A decade ago, a 64-year-old male presenting with fatigue and anemia and a diagnosis suggested of chronic lymphocytic leukemia would be given a standard therapy with an uncertain prognosis. Today, that same patient undergoing molecular profiling of proteins on their lymphocytes detecting ZAP-70 and CD-38 protein markers determines not only the prognosis but how the therapy should be tailored. This is a recurrent theme in the oncology field—breast cancer, lung cancer, AML, CLL, and many other conditions. Yet in cardiology, we have lagged behind our oncology colleagues in our ability to tailor therapies that provide the greatest benefit.

The fundamental principles behind precision medicine are establishing clinical phenotypic characterization with state-of-the-art molecular profiling to enhance diagnostic, prognostic, and therapeutic strategies. It is through this combined approach that a tailored treatment strategy is believed to be able to enhance outcomes. There are many hurdles, however, to accelerating this field. The regulatory environment has not progressed as rapidly as we had hoped. Drug development has increased in time and cost by 75% over the past decade with no ability to prove enhanced safety. Multiple clinical trials in cardiology enrolling thousands of patients over years of exposure often reveal neutral results and subsequent lost datasets which do not allow us to explore potential subgroups with specific molecular signatures which may have enhanced benefit.

We have lagged years behind in our classification of diseases, and it is necessary that a new taxonomy of diseases be a part of our transformation to the better understanding of our cardiovascular patients. Millions of dollars have been invested in electronic health records to store comprehensive individual-specific data; yet our ability to extract this information and utilize it for tailoring therapies is limited. The investment and decision tools and decision support has been significantly hampered by the implementation cost of electronic health records. It will be necessary to integrate these large databases of information with our molecular signature profiles.

In this issue of JACC: Heart Failure, we have emphasized some of the novel investigations looking at better ways to predict, characterize, and tailor diagnostic, prognostic, and therapeutic opportunities for our cardiovascular patients. As we reflect on recent clinical trials, such as TOPCAT, in which the overall primary endpoint was negative, yet there was a strong signal of advantage in patients who had elevated brain natriuretic peptide levels at the time of enrollment, we think about precision medicine across the spectrum of clinical care and research. We should adapt these important signals into clinical guidelines or suggest that they be integrated into clinical practice. We should have a greater willingness to accept results and information in patients who have molecular signatures that afford the potential greatest benefit. It is a commitment of this journal to continue to foster knowledge that will help the cardiovascular heart failure field move forward in the field of predictive and precision medicine so that we may optimize our diagnostic, prognostic, and therapeutic options for the patients that we care for with our ultimate goal to improve their quality of life and their longevity.

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