Approximately 600,000 US citizens die from cardiovascular disease annually, including males and females across all ethnic groups. The development of diagnostics and treatments often ignore the differences in biochemistry and genetics involved in disease development and presentation. Our objective is to define the molecular basis for sex-specific pathophysiologic differences through the study of differential gene expression in heart failure. Using RNA extracted from myocardial tissue and Taqman PCR to measure expression levels of both mRNA and miRNA (inhibitory RNA, which do not become proteins), we have defined sex specific patterns of genes involved in cardiac fibrosis and contractility.