

## ASSOCIATION OF THE GENETIC POLYMORPHISM RS11640851 MT1A 80 C/A AND TYPE 2 DIABETES MELLITUS IN THE CENTRAL BALKAN POPULATION

*Stevan Vujić<sup>1</sup>, Jelena Milenković<sup>2</sup>, Žaklina Šmelcerović<sup>1</sup>,  
Tatjana Jevtović-Stoimenov<sup>1,3</sup>, Aleksandra Klisić<sup>4</sup>*

Type 2 diabetes mellitus (T2DM) is the most common type of diabetes and is becoming an increasingly prevalent global health issue. Polymorphisms in genes coding metallothioneins, a group of small zinc-binding proteins that participate in antioxidative protection, are believed to be involved in T2DM pathogenesis. This study aimed to investigate the potential association of the single nucleotide polymorphism (SNP) rs11640851 MT1A 80 C/A and the T2DM risk and to determine the impact of the genotype and allelic distribution on the diabetes-related biochemical parameters. The study included 298 subjects, 112 with T2DM and 186 healthy, non-diabetic controls. The participants' fasting glycemia and HbA1c levels were measured, while the SNP in the MT1A gene was determined using the PCR-RFLP method. There were no significant differences in the genetic distribution and allele frequency between control subjects and diabetic patients ( $p > 0.05$ ). There was likewise no association between the SNP and diabetes-associated laboratory parameters, fasting serum glucose and HbA1c levels. However, 79.6% of allele C carriers had fasting glucose levels above 7 mmol/L, versus 53.3% of subjects homozygous for allele A ( $p = 0.005$ ). Although our study did not find a direct association between the MT1A genetic variants and the occurrence of T2DM, we observed an effect of the allele C on glycemic control in the patients. Further research in a larger population is needed to expand these findings and to improve the understanding of metallothionein genes and their impact on the development of T2DM.

*Acta Medica Medianae 2024;63(1):56-63.*

**Key words:** *type 2 diabetes, metallothionein, zinc, single nucleotide polymorphism*