Background: Periprocedural bleeding is the most common complication related to coronary angiography (CAG) and percutaneous coronary intervention (PCI) and it is associated with worse short-term and long-term prognosis. Determining risk factors and genetic variations associated with increased bleeding risk may improve use of avoidance bleeding strategies in prevention of bleeding.

Aim: The aim of our study was to a) identify independent risk factors (of the baseline characteristics, clinical, laboratory a procedural data) associated with a higher risk of periprocedural bleeding b) to validate predictive value of CRUSADE and NCDR bleeding risk stratification algorithms c) to analyze the association between the presence of selected single nucleotide polymorphisms of key platelet proteins (GPIa, GPVI, P2Y12, COX-1) and the risk of periprocedural bleeding.

Methods: The study included 73 patients with acute or chronic ischemic heart disease who developed bleeding complication within 30 days after invasive procedure (CAG/PCI). The control group consisted of 331 patients without bleeding. Baseline characteristics, clinical state at admission, laboratory data (creatinine, blood count, INR) and procedural data were evaluated. The CRUSADE and NCDR algorithms for bleeding risk were retrospectively applied on both groups. The single nucleoid polymorphisms GPIa 807C/T, GPVI 13254T/C, P2Y12 32C/T, P2Y12 H1/H2 haplotype, COX-1 -842A/G, COX-1 50C/T were analysed from venous blood samples and their association with the risk of periprocedural bleeding was assessed.

Results and conclusions: The independent risk factors associated with periprocedural bleeding in real clinical practice were identified a) periprocedural administration of ADP antagonists b) administration of low molecular weight heparin after the procedure c) lower baseline haematocrit level d) the presence of acute coronary syndrome e) higher heart rate at

admission. When CRUSADE and NCDR algorithms were applied significantly higher portion of patients with bleeding were retrospectively classified into the high risk group. The prevalence of variant alleles GPIa 807T, GPVI 13254C, P2Y12 34T, P2Y12 H2 haplotype, COX-1 -842A/G and COX-1 50C/T in total study population was 56.7 %, 20.3 %, 56.2 %, 24.3%, 9.9% and 9.6%, respectively. The presence of variant allele was not related to higher risk of periprocedural bleeding: GPIa 807C/T (OR 1.29, 95% CI 0.75–2.24, p=0.334), GPVI 12354T/C (OR 0.82, 95% CI 0.40–1.64, p= 0.551), P2Y12 34C/T (OR 0.71, 95% CI 0.42–1.22, p= 0.189), P2Y12 H1/H2 haplotype (OR 0.69, 95% CI 0.35–1.36, p= 0.258), COX-1-842A/G (OR 1.15, 95% CI 0.46–2.76, p= 0.738) and COX-1 50C/T (OR 0.88, 95% CI 0.31–2.32, p= 0.780). In patients who developed bleeding the tendency of higher frequency of P2Y12 H2 haplotype in its homozygous form (OR 2.79, 95% CI 0.51–13.77, p=0.161) and COX-1 -842A/G polymorphism in PCI subpopulation (OR 2.40, 95% CI 0.6-9.75, p=0.157) was found.