

FREQUENCY DISTRIBUTION OF 6 POLYMORPHISMS OF THE GENES *CYP2C9*
(RS1057910), *HMGCR* (RS17238540, RS17244841), *APOE* (RS429358, RS7412) AND
APOC1 (RS4420638) IN A SAMPLE OF SOUTHEAST EUROPEAN CAUCASIAN
POPULATION (SEC)
COMPARISON WITH OTHER POPULATIONS AND STUDY OF THEIR RESPONSE TO STATIN
THERAPY

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Introduction: This study analyzes the distribution of 6 polymorphisms of the genes *CYP2C9* (rs1057910), *HMGCR* (rs17238540, rs17244841), *APOE* (rs429358, rs7412) and *APOC1* (rs4420638) in a sample of Southeast European Caucasian population (SEC) and uses the TGS (Total Genotype Score) algorithm to assess their effect on statin therapy.

Materials and Methods: A sample of epithelial cells was taken from the buccal cavity of 643 volunteers, followed by DNA isolation and genotyping with the LightSnip method. Frequency distribution of polymorphisms in SEC was compared to AFR, AMR, EUR, EAS, and SAS populations with χ^2 test. Then the TGS was developed and the Kruskal–Wallis test was performed ($\alpha=0,05$).

Results: The results showed statistically significant differences between populations in most comparisons performed. The highest mean TGS was detected in EAS (48.86) and SAS (48.16). Below are the AMR (47.48), SEC (46.42), EUR (45.94) and AFR (42.50). The TGS distributions revealed a statistical significant difference between SEC and AFR, SAS and EAS ($p<0.05$), and highly similar distribution of SEC to native American

($p=0.108$) and European ($p=0.186$) populations. Similar results were obtained without the effect of rs1057910.

Discussion and Conclusions: SEC population is likely to show 1) a better response to statin treatment than AFR, who may require an increased dose, 2) a slightly reduced response to statins compared with both Asian populations, and therefore may require an increased dose and 3) a similar response with EUR and AMR. The same conclusions are drawn whether or not the treatment involves fluvastatin and / or rosuvastatin.