A genome-wide association study identifies a region at chromosome 12 as a potential susceptibility locus for restenosis after percutaneous coronary intervention.

Abstract:

Percutaneous coronary intervention (PCI) has become an effective therapy to treat obstructive coronary artery diseases (CAD). However, one of the major drawbacks of PCI is the occurrence of restenosis in 5-25% of all initially treated patients. Restenosis is defined as the re-narrowing of the lumen of the blood vessel, resulting in renewed symptoms and the need for repeated intervention. To identify genetic variants that are associated with restenosis, a genome-wide association study (GWAS) was conducted in 295 patients who developed restenosis (cases) and 571 who did not (controls) from the GENetic Determinants of Restenosis (GENDER) study. Analysis of ~550,000 single nucleotide polymorphisms (SNPs) in GENDER was followed by a replication phase in three independent case-control populations (533 cases and 3067 controls). A potential susceptibility locus for restenosis at chromosome 12, including rs10861032 (P(combined) = 1.11 x 10(-7)) and rs9804922 (P(combined) = 1.45 x 10(-6)), was identified in the GWAS and replication phase. In addition, both SNPs were also associated with coronary events.
(rs10861032, \(P\text{(additive)} = 0.005\); rs9804922, \(P\text{(additive)} = 0.023\)) in a trial based cohort set of elderly patients with (enhanced risk of) CAD (PROSPER) and all-cause mortality in PROSPER (rs10861032, \(P\text{(additive)} = 0.007\); rs9804922, \(P\text{(additive)} = 0.013\)) and GENDER (rs10861032, \(P\text{(additive)} = 0.005\); rs9804922, \(P\text{(additive)} = 0.023\)). Further analysis suggests that this locus could be involved in regulatory functions.