of the polymorphic variant (857G>A) of the NAT2 gene in patients with lung cancer and the control group.