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**Title:** Searching for CHRNA3, CHRNA4, CHRNA5, and CHRN B4 genes polymorphisms influencing nicotine dependence in the ethnic population of Kashubians, North Poland

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**Body:** Genome wide association studies showed that genes encoding nicotinic receptor CHRN subunits might be potentially involved in the pathogenesis of nicotine dependence. We aimed to investigate whether polymorphisms in the sites rs12914008, rs16969968, rs2236196, rs578776, rs7743870 of CHRNA5, CHRNA3, CHRNA4 and CHRN B4 subunits genes influenced nicotine dependence. The survey was conducted in closed, ethnically homogenic population of Kashubians. The study sample consisted of 455 unrelated subjects, daily or occasional smokers. Several variables of smoking habit were recorded, and the nicotine dependence was scored with the use The Fagerstrom Test for Nicotine Dependence (FTND). Genotyping was performed in blood samples, and genotypes were correlated with the severity of nicotine dependence with the use of multivariate logistic regression analysis. Results: Distributions of genotypes for all polymorphisms did not deviate from expectations predicted by the Hardy-Weinberg equilibrium. We found that A allele carriers of rs16969968 polymorphism had higher risk of heavier smoking, i.e. 10 or more cigarettes per day, than G allele carriers (OR = 1.54; 95% CI: 1.00-2.35). In the separate analysis, performed in the group of subjects with the history of smoking shorter than 5 years, higher risk of a stronger nicotine dependence (i.e. FTND score 4 or more) in A allele carriers of rs12914008 polymorphism than in G allele carriers was found (OR = 14.96; 95% CI: 1.42-158.0). Conclusion: Polymorphisms in the sites rs16969968 and rs578776 of CHRNA5 and CHRNA3 subunits genes may influence the severity of nicotine dependence.