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Role of microRNAs in atrial fibrillation

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Introduction: Atrial fibrillation (AF) is the most common arrhythmia encountered in the US affecting 5.2 million Americans, and the growing burden of AF has profound health implications due to the association of AF with an increased risk of stroke, heart failure, and mortality. MicroRNAs (miRNAs) are small, endogenous, single-stranded, noncoding RNAs that have recently gained status as key determinants in gene expression regulation in cardiovascular development and disease. Few biomarkers exist to identify individuals at risk for AF or response to therapies such as ablation. We conducted the present study to investigate if plasma miRNAs with putative gene targets implicated in cardiac remodeling were associated with AF, and to examine whether or not expression of miRNAs changed after AF ablation.

Methods: We prospectively recruited 211 participants (112 with AF; 99 without AF) presenting to the University of Massachusetts Medical Center. We quantified plasma levels of 86 miRNAs by high-throughput qRT-PCR at baseline in all participants and 1-month post-ablation in 47 participants with AF.We performed global mean normalization prior to analyses and used logistic regression to examine associations between plasma miRNAs and AF.

Results: We observed that plasma levels of 21 miRNAs were associated with AF and 31 plasma miRNAs changed after ablation. Notably, miRs-21 and 150 were associated with AF and changed after ablation.

Conclusion: Our results implicate several miRNAs known to be involved in cardiac development, conduction, and stress response in the pathogenesis of AF. We found that miRs-21-5p and 150-5p were associated with AF. 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.

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