Genetic Evaluation of Cardiomyopathy - A Heart Failure Society of America Practice Guideline

Short Title: Genetic Evaluation of Cardiomyopathy

Ray E. Hershberger[a, b]

Michael Givertz[c]

Carolyn Y. Ho[c]

Daniel P. Judge[d]

Paul Kantor[e]

Kim L. McBride[f]

Ana Morales[a]

Matthew R. G. Taylor[g]

Matteo Vatta[h,i]

Stephanie M. Ware[j,k]

From the [a]Divisions of Human Genetics and [b]Cardiovascular Medicine, The Ohio State University Wexner Medical Center, Columbus, OH; Ray.Hershberger@osumc.edu, Ana.Morales@osumc.edu

[c]Cardiovascular Division, Brigham and Women's Hospital, Boston, MA; mgivertz@bwh.harvard.edu, cho@partners.org

[d]Division of Cardiology, Medical University of South Carolina, Charleston, SC; judged@musc.edu

[e]Division of Pediatric Cardiology, University of Alberta and Stollery Children's Hospital, Edmonton, Canada; Paul.Kantor@albertahealthservices.ca

This is the author's manuscript of the article published in final edited form as:

Hershberger, R. E., Givertz, M., Ho, C. Y., Judge, D. P., Kantor, P., McBride, K. L., … Ware, S. M. (2018). Genetic Evaluation of Cardiomyopathy - a Heart Failure Society of America Practice Guideline. Journal of Cardiac Failure. https://doi.org/10.1016/j.cardfail.2018.03.004

[f]Center for Cardiovascular Research, Nationwide Children's Hospital, and Department of Pediatrics, Ohio State University, Columbus OH; Kim.McBride@nationwidechildrens.org

[g]Adult Medical Genetics Program, Division of Cardiology, University of Colorado Anschutz Medical Campus, Aurora, CO; Matthew.Taylor@ucdenver.edu

[h]Invitae Corporation, San Francisco, CA and Departments of [i]Medical and Molecular Genetics, [j]Medicine, and [k]Pediatrics, Indiana University School of Medicine, Indianapolis, IN; mvatta@iu.edu, stware@iu.edu

Correspondence: Ray Hershberger, Ohio State University Wexner Medical Center, Biomedical Research Tower, Room 304, 460 West 12th Avenue, Columbus, OH 43210; Ray.Hershberger@osumc.edu; telephone 614-688-1388; fax 614-688-1381.

Word counts:

Abstract: 197

Text: 10,776

132 references: 4247

3 tables

Online Supplement: 442 words, 3 tables.

Abstract

This guideline describes the approach and expertise needed for the genetic evaluation of cardiomyopathy. First published in 2009 by the Heart Failure Society of America (HFSA), this guidance has now been updated in collaboration with the American College of Medical Genetics and Genomics (ACMG). The writing group, composed of cardiologists and genetics professionals with expertise in adult and pediatric cardiomyopathy, reflects the emergence and increased clinical activity devoted to cardiovascular genetic medicine. The genetic evaluation of cardiomyopathy is a rapidly emerging key clinical priority, as high throughput sequencing is now feasible for clinical testing, and conventional interventions can improve survival, reduce morbidity, and enhance quality of life. Moreover, specific interventions may be guided by genetic analysis. A systematic approach is recommended: always a comprehensive family history; an expert phenotypic evaluation of the proband and at-risk family members to confirm a diagnosis and guide genetic test selection and interpretation; referral to expert centers as needed; genetic testing, with pre- and post-test genetic counseling; and specific guidance as indicated for drug and device therapies. The evaluation of infants and children demands special expertise. The approach to manage secondary and incidental sequence findings as recommended by the ACMG is provided.

Key Words: cardiomyopathy; genetics; genetic analysis; practice guideline; secondary findings.

Introduction

Continued rapid progress has been made in understanding the genetic basis of cardiomyopathy. This work, which describes the content, approach and expertise needed for a cardiomyopathy genetic evaluation, was first developed in a guideline statement in 2008 and published in 2009 for the Heart Failure Society of America (HFSA).[1] This has now been updated by a writing group organized with the American College of Medical Genetics and Genomics (ACMG) and the HFSA to serve as a practice resource (ACMG) and as a revised guideline statement (HFSA).

This collaboration of cardiovascular and genetics professionals mirrors a recent proliferation of specialized cardiovascular genetics clinics.[2] Most commonly cardiologists, adult or pediatric, with special interest or training in cardiovascular genetics, team up with genetics professionals, usually board-eligible or board-certified genetic counselors and/or clinical geneticists, ideally with cardiovascular expertise, to provide state-of-the-art genetics services to the many patients and families with cardiomyopathy. This growth has been triggered by improvements in technology for clinical genetic testing, resulting in the availability of large clinical genetic testing panels, where numerous genes of interest can be sequenced quickly, efficiently and accurately using continually developing massively parallel DNA sequencing technologies. This growth also recognizes the critical importance of integrated expert phenotypic information with final clinical recommendations in light of burgeoning sequence information.[3]

This collaboration also speaks to the recent prominence of cardiovascular genetics and genomics brought about by the emergence of clinical exome sequencing and the ACMG recommendation, first in 2013[4] and updated in 2016,[5] to return relevant and actionable secondary findings. Of the 59 medically actionable genes cited in 2016, 30 (51%) had cardiovascular phenotypes, and 16 (27%) were genes that included cardiomyopathy

phenotypes. By request from the ACMG, we also provide guidance for secondary findings derived from cardiomyopathy genes.

The rationale for the inclusion of cardiomyopathy genes in the ACMG secondary findings list, and the basis for the clinical screening, counseling and molecular recommendations contained herein, are because the cardiomyopathies are medically actionable: well established treatments or interventions are available to improve survival, reduce morbidity, and enhance quality of life.[6, 7] Cardiomyopathies may present late in their course with advanced disease, which includes heart failure, heart block and/or life-threatening arrhythmias including sudden cardiac death, and thromboembolic events, including stroke from atrial arrhythmias or ventricular thrombus. Thus, the rationale to identify genetic risk is compelling, so that those found to be at-risk can undergo interval screening to detect the earliest manifestations of the cardiomyopathy phenotype. The first evidence of a phenotype then permits earlier interventions,[7] including lifestyle modifications, drugs to slow or halt disease progression or to prevent thromboembolism, and procedures, drugs or devices to reduce the risk of sudden cardiac death.[6] Identification of at-risk individuals, whether affected but asymptomatic or those clinically unaffected may also have implications for genetic counseling and reproductive decision-making.

Cardiovascular physicians are expert at assessing the nuances of cardiomyopathy phenotypes or sub-phenotypes, an essential contribution to cardiovascular genetics care. As in 2009,[1] our current approach continues to be stratified by cardiomyopathy phenotype, as clinical and genetic data collection, analysis and decision making for the cardiomyopathies remain anchored by phenotypic categories.

The Family as the Unit of Care

A critical transition for cardiovascular practitioners who wish to more fully actualize cardiovascular genetic medicine is to adopt the family as the unit of care, a concept inherently understood by genetics professionals. For cardiovascular providers, moving the care paradigm

beyond the patient (proband), who often presents with a fully developed phenotype and at times with advanced life-threatening disease, to at-risk relatives is mandatory to fulfill the promises of precision medicine. Moreover, collaboration with and care for the family unit is an essential component of the genetic evaluation. This includes establishing a genetic etiology for the proband and affected family members, the clinical evaluation of at-risk family members, cascade genetic testing of family members as indicated, and genetic counseling at all steps. All of this will not only augment the evidence of variant pathogenicity but also will provide insight into penetrance, age of onset, pleiotropy and disease expression.

