

PROGNOSTIC SIGNIFICANCE OF SLC2A9 GENE POLYMORPHISM AND SERUM URIC ACID LEVEL IN THE DEVELOPMENT OF ADVERSE CARDIOVASCULAR EVENTS IN PATIENTS WITH ARTERIAL HYPERTENSION AND ATRIAL FIBRILLATION

Barysenka T.L.¹, Snezhitskiy V.A.¹, Kopytsky A.V.¹, Bogdanovich V.Ch.², Korysheva O.R.²

¹Educational Establishment «Grodno State Medical University», Grodno, Belarus, e-mail: t.kepourko@gmail.com

²Health Care Institution «Grodno University Clinic», Grodno, Belarus, regclinic@gocb.by

Aim

The aim of the study is to develop a method for assessing the risk of adverse cardiovascular (CV) events in patients with arterial hypertension (HTN) and atrial fibrillation (AF).

Material and methods

A total of 141 patients, including 50 healthy patients with no history of HTN and AF (1 group), 68 patients with HTN and AF (2 group) and 23 patients with HTN (3 group), were examined.

Serum uric acid (sUA) levels were determined using the enzymatic colorimetric method. Increased sUA levels above 360 µmol/L in women and 400 µmol/L in men and the absence of signs of gouty arthritis and/or subcutaneous tophi were considered to be hyperuricemia [6]. Molecular genetic testing methods included the determination of the SLC2A9 gene rs734553 polymorphism using the polymerase chain reaction technique.

Adverse CV events included hypertensive crises and/or relapses of AF, death of cardiovascular origin. A binary regression equation with a logit-link function was constructed. ROC analysis was carried out, and the cross-validation method was used to determine the classification accuracy of the model. To assess the association of sUA level and SLC2A9 gene polymorphism with the likelihood of developing adverse CV events in patients with HTN and AF, the odds ratio (OR) with a 95%

Results

Hyperuricemia was found in 30 (21.3%) patients, of which 1 patient was in group 1, normal sUA levels were found in 111 (78.7%) patients. In patients with the C/C genotype (420 [413; 424] µmol/l) and with the A/C genotype (330 [284; 412] µmol/l), the value of uricemia was higher than in patients with the A/A genotype (310 [281; 341] µmol/l) (p=0.003).

Results

In total, 41 (45.1%) patients from groups 2 and 3 had adverse CV events, of which 38 (55.9%) patients – from group 2 and 3 (13%) patients – from group 3. Hyperuricemia in patients of the 2nd group with the A/A genotype was diagnosed in 2.9% (n=2), with the A/C genotype – in 17.6% (n=12), with the C/C genotype – in 14.7% (n=10). Hyperuricemia in patients of the 3rd group with the A/A genotype was diagnosed in 4.3% (n=1), with the A/C genotype – 4.3% (n=1), with the C/C genotype – 13% (n=3). In 8 (44.4%) patients with hyperuricemia and registered adverse CV events, the A/C genotype was determined, in 10 (55.6%) patients – the C/C genotype of the SLC2A9 gene rs734553 polymorphism was determined. The A/A genotype was not identified in patients with hyperuricemia and registered adverse CV events. The following predictors were included in the binary regression model with a logit-link function: sUA level, heterozygous genotype A/C, homozygous genotype C/C of the SLC2A9 gene rs734553 polymorphism. A binary regression equation with a logit-link function was constructed, where the linear predictor (Z) is found by the formula: $Z = -3,9084 + 8,4089 \cdot v4 + 1,8106 \cdot v9A/C + 1,7256 \cdot v9C/C$. AUC 0.809 [95% CI 0.733-0.886], which indicates a satisfactory predictive ability of the constructed model, (figure 1). With the selected cutoff threshold $p_0=0.4969$, the sensitivity of the method is 78.05%, specificity – 78%, accuracy – 78.01%. Thus, for patients with $p \geq p_0$, a high risk of developing adverse CV events in patients with HTN and AF is predicted, depending on the sUA level.

Conclusions

1. The sUA level, the heterozygous A/C genotype, the homozygous C/C genotype of the SLC2A9 gene rs734553 polymorphism have been identified as predictors associated with adverse CV events in patients with HTN and AF.
2. The developed logistic regression model has a sensitivity of 78,05% and a specificity of 78%.

Nothing to declare

Figure – ROC curve of the model

