ASHG: 16 additional loci ID'd for coronary artery disease

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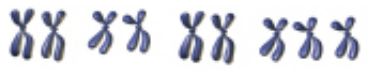

Image courtesy of Blausen Medical

Meta-analyses have identified an additional 16 loci with genome-wide significance for coronary artery disease, according to research presented at the annual meeting of the American Society of Human Genetics, held from Nov. 6 to 10 in San Francisco.

(HealthDay)—Meta-analyses have identified an additional 16 loci with genome-wide significance for coronary artery disease (CAD), according to research presented at the annual meeting of the American Society of Human Genetics, held from Nov. 6 to 10 in San Francisco.

Stavroula Kanoni, Ph.D., from the Wellcome Trust Sanger Institute in Cambridge, U.K., and colleagues conducted a two-stage meta-analysis involving 63,746 CAD cases and 130,681 controls to examine the genes associated with CAD.

The researchers found that 14 loci reached genome-wide significance. Six additional loci were examined in four independent studies, and, in a

three-stage combined meta-analysis, two loci reached genome-wide significance. These results bring the number of loci for CAD to 47, with an additional 103 independent variants that correlate strongly with CAD. Together, these variants account for 10.6 percent of the heritability of CAD. Twelve of the 47 variants with genome-wide significance were significantly associated with a lipid trait, five with blood pressure, and none with diabetes. Five interaction networks were generated from network analysis of 233 candidate genes, which included 85 percent of the putative CAD genes. The four most significant pathways mapping to these networks correlated with lipid metabolism and inflammation.

"We no longer assume that coronary heart disease is triggered by just a handful of genes, each with a strong effect on a person's risk for the disease," a coauthor said in a statement. "Our research supports the current assumption that heart disease risk is determined by a large group of genes, each with a modest effect on risk."

More information: Abstract
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