Ideally family-based cardiovascular genetic medicine also means developing integrated teams with pediatric and adult training and expertise that are able to provide coordinated care across all age groups. Identification of disease and pathogenic variants in an adult parent facilitates testing and potential treatment of pediatric-aged children. Conversely, if the index case is a child, the testing and treatment of adult-aged relatives may also be needed. Thus, we recognize the critical need to address accessible delivery of care of the family across all ages. This also includes managing insurance coverage for the evaluation of asymptomatic relatives based on their family history.

Genetic cardiomyopathy has substantial complexity, as shown by overlap in phenotype as well as an overlap of genes.[8] Despite this complex interplay of genes, variants and phenotypes, current knowledge when combined with expert phenotyping and the sensitivity and specificity of current genetic testing, is sufficient to effectively conduct genetic cardiomyopathy evaluations. We caution, however, that variant interpretation must be thoughtful, rigorous and leverage the most up-to-date approaches, as not all variants identified by genetic testing will be clinically significant or disease-causing. Key resources include use of the most recent ACMG/AMP guidance,[5, 9] now being augmented by ClinGen, a National Human Genome Research Institute-sponsored initiative to curate genes and variants and place them into

ClinVar, a publically accessible database,[10, 11] and other large publicly accessible reference databases.

Types of Cardiomyopathy

The genetic basis of hypertrophic cardiomyopathy (HCM) is well established, largely a disease caused by mutations in genes encoding sarcomeric proteins. That familial dilated cardiomyopathy (DCM) has a genetic basis is also well accepted. By DCM, we clarify that the DCM term herein is used in place of the more technical attribution "idiopathic dilated cardiomyopathy," where the other common and easily clinically detected causes of systolic dysfunction such as coronary artery disease, primary valvular or congenital heart disease, or prior exposure to cancer chemotherapy or other injurious drugs, have been excluded. However, the preponderance of DCM occurs without apparent familial disease, and whether non-familial DCM is principally a genetic condition remains uncertain.[8, 12, 13] The much greater numbers of genes and the diversity of variants identified (allelic and locus heterogeneity) with DCM is more extensive relative to the other cardiomyopathies,[8, 12, 14, 15] making genetic testing inherently more challenging. Arrhythmogenic right ventricular cardiomyopathy (ARVC), which is much less common than HCM or DCM, also has a well-established genetic basis associated with mutations in genes that encoded desmosomal elements. Restrictive cardiomyopathy (RCM), although quite rare, also shares in part a genetic basis with HCM.

In contrast to HCM, DCM, RCM and ARVC, the left ventricular non-compaction (LVNC) phenotype remains enigmatic and without consensus as to whether it should be considered a primary cardiomyopathy,[13] a variant morphologic trait[16] or something else.[17, 18] We favor describing it as a phenotype because an increasing body of population-derived high-quality imaging evidence, not available when LVNC was deemed a primary cardiomyopathy,[13] now shows that increased ratios of non-compacted (trabeculated) to compacted (non-trabeculated) myocardium may be present in 2-10% or more of the population depending on the definition and test sensitivity.[16, 19, 20] Further, studies in highly trained athletes [21, 22] and pregnancy,[23] suggest

LVNC may progress and regress, akin to ventricular remodeling and reverse remodeling. Therefore, LVNC has been included and referred to as a non-compaction phenotype rather than a unique form of cardiomyopathy. Additional background is provided in the online supplement.

Approaches to Review and Publication by the ACMG and HFSA

The writing group was established conjointly with the ACMG and HFSA between 2013 and 2015. The approaches to creating, curating and approving practice guidelines or practice resources for the HFSA and ACMG, respectively, have been outlined in each publication. The material covered in this and the companion document[24] are congruent with one another. Differences in scope, including supplemental materials, are denoted and cross-referenced.

The writing group was comprised of a panel of experts, board certified cardiologists and genetics professionals with experience and expertise in genetic cardiomyopathies (Supplemental Table XX), with a goal to revise a prior HFSA publication in a conjoint effort with a new document for the ACMG. Each author was screened for relevant conflicts of interest and all conflicts shown were considered non-substantial to influence the document. Dr. Vatta was included in the writing group prior to his employment with a for-profit genetic testing company; following his employment potential conflicts of interest regarding genetic testing indications were managed by his recusal from pertinent discussions.

Use of Medical Evidence in this Guideline

We address two questions here. The first question is that of clinical validity: “Does the evaluation or test correlate with the outcome of interest?”[25] Since randomized clinical trials evaluating the clinical accuracy of diagnosis with or without a genetic evaluation or genetic testing are not generally feasible, as in the prior guideline[1] we have used a different format for level of evidence. By genetic evaluation we mean a systematic approach that includes a comprehensive family history, phenotypic evaluation of the proband and at-risk family members,

genetic counseling, genetic testing, if indicated, with pre- and post-test genetic counseling, and guidance as indicated for specific drug and/or device, or other specific therapeutic interventions. By genetic testing we mean DNA sequencing or other DNA testing modalities to identify DNA variants relevant for the phenotype of interest. **Level A:** Genetic evaluation and testing has a high correlation with the cardiomyopathic disease of interest in studies with a moderate or large sample size; **Level B:** Genetic evaluation and testing has a high correlation with the cardiomyopathic disease of interest in smaller or single center studies; and **Level C:** Genetic evaluation and testing correlates with the cardiomyopathic disease of interest in case reports. All levels were assigned based upon literature review and full consensus of the writing group.

The second question is one of clinical effectiveness: "Does performing a genetic evaluation or test result in improved patient outcomes?" This question depends also on the multiple treatment options that follow from a firm genetic and phenotypic diagnosis in cardiomyopathy, as well as the perceived clinical utility, which in this context is the benefit of those who receive a genetic evaluation or test. Again, randomized studies to address this question controlling for genetic diagnosis are not feasible. Moreover, consensus on how to appropriately measure the impact of genetic evaluation and testing on personal utility of patients is still developing,[26] while the impact of genetic evaluation and testing on societal utility is a broader question beyond our current scope. Therefore, while acknowledging these constraints, we have interpreted the level of evidence within the existing HFSA framework,[27] and have based the strength of recommendations on this level, as well as on our current knowledge of clinical effectiveness from the totality of information currently available.

While we recognize that essentially no randomized controlled clinical trials have been conducted to support most of the recommendations herein, this also provides an opportunity to press our constituencies to design and conduct innovative and rigorous research studies to achieve a substantive evidentiary basis for these guidelines. While the present guidance may be

considered “expert” it is well known that well designed and rigorously performed clinical studies have routinely shown that “conventional wisdom” may be simply wrong.

Guideline 1. Obtaining a family history of at least three generations, including the creation of a pedigree, is recommended for all patients with a primary cardiomyopathy.

