Serum Levels of MicroRNAs in Patients with Heart Failure

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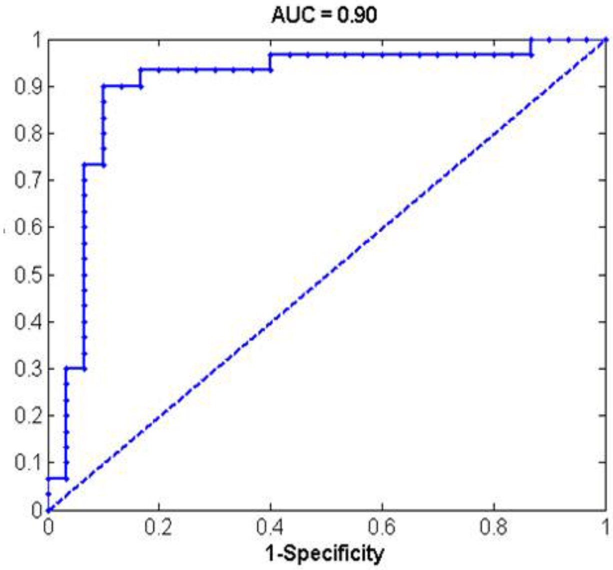

Background: Diagnosis and risk stratification of patients with heart failure remain a challenge. The small noncoding RNAs known as microRNAs, regulate gene expression and seem to play an important role in the pathogenesis of heart failure. In the current study we aim to characterize the levels of microRNAs in the sera of chronic systolic heart failure patients versus controls and assess the possible correlation between elevation in the levels of specific microRNAs and clinical prognostic parameters in heart failure patients.

Methods and results: The levels of 186 microRNAs were measured in the sera of 30 stable chronic systolic heart failure patients and 30 controls using qRT-PCR. The differences in microRNA levels between the two groups were characterized and a score, based on the levels of 4 specific microRNAs with the most significant increase in the heart failure group (miR-423-5p, miR-320a, miR-22, and miR-92b), was defined. The score was used to discriminate heart failure patients from controls with sensitivity and specificity of 90% (Image-1). Moreover, in the heart failure group, there was a significant association between the score and important clinical prognostic parameters such as elevated serum natriuretic peptide levels, wide QRS, and dilatation of the left ventricle and left atrium ($r=0.63$, $p=3e-4$; $p=0.009$; $p=0.03$; $p=0.01$ respectively).

Conclusions: Elevated serum levels of specific microRNAs: miR-423-5p, miR-320a, miR-22,and miR-92b, identify systolic heart failure patients and correlate with important clinical prognostic parameters.