No association of chromosome 9p21.3 variation with clinical and angiographic outcomes after placement of drug-eluting stents.

OBJECTIVES: After novel findings from genomewide association studies that sequence variation on chromosome 9p21.3 is a genetic factor for coronary heart disease, we investigated whether this locus influenced the clinical and angiographic outcomes after implantation of drug-eluting stents in coronary arteries. BACKGROUND: Recently, genomewide association studies have identified a locus on chromosome 9 (approximately 100 kb in band p21.3) as the strongest genetic factor for coronary heart disease. METHODS: We studied the rs7865618, rs1537378, rs1333040, and rs1333049 polymorphisms located on chromosome 9p21.3 in a cohort of 2,028 patients who were treated with percutaneous coronary intervention and implantation of sirolimus- or paclitaxel-eluting stents. Records of 3-year adverse clinical outcomes were obtained from all stented patients. Follow-up angiography at 6 to 8 months after stenting was performed in 1,683 patients (83%). RESULTS: The polymorphisms were not significantly related with clinical outcomes at 3 years, including death (p>or= 0.18), myocardial infarction (p>or= 0.19), repeat revascularization (p>or= 0.08), and the composite end point of adverse events (death, myocardial infarction, repeat revascularization) (p>or= 0.34). No association of the polymorphisms was found with
angiographic measures at follow-up, including minimal lumen diameter ($p \geq 0.51$), diameter stenosis ($p \geq 0.31$), late lumen loss ($p \geq 0.05$), and binary restenosis ($p \geq 0.31$).

CONCLUSIONS: Specific polymorphisms in the chromosome 9p21.3 region that were shown to be associated with coronary heart disease in genomewide analyses were not related to the clinical and angiographic outcomes after the placement of drug-eluting stents in coronary arteries.

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