Cardiomyopathy Phenotype	Level of Evidence
Hypertrophic cardiomyopathy (HCM)	A
Dilated cardiomyopathy (DCM)	A
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	A
Restrictive cardiomyopathy (RCM)	A
Cardiomyopathies with extra-cardiac manifestations	A
Left ventricular non-compaction (LVNC)	see background

Key Points: A genetics professional is skilled at obtaining a reliable family history and identifying those at risk, which is critically important once genetic results have been obtained. Specific questions should be focused to elicit possible affected relatives that may not be identified in a general family history. Primary clinical data should be reviewed, whenever possible, and may require collection of relatives’ records or post mortem reports. These latter may include relevant prenatal (including fetal loss), infant, pediatric, or adult records.

Guideline 1 - Background.

The family history, a key component of any medical and genetic evaluation, is particularly relevant for the cardiomyopathies. The goals of a family history are to ascertain if the cardiomyopathy is inherited, establish the inheritance pattern, identify at-risk family members,

and provide information on disease characteristics within the family (e.g., age of onset, severity, phenotypic variability within the pedigree, and treatment response). Reduced penetrance, defined as individuals possessing a pathogenic variant but not manifesting any evidence of disease, and variable expressivity is not uncommon in cardiomyopathy. For this reason a family history of at least three generations is needed to determine the pattern of inheritance (dominant, recessive, X-linked, mitochondrial).[28] Family history of more distantly affected relatives may be informative regarding the pattern of disease within the family, through increased numbers of affected individuals in the data set.

The writing group strongly recommends placing the family history into a graphical pedigree format to enhance genetic competency for data interpretation, managing family-based clinical screening, determining the mode of inheritance, facilitating the assessment of relatives at risk, and for family counseling.[2]

Most cardiomyopathies presenting in adulthood are inherited in an autosomal dominant manner. Cardiomyopathy presenting in childhood is also frequently inherited as an autosomal dominant condition, but is more likely to have autosomal recessive, X-linked or mitochondrial inheritance than in adults. *De novo* variants may be found in children or adults. In children, *de novo* variants are most commonly identified for autosomal dominant and X-linked syndromic cardiomyopathies. A child may be the first individual in a family to come to attention with a primary HCM, DCM, or ARVC, and have a negative family history. Studies have shown *de novo* events in up to 1/3 of cases with a negative family history, however cardiomyopathy may also occur due to inheritance from an affected but asymptomatic parent unaware they have disease.[29, 30]

Assumptions regarding paternal or maternal transmission should be avoided, as bilineal inheritance of autosomal dominant cardiomyopathy (transmission of disease from both mother and father) can occur and may incur more severe and earlier onset disease. Compound or digenic heterozygous variants classified in earlier studies have been shown in up to 5% of HCM

and up to 20% in ARVC patients,[31-33] although a re-evaluation of the previously published HCM double variants applying the 2015 ACMG approach[9] indicated double pathogenic or likely pathogenic double variants were much less common.[34] Reliable data for DCM are not yet available but also may be prevalent.[35] If the inheritance pattern can be established, accurate risk assessment of relatives can be provided. While some digenic conditions have been clearly established,[36] well-designed rigorous studies investigating di- or multigenic inheritance for the cardiomyopathies are needed.

A family history provided by patients is frequently inadequate and may miss familial cardiomyopathy.[37] Details from patients regarding heart disease in their family may be lacking, and vague terms such as “heart attack” or “stroke” may be used for any sudden or unexplained death. Ideally family history should be obtained from the most informed family member. Similar to medical history, family history is dynamic and should be updated at regular intervals. Specific, focused questions should be asked to ensure affected relatives are identified. Key elements include: 1) cardiovascular symptoms (e.g., shortness of breath, paroxysmal nocturnal dyspnea, or dyspnea on exertion), or symptoms suggestive of arrhythmia, including palpitations, presyncope or syncope with or without exercise; 2) cardiovascular diagnoses such as cardiomyopathy, heart failure or valve disease, or prior procedures including cardiac catheterization, arrhythmia ablation, cardioversions, heart surgery, heart transplant, or use of pacemakers or implantable cardioverter defibrillators (ICDs); all of these should include age at time of symptom onset, procedures, or death; 3) sudden death, particularly under age 40, with special attention to single vehicle accidents, drowning, or sudden infant death; 4) previous genetic testing; 5) specific details on deaths attributed to “heart attack”; and 6) features of syndromes, especially any features suggesting skeletal muscle disease. Also, if applicable; e.g. short stature and learning problems suggesting Noonan, acroparesthesias and renal failure consistent with Fabry or skeletal myopathy.

A critical component to validate family history often includes obtaining medical records and/or post mortem reports. Obtaining a family history and related activities outlined are time and effort intensive. Alternatively, focused family history interviews can be accomplished by trained allied health professionals. Practitioners may choose to refer patients with cardiomyopathy to centers expert in genetic cardiomyopathies, to obtain detailed family histories, provide genetic counseling and genetic testing, compile clinical and genetic databases, and provide opportunities to participate in research studies that are essential for progress in the field.

As noted above (Introduction, Supplementary Material), left ventricular noncompaction (LVNC) observed in conjunction with HCM, DCM, ARVC or RCM follows guidelines for that of the associated subtype of cardiomyopathy. If isolated noncompaction is identified serendipitously in an individual who is otherwise normal (asymptomatic with a normal ECG and normal ventricular size and function), it is always reasonable to obtain a family history to ensure there is no evidence of cardiomyopathy in the family, although formal population-based family studies of such individuals have not been published. Please see additional discussion at Guidelines 2 and 4.

Guideline 2. Clinical (phenotypic) screening for cardiomyopathy in at-risk first-degree relatives is recommended.

Cardiomyopathy Phenotype	Level of Evidence
Hypertrophic cardiomyopathy (HCM)	**A**
Dilated cardiomyopathy (DCM)	**A**
Arrhythmogenic right ventricular cardiomyopathy (ARVC)	**A**
Restrictive cardiomyopathy (RCM)	**A**
Cardiomyopathies, overlapping, or extra cardiac	**A**
Left ventricular noncompaction (LVNC)	**see background**

Key Points: Cardiomyopathies are frequently clinically silent for extended periods of time. Thus, first-degree relatives may be reportedly unaffected, and cardiomyopathy can only be detected by clinical testing (denoted hereafter as "phenotype screening"). Relatives who complete phenotype screening with no evidence of disease are denoted as "clinically unaffected." Relatives who are asymptomatic but have not completed phenotype screening are denoted hereafter as "reportedly clinically unaffected." Development of disease is age dependent, thus assessments of at-risk relatives may require repeated phenotype screening.

a. Baseline phenotype screening is recommended for all at-risk first-degree relatives, including those who have tested negative for a known familial variant. (Level of Evidence = A)

The rationale for baseline phenotype screening for at risk family members is that, as noted above, cardiomyopathy is commonly clinically silent and can only be detected by clinical screening. The rationale for phenotyping family members who test negative for a familial variant known to be actionable (i.e., pathogenic or likely pathogenic) is because in some cases non-segregation (an individual with the cardiomyopathy phenotype who tests negative for a pathogenic or likely pathogenic variant in the pedigree) will be unmasked, thus prompting the need for expanded genetic evaluation. We also note that determining whether a variant of uncertain significance (VUS) identified in the proband segregates with cardiomyopathy in a family can only be accomplished with up-to-date clinical phenotype information in all at-risk members of the pedigree. Furthermore, many variants continue to be novel for the cardiomyopathies (the exception being for some variants in *MYH7* and *MYBPC3* where larger numbers of pathogenic variants have been identified in HCM[38]) and thus if only observed in the proband will likely be assigned as a VUS, whereas knowledge of other affected family members who also carry a variant initially assigned as a VUS may enable its reclassification to likely

pathogenic or pathogenic, which can then be used for predictive testing. For these reasons we advocate that baseline clinical phenotype screening be conducted for all at-risk family members in conjunction with initial cascade genetic testing of a family's disease-causing variant or variants. Please see Guideline 3 for comments specific to children.

