Circulating MicroRNAs in Cardiovascular Disease

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MicroRNAs (miRNAs) are short, single-stranded, non-coding, highly conserved posttranscriptional regulators found in a variety of tissues including circulating blood. MicroRNAs regulate gene expression posttranscriptionally through inhibiting translation from and/or inducing degradation of specific RNAs. Certain miRNAs are expressed and function cell-type specifically or in association with particular physiological processes. MicroRNAs contribute to cardiac development and remodeling, and miRNAs found in cardiac tissue show dynamic changes in the setting of heart disease, suggesting their involvement in the regulation of cardiovascular disease (CVD). Mouse and human studies have emphasized the importance of individual miRNAs in different forms of CVD, including myocardial infarction (mirR-1, miR-133a, miR-208a, and mir-499), atrial and ventricular arrhythmias (miR-1, miR-133, and miR-328), fibrosis (miR-21 and miR-29), and ventricular hypertrophy (miR-208 and miR-133).

Intracellular levels of miRNAs provide information about regulatory pathways involved in mediating the cardiomyocyte injury response. MicroRNA 133a, for example, has been shown to target the ion-channel–encoding genes HCN2 and HCN4. mir-208a is encoded in the intron of the heavy chain gene and indirectly influences myosin heavy chain and connexin-40 expression, and mir-499 is intronic with the myosin gene Myh7b. Intronic miRNA are coded within a host gene, often regulating pathways similar to those of the protein encoded by that gene and frequently acting to regulate a single biological process. Whether circulating miRNAs such as miR-133a and miR-499 function as signaling molecules or are simply released after cardiomyocyte injury remains unknown, but the functional redundancy of miRNAs would suggest that miRNAs help to mitigate biological perturbations such as occur during an ACS. Although De Rosa’s findings firmly establish that miR-133a and miR-499 are produced by the heart and are specific to an ACS, important questions remain unanswered, such as whether or not secreted miRNAs serve to influence gene regulation in other parts of the heart (eg, in peri-infarct or noninfarcted zones) or in other organs.

As evidenced by the authors’ surprising finding that miR-126 levels decrease across the transcoronary circulation (Figure), much remains unknown about the acute processes regulating circulating miRNA levels, especially in the setting of an ACS. The authors propose that the negative miR-126 transcoronary gradient may be explained by the secretion of proteases and/or RNases by injured or ischemic myocytes. Although nonspecific degradation of circulating proteins conjugated to miRNAs or miRNAs themselves may explain the negative miR-126 transcoronary gradient, an alternative hypothesis is that miRNAs such as miR-126 function as signal-
ing molecules and are taken up by injured cardiomyocytes in a specific fashion. More information is needed about the biochemical composition of important circulating miRNAs and how this relates to miRNA stability and uptake.

Modulation of miRNAs has opened exciting opportunities for miRNA-based therapies in the treatment of CVD. Indeed, miRNA mimics and anti-miRs are currently under development and have been advanced to clinical trials. Further study is warranted of circulating miRNA secretion, clearance and potential function in patients with CVD. In addition to the potential role of miRNA as biomarkers, miRNAs will provide new insights into CVD pathogenesis and new applications for CVD prevention and treatment in the near future.

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None.

**References**


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