

## **Expression Profiling of Peripheral Blood Cells Identifies Genes That Distinguish Patients With and Without Coronary Artery Stenosis**

### **Category:**

Vascular Disease, Hypertension and Prevention

### **Sub-category:**

Vascular Biology/Atherosclerosis/Thrombosis/Endothelium

### **Abstract No.:**

1007-210

### **Meeting:**

ACC.08

### **Citation:**

*J. Am. Coll. Cardiol.* 2008;51;A289

### **Authors:**

James A. Wingrove, Amy J. Sehnert, Whittemore G. Tingley, Michael Elashoff, Susan E. Daniels, Nicholas F. Paoni, Lori Littleford, Rachel L. Nuttall, Michael Doctolero, Steven Rosenberg, Lutz Buellfeld, Eberhard Grube, L. Kristin Newby, William E. Kraus, Duke University, Durham, NC, CardioDx, Inc, Palo Alto, CA

### **Abstract:**

**Background:** Coronary artery disease (CAD) is characterized by vessel wall inflammation and cytokine release; how this relates to gene expression in circulating cells is unknown. To address this, we compared global gene expression of blood cells between patients with and without angiographic evidence of CAD.

**Methods:** Total peripheral blood mononuclear cell (PBMC) RNA was isolated from patients undergoing coronary angiography. Cases had 70% stenosis in >1 vessel or 50% stenosis in >2 vessels; controls had 0% luminal stenosis. We performed whole genome microarrays on 41 subjects (27 cases, 14 controls), then performed RT-PCR on two independent cohorts comprising 214 subjects (160 cases, 54 controls), using either PBMC or total blood RNA.

**Results:** Array analysis yielded 520 genes with >1.3 fold differential expression ( $p < 0.05$ ). Of these, 110 genes, including the most significant genes from microarrays and additional literature genes, were tested by RT-PCR on the two independent cohorts. 52 genes ( $p < 0.05$ ) discriminated patients with and without CAD; 16 were significant in both cohorts. These included S100 family members, CSF, cytokine and scavenger receptors, and complement and proteoglycan components. The figure shows the relationship between gene expression and CAD severity.

**Conclusion:** Peripheral blood gene expression can reflect the presence or absence of CAD and represents a possible tool for development of a diagnostic classifier to distinguish these patients.