b. Serial phenotype screening for cardiomyopathy is recommended in clinically unaffected, at-risk relatives who are known to carry one or more disease-causing variants. (Level of Evidence = A)

Serial screening means, following a baseline-screening event, regular and repeated phenotype screening events are then conducted over a period of years.

c. Serial phenotypic screening for the emergence of cardiomyopathy is recommended for clinically unaffected at-risk first-degree relatives whose genetic status is unknown. (Level of Evidence = A)

An unknown genetic status can occur when an at-risk individual has not yet been tested for a previously detected disease-causing variant in the family, or if no pathogenic or likely pathogenic variant has been identified in the proband. It can also occur if a VUS has been identified in the proband and the family-based or other data are insufficient to allow reclassification as a likely pathogenic variant.

d. Serial screening of clinically unaffected relatives who have negative genetic testing for a pathogenic variant is not recommended. (Level of Evidence = A)

This recommendation is based upon the certainty that the variant identified in a family is indeed pathogenic and is discussed below at Guideline 4. However, relatives should be counseled to present for evaluation if they develop signs or symptoms suggestive of disease.

e. Clinical phenotype screening is recommended. (Level of Evidence = A)

Clinical phenotype screening (Table 1) includes:

- Medical history, with special attention to heart failure symptoms, arrhythmias, presyncope or syncope, and thromboembolism.
- Physical examination.
    - Special attention should be given to cardiac and neuromuscular systems.
    - Examination is indicated of the integumentary system when ARVC is suspected.
- Electrocardiogram.
- Cardiovascular imaging. This includes, minimally, a two-dimensional trans-thoracic echocardiogram (2D-TTE) for all cardiomyopathies, augmented with tissue Doppler interrogation, if available, for HCM. Cardiac MRI is rapidly emerging as a definitive imaging modality; it should be used if echocardiographic imaging is inadequate or equivocal. Additional studies may be considered based on the type of cardiomyopathy and/or if symptoms are present.

f. Suggested Clinical Screening Intervals for At-Risk Family Members.

Clinical screening intervals are suggested (Table 2).

Guideline 2 - Background.

Cardiomyopathies span all ages – from prenatal to the elderly. The approach to clinical phenotype screening of family members always relies on cardiac electrical, structural and functional evaluations, with age- or phenotype-specific additions as needed. An ECG and an echocardiogram are usually foundational in the initial phenotype screening for all ages of at-risk pediatric and adult first-degree relatives.

Integration of the considerations given above, most importantly the type of cardiomyopathy, should also be taken into account in screening of children. While children, even neonates, do manifest cardiomyopathy, most disease is adolescent- or adult-onset. Hence these recommendations should be integrated with the type of cardiomyopathy, the age of onset of other affected members in the pedigree when such data are available, the identity of the cardiomyopathy gene, if known, and other features. Additional guidance for the evaluation of cardiomyopathy in pediatrics is covered in the next section.

Adult-onset cardiomyopathies commonly show variable expressivity, a variable age of onset and reduced penetrance. Clinical screening of first-degree relatives of adults diagnosed with cardiomyopathy is indicated, regardless of whether a disease-causing variant has been identified in the index patient. In cases where first-degree relatives are all clinically unaffected, it is reasonable to initiate genetic testing in the affected patient since identification of a previously known disease-causing variant could lead to cascade testing in first-degree relatives. Because of the variable age of onset, clinical screening repeated at intervals is recommended, even if clinical genetic testing has not identified a disease-causing variant in the proband.

The risk for developing HCM after 50 years of age is reduced but not eliminated[39] as is that for ARVC after age 50.[40] The favorable utility and role of Holter monitoring in the diagnosis of ARVC has been reviewed.[40] Magnetic resonance imaging is useful for the diagnosis of ARVC in centers experienced in its use and interpretation for ARVC;[41] data are not yet available to guide the frequency of its application for screening at-risk family members.

As noted above (Introduction, Supplementary Material), LVNC may be observed in conjunction with other cardiomyopathy phenotypes, and if so, recommendations for that cardiomyopathy drive clinical screening recommendations. We lack data on whether, in the setting of normal ventricular size and function, the LVNC phenotype foreshadows the later development of a specific cardiomyopathy or other forms of cardiovascular disease in an extended pedigree. This is because the present literature of family-based screening has been

derived from LVNC identified at referral centers, in most cases in the setting of other cardiovascular disease.[42-44] Large systematic population-based studies to identify individuals with the LVNC phenotype but otherwise with normal cardiac morphology and function, followed by studies of their family members have not been done, although limited preliminary data are available.[42, 43] Because of the high prevalence of the LVNC phenotype in otherwise normal individuals in population-based studies,[19, 20] the limited evidence of disease causation from the LVNC phenotype itself, and the limited individual and pedigree natural history data from population-based studies, we provide no recommendations regarding family-based phenotype screening of LVNC that is not accompanied by other cardiovascular phenotypes with known disease risks.

Guideline 3. Referral of patients with genetic, familial or other unexplained forms of cardiomyopathy to expert centers is recommended.

a. **Infants and children with cardiomyopathy should be evaluated by clinicians with specific expertise in the recognition and testing of syndromic and non-syndromic presentations of cardiomyopathy in this age group.**

Key Points: Expert centers are those with expertise in the evaluation, diagnosis and management of genetic heart disease. Core competencies of expert centers include expertise with cardiovascular phenotypes as well as the conduct of genetic evaluations. Such centers should also have expertise in adults and/or children, dependent upon the ages of patients referred. Especially for infants and children, this includes clinicians who are able to recognize and characterize syndromes, dysmorphology, and metabolic abnormalities. Personnel at expert centers include physicians who are board-eligible or board-certified in cardiovascular disease,

working collaboratively with genetics professionals, including genetic counselors and/or clinical geneticists, ideally with cardiovascular expertise.

Guideline 3 - Background.

This recommendation is based on the marked genetic heterogeneity observed in cardiomyopathy, the increasingly complicated interpretations of human DNA variation, and the syndromic associations with some forms of cardiomyopathy. As noted below, both pre- and post-test genetic counseling should be provided by a healthcare professional who is board-eligible or board-certified in genetic counseling or clinical genetics, ideally with specialty training and experience in cardiovascular genetics. Although all healthcare professionals are expected to have core competencies in genetics, most cardiovascular providers do not have specific training or certification in clinical genetics or genetic counseling.[2] The 2009 HFSA practice guideline in genetic evaluation of cardiomyopathy acknowledged the challenges of obtaining a family history.[1] The 2013 ACC/AHA guidelines also highlight the importance of obtaining at least a 3-generation family history in the evaluation of cardiomyopathy.[6] However, the genetic evaluation of cardiomyopathy is more complex than identification of a familial pattern of disease. This includes expert phenotyping to guide test selection and rigorous interpretation of genetic testing results. Also, one recent study of genetic testing in clinical practice cited problems with incorrect or inappropriate ordering, errors in analysis, incorrect interpretations, and incorrect follow-up regarding VUSs, potentially jeopardizing patient safety.[45]

In contrast with other subspecialty areas in cardiovascular disease, no consensus or formal definition of the requirements for expertise in cardiovascular genetics is currently available. Some training programs in Advanced Heart Failure and Transplant Cardiology or in Cardiac Electrophysiology include genetics exposure, but typically training is insufficient to achieve expertise to conduct an independent cardiovascular genetic evaluation. Similarly, training programs in Clinical Genetics typically provide exposure to diagnostic evaluation of

cardiomyopathy, but may not provide sufficient training or experience in the recognition, management and risk stratification of the heterogeneous cardiac phenotypes found in this patient population. Clinical practice in cardiovascular genetics requires that practitioners remain up to date with the wide range of genes in which pathogenic variants cause cardiac phenotypes, including various forms of cardiomyopathy, arrhythmia, and syndromes in which these cardiovascular manifestations occur. For these reasons the ideal construct includes a close collaboration of specialists in both fields.

