

Preface



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Guest Editor

Until recently, the classification of heart failure (HF) has focused on the anatomic cause of failure of the cardiac pump (eg, valvular heart disease, hypertension, chronic coronary artery disease, and so forth), the pathophysiology (eg, reduced or normal ejection fraction), and the clinical features (eg, the acuity and severity of the HF). A biomarker profile can be a valuable addition to this approach. The major classes of biomarkers for HF discussed in this issue of *Heart Failure Clinics* are usually considered individually, as they were done so expertly in this issue. However, investigators are finding increasingly that a multimarker strategy may be useful in refining risk stratification in patients who have acute coronary syndrome,¹ and there is a growing interest in utilizing this approach in HF as well.²

It has been demonstrated that using troponin together with BNP can achieve a more accurate stratification of risk than can be obtained with either biomarker alone.^{3–5} The accuracy of risk prediction was also enhanced when a natriuretic peptide was coupled with other biomarkers of myocardial stress—adrenomedullin⁶ and ST-2⁷—as well as with the inflammatory biomarkers C-reactive protein (CRP) and myeloperoxidase.⁸ Zathelius and colleagues have shown that the combination of four biomarkers (Tnl, NTproBNP, CRP, and cystatin C) improves risk stratification for total cardiovascular mortality in elderly men.⁹

From the foregoing, the next logical step is to obtain a profile using the seven classes of biomarker described in this issue (**Fig. 1**). This profile should provide not only a more accurate risk stratification, but it may provide clues to the pathophysiology of HF in any given patient and point the way to individualized therapy. New

approaches to bioinformatics, including the use of neural networks, will be needed to assist in data analysis and its clinical application.

We are now moving rapidly into the proteomic era, which provides a greatly expanded approach to the study of proteins, their variations, and their concentrations. The evaluation of proteins using mass spectrometric analysis coupled with high pressure liquid chromatography is likely to yield totally new classes of biomarkers of HF.¹⁰ Large platforms of hundreds of proteins are likely to provide deeper insights into the detection of ventricular dysfunction, elucidating pathogenesis, and in monitoring the therapy of HF. As a result of these expanding technologies, advances in

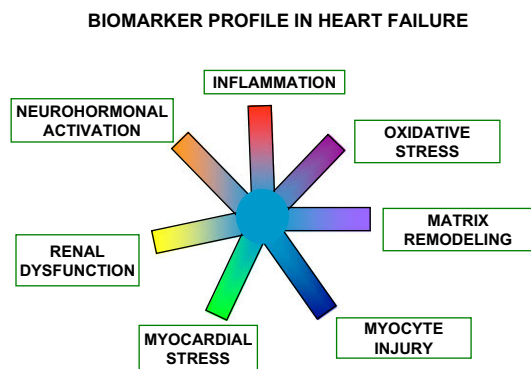


Fig. 1. Seven axes representing the classes of biomarkers discussed in this issue. It is proposed that a representative marker of each class be measured in patients who have established HF, or who are at risk for HF. The resultant biomarker profile should enhance prevention, treatment, and prognostication. Other classes of biomarkers are likely to be added in the future.

biomarkers in the next ten years may be expected to be greater and to have even more impact on the detection, risk assessment, and management of patients who have HF than those advances that have occurred since work in this field began a half of a century ago.

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