**GENETICS IN THE MANAGEMENT OF DILATED CARDIOMYOPATHY**  
**L. Mestroni**

University of Colorado Anschutz Medical Campus, Aurora, CO, USA

Nonischemic dilated cardiomyopathy (DCM) is a common heart disease, associated with high risk of progressive heart failure, arrhythmia and sudden cardiac death. In a large proportion of patient, DCM has a genetic etiology and a familial transmission. Compared to other cardiomyopathies, such as hypertrophic cardiomyopathy, a large number of mutant genes and alleles have been associated with DCM. While in the past, the genetic heterogeneity of DCM was an important technical limitation for genetic testing, the current sequencing technology allows comprehensive genetic testing, encompassing large gene panels with over 100 cardiomyopathy genes. Genetic diagnosis can help predict prognosis, and recently, special attention has been given to a subgroup of DCM patients with high risk of sudden cardiac death and life-threatening arrhythmias. In this group of arrhythmogenic DCM patients, the most frequent and best known causal gene is the lamin A/C gene (*LMNA*), which has been established by the 2017AHA/ACC/HRS as a special indication for implantable defibrillator in selected cases, regardless of the severity of the left ventricular dysfunction. The identification of the causal gene allows for cascade genetic testing in family members, and can identify carriers of the mutant gene who are at-risk of disease, providing opportunities for prevention of complications and early intervention. In the management of dilated cardiomyopathy, the role of genetic evaluation, including an accurate family history, genetic testing and genetic counseling, is now established. Although, the classification of cardiomyopathies based on cardiac morphology is still of clinical use, genetics is now positioned to contribute to the subclassification of cardiomyopathy and DCM, guide in the management and provide the framework for the development of novel therapies.