**VALIDATED GENETIC BIOMARKERS FOR PREDICTION OF INDIVIDUAL RISK OF MYOCARDIAL INFARCTION IN RUSSIANS**

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*Background*. Myocardial infarction (MI) remains the cause number one of death and disability worldwide. In spite of progress in cardiovascular genetics, data on genetic background of MI are still limited and need to be validated in order to be used for prediction of individual risk.

*Methods and Results*. In this study we found that the carriage of TGFB1 rs1982073\*TT, FGB rs1800788\*T, CRP rs1130864\*TT was associated with MI in the discovery group of Russian descent from the Moscow region (325 patients and 185 controls). We also found several MI-associated biallelic combinations. One of them, namely IFNG rs2430561\*A + PTGS1 rs3842787\*T, showed nonlinear (epistatic) interaction between the genes according to our original two-component procedure that consisted of the evaluation of the Synergy Factor and the exact Fisher-like interaction numeric test. All these association data were replicated in the independent group of Russians from the Republic of Bashkortostan (220/197 samples, men only). Multiple logistic regression analysis was performed for the four identified genetic markers: three single gene variants and the epistatic pair, which was considered as an independent marker. The composite model demonstrated a rather moderate AUC of 0.66 and performed very well when applied to the independent replication sample from Bashkortostan: the two ROC curves were almost identical. *Conclusions*. The prognostic significance of TGFB1, FGB, CRP, and the biallelic combination of IFNG and PTGS for MI was shown. Results appeared to be very similar in the two groups of Russians from different regions of European Russia. In the future, the discovered genetic variants that replicably predict MI could be used as substantial components for the creation and implementation of prognostic tests for individual risk of MI. This work was supported by the Russian Science Foundation (project 16-14-10251).