Because of the genetic and phenotypic heterogeneity inherent among different forms of cardiomyopathy, a single healthcare provider is unlikely to be able to provide expert care alone. Often, the range of expertise required is best achieved with a team of personnel who have complementary training and experience, as a multidisciplinary approach is frequently essential for optimizing diagnosis and management.[2, 46, 47] Often a board-eligible or board-certified genetics professional will work in conjunction with clinicians who are board-eligible or board-certified in Cardiovascular Disease, pediatric, adult or both. One or more members of an expert team involved with evaluation of cardiomyopathies may have subspecialty certification in Advanced Heart Failure and Transplant Cardiology, and/or subspecialty certification in Cardiac Electrophysiology. The evaluation of genetic heart disease includes whole families, so expert centers ideally have teams of physicians and counselors who are experienced with providing care for both adults and children with genetic forms of heart disease. Expert centers should be able to advise patients properly about patterns of inheritance, family members who are at risk of developing genetic heart disease, and reproductive risks related to variants in genes involved with cardiomyopathies.

Although referral to an expert center is recommended for genetic evaluation of patients with familial or otherwise unexplained forms of cardiomyopathy, the practicality of this recommendation varies regionally. Travel to an expert center for genetic evaluation of cardiomyopathy may not be feasible for some patients and their families. Additional options

through telephone-based genetic counseling and telemedicine-based genetic evaluation may help in part to address this shortcoming.[48]

The Evaluation of Cardiomyopathy in Children Requires Special Expertise:

Cardiomyopathy in children presents a unique differential diagnosis list, as compared to adults, and geneticist evaluation may be required as syndromic and metabolic causes of disease represent a higher proportion in children than in the adult population.[49, 50] This is particularly relevant in patients with intellectual disability of unknown etiology. Other extra-cardiac findings that should prompt further evaluation and referral include dysmorphic features, short stature, congenital anomalies, muscle weakness, or sensory deficits of unknown etiology. Age at presentation may greatly aid in refining the differential list, with a specific set of disorders more common in infancy. While there are many conditions that may cause cardiomyopathy in childhood (see Supplemental Table for examples), a few are notable for having specific, time-critical treatments available, or because the identification of the cardiomyopathy in the presence of other findings may solidify the diagnosis of a specific syndrome. A number of conditions can be screened by relatively inexpensive and rapid biochemical tests, followed by genetic testing for a molecular diagnosis.

Aside from neuromuscular disorders, inborn errors of metabolism, and specific syndromes noted in children, the same causes of familial HCM and DCM common in adults are also encountered throughout childhood.[51]

Equally, syndromes with cardiomyopathy as a component may not be diagnosed until adulthood, and thus syndromic cardiomyopathies should also be part of the differential diagnosis among adults. In some cases, the dysmorphic features that form an integral part of the diagnosis in infancy and childhood may not be as prominent later in life.

Infancy. Inborn errors of metabolism (IEMs) constitute an important group of conditions that may manifest early in life. While expanded newborn screening may identify potentially

affected individuals, false negatives and missed screening confirmations can occur. Not all diseases are screened in all jurisdictions, and some conditions are not currently amenable to screening. Disorders of energy metabolism in particular should be considered: these may present as either HCM or DCM, and include fatty acid oxidation defects (eg. very long-chain acyl-CoA dehydrogenase [VLCAD], carnitine palmitoyl transferase 2 [CPT2], long-chain 3-hydroxyacyl-CoA dehydrogenase [LCHAD] deficiency) and mitochondrial oxidative phosphorylation disorders. If suspected, acylcarnitine profile, serum amino acids, urine organic acids, liver transaminases, serum lactate, and comprehensive metabolic profile are recommended first line studies. HCM in infancy should always invoke investigation for infantile Pompe disease (glycogen storage disease type II) by enzyme assay for acid alpha-glucosidase deficiency as early diagnosis is crucial for successful treatment by enzyme replacement therapy. Of note, HCM may also occur secondary to corticosteroid use in preterm infants with respiratory distress syndrome[52, 53] or maternal diabetes[54] and should resolve spontaneously. Persistence of HCM more than 4 weeks after cessation of steroids or past 6 months of age in an infant of a diabetic mother should prompt evaluation for other causes.

Some syndromes with cardiomyopathy may present in infancy. Noonan syndrome or other RASopathies are the most common syndromes associated with HCM, and may have extra-cardiac manifestations of short stature and dysmorphic features that may be subtle and difficult to recognize. HCM occurs in up to 20-30% of cases, with half presenting prior to 12 months of life with a more severe hypertrophy that paradoxically may improve over time.[55, 56] This may be biventricular, or involve predominantly the right ventricle. HCM rarely newly develops past age of 5 years.[57] Molecular testing for RASopathies gene panel testing may or may not be included with sarcomeric HCM genetic testing panels.

Childhood. Cardiomyopathy due to IEM may present in early or late childhood, typically in individuals previously diagnosed with a specific disorder who receive cardiac screening. Examples include the amino acid metabolism disorders methylmalonic acidemia and propionic

acidemia, glycogen storage disease type III (or very rarely type IV), and mucopolysaccharidoses (MPS). Occasionally these conditions escape diagnosis or are misdiagnosed.

Neuromuscular disorders may first manifest with DCM in childhood, and include muscular dystrophies (dystrophinopathies, laminopathies, desminopathies, sarcoglycanopathies, and other recessive and dominant limb-girdle muscular dystrophies) and Friedreich ataxia. Myotonic dystrophy, Types I and II, also present with cardiomyopathy although more commonly in adults, especially type II. Both types also have risk for conduction system disease.[58] Mitochondrial disorders may also present primarily as symptomatic cardiomyopathy throughout childhood. Finally, boys with early onset cardiomyopathy should be carefully evaluated for Barth syndrome (skeletal myopathy, small size, cyclical neutropenia, delayed puberty, 3-methylglutaconic aciduria), an X-linked condition due to pathogenic variants in *TAZ,* which is important for mitochondrial function.[59] Mitochondrial disorders may exhibit HCM (~60%) or DCM (~30%).[60]

Selected Syndromes with Cardiomyopathy. Careful history and physical exam are essential to identify possible extra-cardiac manifestations of syndromes which may change investigation and management. It is estimated that up to 10% of children with cardiomyopathy have an underlying genetic syndrome. Over 100 different syndromes have been described with cardiomyopathy as a feature. While most are very rare, several occur with higher frequency and should be considered in the differential diagnosis (see Supplemental Table).

