May 22nd, 4:30 PM - 6:00 PM

Circulating microRNAs are associated with Paroxysmal or Persistent Atrial Fibrillation

David D. McManus
University of Massachusetts Medical School

Jeanine Ward
University of Massachusetts Medical School

Amir Y. Shaikh
University of Massachusetts Medical School

See next page for additional authors

Presenter Information
David D. McManus, Jeanine Ward, Amir Y. Shaikh, Khushleen Jaggi, Victor R. Ambros, Jane Freedman, and John F. Keaney Jr.

CIRCULATING MICRORNAS ARE ASSOCIATED WITH PAROXYSMAL OR PERSISTENT ATRIAL FIBRILLATION

David D. McManus, MD[1]; Jeanine A. Ward, MD PhD[2]; Amir Y Shaikh, MD[1]; Khushleen Jaggi, MD[1]; Victor Ambros, PhD[3]; Jane E. Freedman, MD[1]; John F Keaney Jr., MD[1]

[1]Departments of Medicine, [2]Emergency Medicine, and [3]Molecular Medicine, University of Massachusetts Medical School, Worcester, MA 01655

Contact information: David D. McManus, MD; Phone 508-856-3905; Email mcmanusd@ummhc.org

Abstract:

Introduction: Novel methods of identifying individuals at risk for atrial fibrillation (AF) are needed. MicroRNAs (MiRNAs) regulate gene expression in a number of cardiovascular diseases, including AF. It is unknown, however, if key circulating, cardiac-specific miRNAs differ between individuals with paroxysmal or persistent AF and those in sinus rhythm.

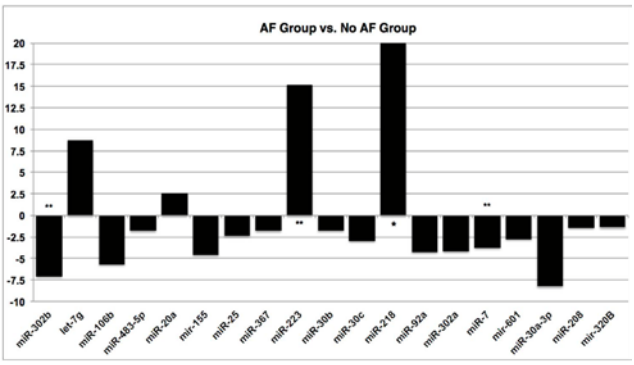
Methods: 17 individuals with a history of AF were recruited prior to catheter ablation. 24 hospitalized patients in normal sinus rhythm and no history of AF comprised the control group. 94 plasma miRNAs were selected based on *a priori* associations with processes implicated in AF for evaluation using the TaqMan miRNA expression profiling system.

Results: We found that miRNA expression differed by at least 2-fold for 14 miRNAs, including several previously implicated in cardiovascular remodeling and disease (**Figure 1**). Levels of miR-7, miR-208, and miR-302b were statistically significantly up- or down-regulated in AF patients relative to controls ($p<0.05$) and levels of miR-218 differed by greater than 20-fold ($p=0.095$).

Application: Although power was limited by the modest sample size, these data support the rationale for using circulating miRNA as AF biomarkers. Moreover, since miRNA can modulate disease pathways, miRNA-based therapeutics would theoretically enable targeting of novel gene regulatory pathways implicated in AF in a unique and powerful manner.

Next Steps/ Future: Further investigations involving well-characterized, large samples from longitudinal studies with standardized miRNA assessment and evaluation for AF are required to validate the observed associations.

Figure 1. MiRNAs Differentially Expressed (Fold-Difference) in Patients with AF as compared without AF



*miR-218 expression was >20-fold higher in AF patients than in controls (p value = 0.095)
**Fold-difference in miR-302b, miR-223, and miR-7 were significantly different between AF and controls ($p<0.05$)