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Polygenic risk score reliably predicts coronary artery disease

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(HealthDay)—Genome-wide polygenic risk scores (PRS) can predict coronary artery disease (CAD), according to a study published online June 11 in *Circulation: Genomic and Precision Medicine*.

Noting that two recently derived genome-wide PRS have shown high specificity and sensitivity to identify CAD cases in European-ancestry participants from the U.K. Biobank, Florian Wünnemann, Ph.D., from the Montreal Heart Institute, and colleagues calculated both PRS (GPS_{CAD} and $metaGRS_{CAD}$) in French-Canadian individuals from three cohorts totaling 3,639 prevalent CAD cases and 7,382 controls. The impact of the founder French-Canadian familial hypercholesterolemia deletion (*LDLR* delta > 15kb deletion) was estimated on CAD risk in one of these cohorts; this estimate was used to calibrate PRS impact.

The researchers confirmed the ability of both PRS to predict prevalent CAD comparable to the original reports (area under the curve [AUC], 0.72 to 0.89). Consistent with previous estimates, the PRS identified about 6 to 7 percent of individuals at CAD risk similar to that for carriers of the *LDLR* delta > 15kb mutation. For predicting incident or recurrent CAD, the PRS did not perform as well (AUC, 0.56 to 0.60), possibly due to confounding as more than three-quarters (76 percent) of participants were on statin treatment.

"Using the polygenic risk score, even in a normal population, we can find people whose risk is as high as those who have [familial hypercholesterolemia]," a coauthor said in a statement.

More information: Abstract/Full Text (subscription or payment may be required)