Several syndromes present more commonly in childhood. Alström syndrome may present with transient DCM in infancy and later reoccurrence of DCM or restrictive cardiomyopathy in adolescence. Other features include visual impairment (due to cone-rod dystrophy) with nystagmus, progressive sensorineural hearing loss, obesity and diabetes due to insulin resistance. Danon disease, an X-linked condition due to pathogenic variants in *LAMP2*, frequently manifests in early childhood.[61] It resembles infantile Pompe disease with severe HCM but less pronounced skeletal myopathy, and has additional problems of cardiac pre-excitation,

intellectual disabilities, and retinal pigmentary disease. The variability in extra-cardiac features is not well understood. Female carriers may present with either HCM or DCM, most often in the second or third decades. Severe HCM due to 5′ AMP-activated protein kinase (AMPK) deficiency encoded by *PRKAG2* leading to non-lysosomal glycogen accumulation may also present in childhood, frequently with arrhythmias, heart block and Wolf-Parkinson-White.[62] Fabry disease, an X-linked disorder resulting from mutations in *GLA,* causes deficiency of alpha-galactosidase. Fabry may present as early as adolescence with LV hypertrophy. Manifestations of classic Fabry include extra-cardiac features of angiokeratomas, painful acroparesthesias, corneal opacities, reduced sweating, and end stage renal disease due to loss of enzyme activity (typically <1%). However, variants in *GLA* that leave some residual enzymatic function may result in cardiac variant Fabry, which usually presents at 40 years and older, in which left ventricular hypertrophy is identified with or without proteinuria and without other extra-cardiac manifestations.[63] Early enzyme replacement therapy, particularly for males and severely affected females of this X linked disorder, may slow progression of disease. Atypical forms of Fabry include a cardiac variant consisting of HCM, arrhythmia and conduction abnormalities without renal failure, neuropathy or skin findings and present at a later age.

Guideline 4. Genetic testing is recommended for patients with cardiomyopathy.

a. **Genetic testing is recommended for the most clearly affected family member.**

b. **Cascade genetic testing of at-risk family members is recommended for pathogenic and likely pathogenic variants.**

c. In addition to routine newborn screening tests, specialized evaluation of infants with cardiomyopathy is recommended, and genetic testing should be considered.

Cardiomyopathy Phenotype	Level of Evidence
Hypertrophic cardiomyopathy (HCM)	**A**
Dilated cardiomyopathy (DCM)	**A**
Arrhythmic right ventricular cardiomyopathy (ARVC)	**A**
Restrictive cardiomyopathy (RCM)	**B**
Cardiomyopathies associated with other extra-cardiac manifestations	**A**
Left ventricular noncompaction (LVNC)	**See background**

Key Points: Genetic testing is recommended to determine if a pathogenic variant can be identified to facilitate patient management and family screening. The identification of at risk family members is critical because the first presentation may be sudden death. Cascade genetic screening identifies asymptomatic affected family members and clinically unaffected carriers of pathogenic variants.[64] Institution of therapy in asymptomatic affected individuals improves outcomes and decreases hospitalization and death due to heart failure.[65, 66] Preliminary studies indicate that treatment of clinically unaffected carriers of pathogenic variants may improve outcome as well although larger studies are needed.[67] Genetic testing and cascade screening for HCM have been shown to be cost-effective in Australia and the United States.[68, 69] The identification of a molecular cause may also lead to critical gene-specific cardiac or extra-cardiac management recommendations. For example, cardiac hypertrophy seen in *LAMP2*, *PRKAG2*, *PTPN1*1 and *RAF1* pathogenic variant carriers can represent a genocopy of hypertrophy seen with sarcomeric pathogenic variants; yet *LAMP2*, *PRKAG2*, *PTPN1*1 and *RAF1* patients have different clinical courses and management needs.[70, 71] In sarcomeric

carriers, genotype status is associated with long term outcomes, including all-cause mortality.[72, 73] In DCM, there is evidence for prognostication value of genetic testing[74-77] and management implications for specific genetic findings, such as consideration of ICD for primary prevention in carriers of *LMNA* pathogenic variants.[78] In ARVC, ICD placement for primary prevention in asymptomatic male carriers of a malignant pathogenic variant showed significant impact on long-term clinical outcome.[79]

Testing should ideally be initiated on the person in a family with the most definitive diagnosis and most severe manifestations. This approach will maximize the likelihood of obtaining diagnostic results and detecting whether multiple pathogenic variants may be present and contributing to variable disease expression or severity. Please see Guideline 3 for additional comments on specialized evaluation of infants and children.

Guideline 4 - Background

Nomenclature follows the ACMG approach[9] for calling variants as pathogenic (P), likely pathogenic (LP), variants of uncertain significance (VUS), likely benign and benign. The indications for genetic testing include guiding patient management and facilitating family screening and reproductive risk assessment.

Test Selection: Genes and Gene Panels

Since the 2009 HFSA guideline,[1] the number of genes known that harbor rare pathogenic variants that cause cardiomyopathy has increased, the number of clinical laboratories performing high volume cardiovascular genetic testing has expanded, and the number, type, and technologies available for gene-based sequencing have been in constant evolution. While the 2009 guideline suggested that “genetic testing should be considered,” additional data on the importance of genetic testing for prognostication and management as well

as cascade screening and risk stratification of relatives support the current genetic testing recommendation. Furthermore, the cost for most large genetic panels is substantially lower than it was in 2009, with expectations for continued decline.[80] Nevertheless, genetic testing is probabilistic in nature and interpretation of genetic variation will continue to be refined as additional sequencing information becomes available from both affected and unaffected individuals.

The rationale for level of evidence presented in this guideline is derived largely from the published sensitivity of genetic testing. These guidelines do not address molecular testing in prenatal, newborn screening or *in-vitro* fertilization settings.

We also note ongoing challenges of variant interpretation in non-Caucasian, non-Northern European populations, as most genetic testing, and hence repositories of known pathogenic variants, has previously been conducted principally in the Caucasian/Northern European population. The recent development of very large population databases (e.g., ExAC, http://exac.broadinstitute.org, or gnomAD, http://gnomad.broadinstitute.org) now provides limited numbers of reference alleles from non-European cohorts, which has greatly assisted variant interpretation. However, genetic test interpretation of variant alleles from ethnic groups not represented or represented in low numbers in reference datasets become extremely challenging, and must be approached with considerable caution.

A variety of resources are publicly available that provide additional relevant information (e.g., GeneReviews, http://www.ncbi.nlm.nih.gov/books/NBK1116), on individual genes (e.g., Online Mendelian Inheritance in Man, http://www.omim.org), specific genetic variants and their population frequencies (e.g., dbSNP, http://www.ncbi.nlm.nih.gov/snp; ExAC browser, http://exac.broadinstitute.org; Genome aggregation database (gnomAD) http://gnomad.broadinstitute.org/; exome variant server, http://evs.gs.washington.edu/EVS or 1000 Genomes, http://www.1000genomes.org), and information for the interpretation of these

variants (e.g., ClinVar, http://www.ncbi.nlm.nih.gov/clinvar and ClinGen, http://www.clinicalgenome.org).

We also note that large insertion/deletion variants (e.g., > 25 nucleotides) and other structural changes in DNA, referred to as copy number variants, in a preliminary study represent < 1% of cardiomyopathy cases,[81] although structural variants have received minimal investigation in the cardiomyopathies and may have greater relevance than is currently understood.

