

Genetic study reveals ancestry-specific risk factors for coronary artery disease

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A large team of researchers affiliated with a host of institutions across Japan has identified multiple loci associated with ancestry-specific risk factors for coronary artery disease. In their paper published in the journal *Nature Genetics*, the group describes their analysis of genetic information from several publicly available databases and its results.

Coronary artery disease is a condition that develops in patients who experience thinning or blocked coronary arteries, usually because of atherosclerosis. Patients with the disease can experience shortness of breath, [chest pain](#) and sometimes a heart attack. In recent years, medical scientists have discovered that there is a genetic component involved with [coronary artery disease](#) that makes some people more susceptible to developing the disease. Studies have sought to identify [genetic markers](#) for coronary artery disease susceptibility, but as the authors with this study note, most of them have involved study of people living in the West. In this new effort, the researchers sought to find markers present in Asian people, most specifically, those with Japanese backgrounds.

The work began with obtaining and analyzing [genetic data](#) from the BioBank Japan effort. Data

in the BioBank included results from whole-genome sequencing for almost 1,800 people with coronary artery disease and 2,636 without. The team next included data from a host of other databanks of information regarding results of whole-genome sequencing. In all, the team analyzed data for 25,892 people with coronary artery disease and 142,336 without. They found eight previously unidentified loci that could be associated with coronary artery disease—and several variants that could be associated with the severity of the disease. Emboldened by their findings, the researchers obtained more data from other databanks and added it to their study. As a result, the researchers identified 175 loci with ties to coronary artery disease.

The researchers then created a map outlining [risk factors](#) for patients with the markers they identified, which they used to create scores. They suggest that in the future, the scores they derived could be used to assist in early diagnoses and treatment for people who have a heightened risk of developing [coronary artery](#) disease.

More information: Satoshi Koyama et al. Population-specific and trans-ancestry genome-wide analyses identify distinct and shared genetic risk loci for coronary artery disease, *Nature Genetics* (2020). [DOI: 10.1038/s41588-020-0705-3](https://doi.org/10.1038/s41588-020-0705-3)

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