SUMMARY

Inherited hyperbilirubinemias are a group of metabolic disorders, characterized by increased levels of total serum bilirubin or its conjugated fraction. Most of these hyperbilirubinemias are inherited autosomal recessively and are manifested in young age. Increased bilirubin reflects the genetic disturbances in one of the enzymes of heme degradation pathway, the defect of bilirubin conjugation (*UGT1A1 gene*) or its transport (*ABCC2, OATP1B1, OATP1B3*). All of these proteins are involved not only in elimination of bilirubin, but various substrates; therefore the performed studies have a great pharmacogenomics impact. We have studied the molecular pathology of hereditary hyperbilirubinemias in Caucasian and Roma population and to compare the clinical and biochemical results with the molecular genetic data. We described the impact of compound defect of c.-3279T>G and g.175492_175493insTA on total serum bilirubin and calculated the linkage disequlibrium of these two variants in promoter region of *UGT1A1* gene. We also verified, that the population distribution of both variants is in concordance with the literature.

In our second study, we have described the rare conjugated hyperbilirubinemia Dubin-Johnson type among 7 Roma families. We have found a novel variant NG_011798.1:c.[1013_1014delTG] together with the dual genetic defect – a combination of Dubin-Johnson and Gilbert`s syndrome. We have described a founder effect of the mutation in *ABCC2* and found a common haplotype of 86 bp encompassing the gene. We have also characterized the excretion of coproporphyrin isomers in patients with DJS and compared it with those with dual hereditary jaundice.

KEY WORDS

Bilirubin, jaundice, hyperbilirubinemia, *UGT1A1, ABCC2*, coproporphyrin isomers