Whom to test. In order to yield the most conclusive, informative results, diagnostic genetic testing is optimally initiated on a confirmed affected individual. Furthermore, as there are sometimes multiple genetic variants contributing to disease in a single family, the testing should ideally be initiated on the person who is most likely to harbor the disease-causing variant or variants. This is frequently the individual in the family with the most severe disease and/or the earliest disease onset. This is a well-established principle in clinical genetics, as selecting the individual with the most evident disease increases the likelihood of finding a genetic cause. If the ideal person for initiation of genetic testing in a family is unavailable or unwilling to proceed, then comprehensive genetic testing should be considered for another affected family member.

When to test. The timing for ordering genetic testing in a patient with cardiomyopathy has not been studied. Because results may guide management, we recommend genetic testing at the time a new cardiomyopathy diagnosis is made, but it can be conducted at any time following diagnosis. Education and counseling regarding genetic testing options are a key component of the process. For those who have had genetic testing in the past, re-testing may be appropriate if the previous testing produced negative or inconclusive results and the test's detection rate has improved. This latter point is particularly relevant for DCM as the gene panels have rapidly expanded (e.g., inclusion of *TTN*[15, 82, 83] and others) and are anticipated to continue expanding.

Genetic testing for the cardiomyopathies may best be viewed as continuously evolving, as new genes, and hence larger panels with greater sensitivity, continue to emerge. Although no data are available, we suggest that repeat genetic testing is reasonable if test sensitivity has increased by 5-10%. An alternative approach is to tailor retesting if particular characteristics of the patient's phenotype are consistent with a newly identified gene. Further, the genetics provider involved in a patient's care should periodically revisit results as variants may be reclassified over time.[46, 84, 85] Such reclassification includes upgrading variants from VUS to likely pathogenic or pathogenic, as additional probands and affected family members with the phenotype of interest are found to carry the variant. Conversely, some variants, previously considered pathogenic, are downgraded to a VUS, or likely benign or benign, as larger datasets from expanded ethnicities become available.

How to test. With the development of next generation sequencing (NGS), panels incorporating dozens of genes relevant to the phenotype have become the norm, as they are technically feasible and less costly.[80] As a result, clinical genetic testing panels for these disorders are changing rapidly. Molecular genetic testing for multiple genes using a multi-gene panel is now the standard of practice for cardiovascular genetic medicine. Furthermore, multi-gene panel genetic testing is recommended over a serial single-gene testing approach due to the genetically heterogeneous nature of cardiomyopathy. Genetic testing and cascade screening have been shown to be cost-effective.[68, 69]

Large gene panels for cardiomyopathy may include genes that cause genetic syndromes associated with cardiomyopathy (eg. Fabry disease, Danon disease, Alström syndrome), neuromuscular conditions associated with cardiomyopathy (eg. limb girdle muscular dystrophies) or metabolic conditions. These large gene panels have the advantage of increasing the likelihood of identifying a molecular etiology, especially in patients with mixed phenotypes or those who lack pathognomonic features.[86, 87] Considerable overlap of genes among different types of cardiomyopathy (and other phenotypes) is also well established (Supplemental Figure

1). Panels also increase the likelihood of identifying individuals who carry disease-causing variants in multiple genes, and this knowledge is extremely important for appropriate targeted testing of family members.

With larger gene panels, the likelihood of identifying a VUS increases in proportion to the number of genes tested, increasing the complexity of the interpretation and genetic counseling. Importantly, the strength of evidence for gene-disease pairs on current panels differs, with some well-established genes having a wealth of information regarding disease-causing variants, while more recently identified genes having much less information available. The latter case increases the likelihood of a variant being classified as a VUS. The composition of gene panels varies by testing lab. It is critical that the ordering physician has an understanding of the uses, benefits, and limitations of specific test types in order to select the most appropriate test for their patient (Table 4.1). Addition of *TTN* and *BAG3* to DCM panels increased genetic testing yield by more than 10%,[15, 82, 83] but for HCM, recent studies have shown that expanded panels do not currently increase sensitivity.[69] Thus the decision to order a panel that includes a larger number of genes should be based on the specifics of the patient's medical history, physical exam findings, and family history.

HCM. The level of evidence for testing in HCM is based on studies showing a high diagnostic yield of genetic testing in children and adults and prognostic value of genotype status.[30, 69, 72, 73, 88] HCM is considered a disease of the sarcomere, and variations in genes encoding sarcomeric proteins, in which there is low tolerance for genetic variation, are common causes.[89] The diagnostic yield of HCM testing is approximately 30-60% (Table 4.2). The yield of testing is higher in individuals who have a known family history of HCM.[69, 88] Pathogenic variants in *MYH7* and *MYBPC3* account for approximately 80% of all cases for which a molecular diagnosis is achieved.[90, 91] Beyond sarcomeric genes, core genes to screen in patients with HCM include *GLA, PRKAG2,* and *LAMP2*, as reviewed in the Background of Guideline 3.

Infants and children with HCM may require more specialized evaluation and diagnostic testing as noted in Section 3 because of the rate of syndromic conditions and inborn errors of metabolism associated with HCM at these ages.[49, 50, 92] Consultation with a geneticist is indicated.

DCM. Evidence indicates that clinical genetic testing can identify the cause of DCM in families with autosomal dominant inheritance in approximately 25-40% of cases, whereas in isolated cases of DCM, the yield of testing is commonly estimated at 10-25%.[35, 93-95] Core genes to be tested in individuals with DCM include genes encoding sarcomeric and cytoskeletal proteins (Table 3), although DCM testing panels typically carry several dozen genes, some with uncertain significance. In most cases, all HCM and ARVC genes are included in DCM panels because of gene/phenotype overlap.

Protein-truncating variants in *TTN* (*TTN*tv) represent the most common genetic testing finding in DCM, ranging from 10-20% of cases.[15, 82, 83] While many commercial testing laboratories will adjudicate all *TTN*tv's, whether singleton or familial, as pathogenic or likely pathogenic, variant interpretation is challenging due to the large size of the gene and the frequency of truncating *TTN* variants in reference populations.[82, 83, 96, 97] Most studies have not been family-based, where segregation could be evaluated, but some non-segregation of *TTN*tv's has been identified.[98] Further, recent cardiac magnetic resonance data of normal individuals from a population-based study showed a small but significant decrement in LV function with *TTN*tv's in constitutive cardiac exons,[97] suggesting that in some cases a *TTN*tv may function as a risk allele.

The *LMNA* gene is the second most commonly identified cause of DCM with a diagnostic yield of 5.5%, and gene-specific management recommendations, reviewed below, are available.[99, 100] More recently identified genetic causes of DCM such as *BAG3*, a chaperone regulator, and *RBM20*, a protein required for RNA splicing, identify novel molecular mechanisms for disease[101, 102], and are each identified in approximately 2% of DCM cases. DCM is a

common complication of neuromuscular disease such as Duchenne or Becker muscular dystrophy. Genetic testing is important in mothers of individuals with Duchenne or Becker to determine carrier status because carrier females may develop DCM in the third to fifth decade of life.[103] As in HCM, infants and children with DCM may require additional diagnostic genetic evaluation.

