

## Cappola et al Clinical Perspective

Heart failure is a common, heterogeneous disorder that leads to substantial morbidity and mortality in the developed world. Although population-based studies have demonstrated a genetic component to common forms of heart failure, specific risk loci have been difficult to identify. Here we tested the broad hypothesis that common genetic variation in ~2000 candidate genes of known importance to cardiovascular biology contribute to heart failure risk. We found that common SNPs in *HSPB7* (rs1738943) and *FRMD4B* (rs6787362) were associated with advanced heart failure in two Caucasian referral populations, but not in African Americans. For both SNPs, the minor allele was less frequent in cases than in controls, indicating that patients who carry the minor allele are at lower risk for heart failure, though the magnitude of these changes in risk are too small to be applied clinically. Our findings thus identify *HSPB7* and *FRMD4B* as novel heart failure susceptibility loci and should stimulate resequencing efforts and mechanistic studies to identify the underlying mechanisms.