NEWS

Press release

EMBARGOED UNTIL
Thursday, Oct 25 at 8:00 AM PT

GENETIC ADVANCES IN CARDIOVASCULAR DISEASE ANNOUNCED

San Diego—Thursday, October 25, 2007. Two reports on important genetic breakthroughs related to cardiovascular disease will be presented at the 57th Annual Meeting of the American Society of Human Genetics in San Diego, California, October 23-27.

deCODE Genetics Finding May Help Prevent Stroke

Researchers at deCODE Genetics and collaborating institutions have identified two genetic variations (SNPs) associated with increased risk of atrial fibrillation (AF), which is the most common sustained cardiac arrhythmia in man and is the leading cause of cardiogenic stroke.

On the heels of this discovery, deCODE has launched a reference laboratory test (deCODE AF™) for the two SNPs. The company believes that testing for these SNPs will provide doctors with a targeted and cost-effective means of identifying those who should be intensively monitored for AF. Current best clinical practice recommends that stroke patients with AF can significantly reduce their risk of a second stroke by taking the anticoagulant drug warfarin.

In their work, the researchers first showed, in a genome-wide association study, that SNPs on chromosome 4q25 are associated with the risk of AF in an Icelandic population. Additional studies in European-descent populations from Iceland, Sweden, the United States, and Norway confirmed that two of the SNPs are strongly associated with the risk of AF in these additional populations. The researchers estimate that approximately 35% of those of European descent carry at least one of the two SNPs and that the risk of AF is increased by approximately 70% or 40% per copy in these individuals, depending on the SNP.

Additional testing in a Chinese population showed that 75% of this population carried the stronger of the two SNPs. The risk of AF is increased by approximately 40% per copy for this stronger SNP in the Chinese population.

The authors noted that the SNPs are in the same linkage disequilibrium block (i.e., in the same region of chromosome 4q25) and that this block is adjacent to the *PITX2* gene, which is known to play a critical role in left-right asymmetry of the heart.

If you have any questions, please contact Ms. Berglind Olafsdottir at DeCODE. Tele: 354-664-2393

deCODE Extends Studies on Heart Attack Risk Factor; Offers Test

Researchers at deCODE Genetics and collaborating institutions have shown that a single sequence variant (a SNP) in chromosome region 9q21 is associated with atherosclerosis in multiple different vascular regions. Atherosclerotic cardiovascular disease (CVD) is the leading cause of death worldwide. In earlier work, the authors had shown that this particular SNP is associated with increased risk of myocardial infarction/coronary artery disease (MI/CAD).

This month, deCODE began offering a reference laboratory test for this SNP (rs10757278) to gauge individual risk of heart attack. Because this SNP represents a genetic risk factor that is independent of other risks such as cholesterol, obesity, and smoking, the company believes it provides a novel means of identifying individuals who may derive particular benefit from earlier and more aggressive prevention efforts.

SNP rs10757278 is located adjacent to two tumor-suppressor genes, *CDKN2A* and *CDKN2B.* These genes are known to play key roles in processes - cell proliferation, cell aging, and programmed cell death – involved in the development of atherosclerotic plaques within arteries.

Approximately 21 percent of the Caucasian population is homozygous for this SNP and this leads to a risk of MI that is 1.64-fold (64%) greater than that for those who do not carry the variant. The risk of early-onset MI is 2.02-fold (102%) greater in homozygotes than in non-carriers.

In the current work, the authors extend their studies of SNP rs10757278 to those with other atherosclerosis phenotypes—including peripheral artery disease, large vessel disease stroke, and abdominal aortic aneurysm. For each of these phenotypes, the researchers studied two to five Caucasian case-control groups. They found significant association between SNP rs10757278 and each of the tested phenotypes in all the groups tested.

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The authors also report replication of the association of another 9q21 SNP (rs10811661) with type 2 diabetes (T2D) in patient groups from Iceland, Denmark and the United States. They did not, however, see an association between T2D and SNP rs10757278.

If you have any questions, please contact Ms. Berglind Olafsdottir at DeCODE. Tele: 354-664-2393

For more information please contact Jane Nelson, ASHG Communications, on site at the San Diego Convention Center at 619-525-6413 (Room 24C)