Genomic Test Validated for CAD Assessment

VITALS

Major finding: A genomic test bested two standard risk-factor assessments for predicting CAD.

Source of data: Prospective comparison of three screening tests in 525 patients.

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BY MITCHEL L. ZOLER

ORLANDO — A genomic test surpassed conventional risk-factor assessment for predicting the presence of an obstructive coronary lesion, based on results from a prospective study of 525 patients with suspected coronary disease.

The results performed better than either the Diamond-Forrester method or the Framingham risk score for predicting the presence of obstructive coronary artery disease, Dr. William E. Kraus said at the annual scientific sessions of the American Heart Association.

The Corus CAD genomic test examines RNA expression for 23 genes in a peripheral blood sample. The genes primarily control immune responses, including neutrophil activation, natural killer cell activation by T cells, and adaptive immunity. The functions of other genes that are part of the test are unknown, but prior results identified their expression as tied to coronary disease risk, said Dr. Kraus, a cardiologist at Duke University, Durham, N.C.

The Personalized Risk Evaluation and Diagnosis In the Coronary Tree (PREDICT) study enrolled patients at 43 U.S. sites with suspected coronary disease who were scheduled for coronary catheterization and angiography. Angiography identified a coronary stenosis that obstructed at least 50% of at least one major coronary artery (diameter of at least 1.5 mm) in 192 of the 525 patients (37%).

The genomic test algorithm prospectively divided the participants into a low-risk group of 174, a medium-risk group of 177, and a high-risk group of 174. Subsequent angiography found a coronary disease prevalence of 17% in the low-risk group, 33% in the medium-risk group, and 60% in the high-risk group.

The genomic test performed better than the Diamond-Forrester method or the Framingham risk score for predicting obstructive coronary artery disease.

The gene-test algorithm results accounted for 72% of the coronary artery disease found in the study. In contrast, applying the Diamond-Forrester method for determining coronary disease risk in these patients accounted for 66% (N. Engl. J. Med. 1979;300:1350-8).

A more detailed comparison showed that Diamond-Forrester identified 150 of the patients (29%) at medium risk for coronary disease, and the overall rate of actual disease in these people was 39%.

With the genomic test algorithm, 32 were identified as actually having a low risk, 53 as medium risk, and 65 as high risk. The actual coronary disease rate found within each of these subgroups confirmed the validity of the gene-test reclassification: In the 32 people categorized as low risk by the genomic test but medium risk by Diamond-Forrester, the actual rate of coronary disease was 25%. Among the 53 medium-risk patients, the prevalence of actual coronary disease was 30%. And in the 65 high-risk patients, the actual prevalence was 52%.

The genomic-test algorithm has similar success reclassifying the coronary disease risk when the first determinant used was the Framingham risk score.

The gene-test algorithm also performed better than myocardial perfusion imaging. Among the 310 of the 525 patients who underwent myocardial perfusion imaging, the imaging identified 87 at low risk for coronary disease and 223 at high risk. Within the high-risk subgroup, the genomic tests rated 57 as being at low risk, and in these people the prevalence of coronary disease on angiography was 11%. That compared with a 56% coronary disease prevalence in those identified as high risk by the genomic test. ■