

**American College of Cardiology – March 8, 2004 – New Orleans, LA**

***Poster presentation:***

Novel Genetic Markers Associated With Myocardial Infarction: A Genomic Scale Scan of Putative Functional Polymorphisms

***Background:***

Scientists from Celera Diagnostics and the University of California, San Francisco conducted a genetic study to identify gene variants associated with increased risk for myocardial infarction (MI), commonly known as heart attack.

Celera Diagnostics used industrial-scale high-throughput genotyping to discover and replicate single nucleotide polymorphisms (SNPs) associated with MI. Two approaches were employed:

Candidate gene study – More than 250 genes suspected to be associated with MI were included and 288 SNPs within those genes were genotyped.

Genome wide scan – Using pooled DNA, the allele frequencies of 16,000 functional SNPs were determined. Functional SNPs are those predicted to alter the amount, activity or stability of encoded proteins.

***Key Points:***

- This poster identifies the SNPs in the three genes that Celera Diagnostics and UCSF first reported to be novel associations with risk for MI in September 2003 at the International Symposium on Atherosclerosis. [\[Read press release.\]](#)
- An additional novel association with a SNP in a fourth gene is identified for the first time.
- These findings have been replicated in a second independent large sample set.
- The increased risk for MI associated with each of these polymorphisms individually is comparable to traditional individual risk factors for MI (smoking, blood pressure, cholesterol, family history of early heart disease, age).
- None of these genes is in an established pathway known to be associated with MI.

***Significance:***

Using a combination of a candidate gene approach and a genome wide scan, Celera Diagnostics was able to efficiently analyze allele frequency differences in studies of 3,958 case and control samples. The large number of cases and controls provide statistical power to the associations reported.

To increase the speed and capacity of the whole genome scan, allele frequencies were measured in pools of DNA from multiple individuals.

Oftentimes, initial reports of gene-disease associations are not subsequently replicated. For gene-disease associations to be broadly useful for diagnostic and therapeutic applications, replication of associations is essential. All the results reported by Celera Diagnostics and UCSF at the ACC conference have been replicated in a second independent sample set.