**MICRORNAS AS A WINDOW INTO CELLULAR PROCESSES OCCURRING SOON AFTER ACUTE MYOCARDIAL INFARCTION**

**C. Watt**, P. Sirish, N. Chiamvimonvat, J. López.

University of California, Davis, Sacramento, CA, USA

Objectives: To identify dysregulated cellular processes in acute myocardial infarction (MI) patients by measuring circulating microRNA expression signatures and performing gene ontology analysis.

Background: Using biomarkers to identify cellular processes occurring shortly after MI offers a novel approach to predicting disease activity.

Methods: MicroRNAs in blood from two patients presenting with acute ST-elevation MIs (STEMI) were sampled at hospital discharge. We compared microRNA expression profiles from microarrays to those of two individuals without heart disease (controls) and identified dysregulated microRNAs attributed to MI and therapies during hospitalization. To identify cardiac-enriched candidate microRNAs, 27 microRNAs known to play roles in cardiac disease were identified from literature. Candidates for target gene annotation and gene ontology analysis were selected by representation in these cohorts.

Results: 38 microRNAs were differentially expressed with fold change >2.0 between STEMI patients and controls. These microRNAs were compared against cardiac-enriched microRNAs. Five dysregulated microRNAs (miR-21\*, -29a, -126\*, -199b-5p, and -423-5p) were found to be cardiac-enriched. Target gene annotation yielded 1400 targets. Gene ontology analysis generated cellular processes known to play roles in cardiac remodeling. The most highly enriched process was the blood clotting cascade.

Conclusions: We have performed gene ontology analysis of dysregulated microRNAs in STEMI patients and have predicted cellular processes such as clotting and inflammation that play roles in cardiac remodeling soon after acute MI.