ARVC. The genetic basis of ARVC was initially identified as a disease of the desmosome.[104] Genetic testing of *PKP2, DSP, DSG2, DSC2, JUP, TMEM43*, and *PLN* resulted in a molecular diagnosis in 63% of patients who fulfilled Task Force criteria for ARVC.[105] Digenic inheritance and compound heterozygosity are frequent[106] and, combined with decreased penetrance that is a feature of ARVC, may significantly complicate genetic counseling. ARVC overlaps with arrhythmogenic left ventricular cardiomyopathy, sometimes more broadly referred to as arrhythmogenic cardiomyopathy.[107] This reflects genetic and phenotypic overlap among these forms of cardiomyopathy. Accordingly, genetic testing for ARVC using a larger cardiomyopathy panel may identify non-desmosomal genes with pathogenic variants. Similarly, desmosome gene mutations have also been identified in patients diagnosed with DCM.[108] Exercise has a well-established role in the pathogenesis of desmosomal cardiomyopathies, and recognition of a desmosome gene mutation can help to determine optimal exercise recommendations.[109]

RCM. Genetic causes of RCM continue to be identified, but because RCM is a relatively rare form of cardiomyopathy, numbers remain limited. A recent study identified a pathogenic variant in 60% of subjects, primarily occurring in genes known to cause HCM.[110] Family members were frequently identified with HCM or HCM with restrictive physiology. Cardiac amyloidosis resulting from pathogenic variants in *TTR* needs to be differentiated from other forms of RCM due to the age demographic in which this occurs, the slowly progressive nature of this disease, and therefore different management strategies.[111, 112] The *TTR* allele p.Val142Ile (commonly referred to as Val122Ile based on nomenclature for the circulating protein after N-

terminal peptide cleavage) has been found in 10% of African Americans older than age 65 with severe congestive heart failure.[113] Substantial recent progress with amyloidosis, both in imaging strategies, including cardiac magnetic resonance and pyrophosphate scanning, and therapeutic interventions in ongoing clinical trials, provide new incentives for genetic diagnosis.[114] Hemochromatosis is uncommon but easily excluded with iron studies, such as percent saturation of transferrin, and if present can be treated with iron removal.[115]

LVNC. As noted above, the LVNC phenotype may be observed in conjunction with all other cardiomyopathy phenotypes, so considerations related to genetic testing should always be directed by findings of a cardiomyopathy (or other cardiovascular) phenotype.[16, 116] Genetic testing is not recommended when the LVNC phenotype is identified serendipitously in asymptomatic individuals with otherwise normal cardiovascular structure and function.[117]

Special Circumstances: A genetic etiology should be considered and a genetic evaluation conducted in cases of peripartum cardiomyopathy, as rare variants in genes known to cause DCM have been identified in patients with peripartum cardiomyopathy,[118-120] and *TTN* truncating variants are present at rates similar to those found in the DCM population.[120] In cases of sudden death with an autopsy diagnosis of cardiomyopathy, genetic testing may facilitate risk stratification of family members.[121, 122]

Interpretation of genetic testing.

Genetic testing results are probabilistic rather that determinative, and thus rely on strength of evidence, both for and against, of specific variants causing or contributing to disease. New guidelines have attempted to standardize and increase the stringency of interpretation, with greater clarity regarding the criteria for strength of evidence and the weighting of multiple sources of information that need to be incorporated to arrive at the interpretation.[9] Despite this, the interpretations provided for a given variant may differ between clinical genetic testing laboratories.[123, 124] In addition, updates and revisions of the laboratory

interpretation may occur as more information is obtained from larger cohorts, sometimes leading to re-issuing of a clinical report with changed interpretation by diagnostic laboratories.

Because of their probabilistic nature, results of genetic testing must always be interpreted in the context of the patient's medical and family history.[85] For example, family history information and the segregation of a putative disease-causing variant within the family may be important information to guide clinical interpretation, especially in cases where novel genetic variants are identified. Also, family studies have noted more than one pathogenic variant in up to 10% of families with ARVC.[125] Two or more variants have been seen in 3-5% of HCM cases,[31-33] particularly if onset is early or severe.[30] Although not reported systematically, digenic inheritance has been suggested to occur at even higher frequency with DCM.[35]

The diagnostic yield of genetic testing for each subtype of cardiomyopathy is much less than 100% (Table 2) and a negative genetic test result (in this setting including VUS and likely benign or benign variants) *does not rule out a genetic cause*. Such an uninformative result in a proband simply indicates that the genetic testing performed was unable to identify the specific cause of disease in the given family. In these circumstances, an uninformative genetic testing result cannot be used for predictive, cascade genetic testing in unaffected relatives. Rather, family screening using phenotypic evaluations is recommended (Guideline 2). Larger panels, better coverage of the relevant genes, analysis for deletions, duplications, and rearrangements in the genes of interest, or exome sequencing in families with multiple living affected individuals may identify a genetic etiology.

Finally, the recent availability of and much greater focus on extensive genetic testing panels should not diminish or distract from the critical importance of expert phenotyping of patients and families, and the relevance of highly insightful phenotype and gene-variant correlations. Current genetics practice suggests that results provided by molecular genetics laboratories drive clinical decision making, specifically actionability, in a genetic evaluation. In the Family Management section below, this guidance states that a VUS cannot be used for

predictive testing, which the writing group firmly supports. However, we acknowledge that compelling clinical data, for example, the pre-genetic test specification of a disease gene highly likely to harbor a disease-associated variant of interest, seldom impacts the clinician's decision of whether a variant classified as a VUS by a laboratory report is actionable. More specifically, cardiovascular genetics experts have become quite sanguine, for example, at specifying the pretest likelihood of identifying a *LMNA* variant based upon phenotype and/or family data. However, finding a novel missense or nonsense variant in any gene, even with such a pretest specification, cannot be classified with current ACMG rules as likely pathogenic (or pathogenic), and thus actionable, unless data regarding the same variant is available from multiple probands and/or affected family members. While we propose no solution to this present conundrum, we do acknowledge its existence. Efforts to accumulate extensive catalogs of expertly adjudicated phenotype and variant information, such as the ClinGen effort,[10] may eventually partially mitigate this situation.

Considerations of Family Management

Predictive Genetic Testing

Risk stratification in family members is an important and valuable reason for genetic testing. If a pathogenic or likely pathogenic variant is identified in the index patient initially tested, opportunities emerge for the predictive testing of at-risk family members. As noted above, variants of uncertain significance (VUS) are not useful to conduct predictive genetic testing.

Negative cascade genetic testing in an at-risk family member. If genetic testing is negative in an at-risk phenotype-negative family member for a pathogenic or likely pathogenic variant present in the proband, that family member's risk of developing the cardiomyopathy is substantially reduced. In this situation the need for serial phenotype screening after a baseline clinical evaluation in such a genotype-negative family member in most cases is unnecessary,

and the family member can be discharged from serial clinical phenotype screening. However, the strength of the recommendation to release a family member from ongoing interval phenotype screening is based upon the strength of the evidence that the variant indeed is the cause of disease in the family under care. In most cases this evidence must be assembled from prior patients and families, usually in publicly accessible databases or the medical literature, and/or from evidence gathered and assessed from the family under care. The family member should be counseled that their risk has been substantially reduced, but is not reduced to zero, with the caveat that if they develop relevant symptoms, phenotype screening should be reconsidered because of the possibility that one or more yet undetected variants may be at play.

Positive cascade genetic testing in an at-risk family member. On the other hand, if a pathogenic or likely pathogenic variant is identified in an asymptomatic, at-risk phenotype-negative family member, the confidence is much greater to infer risk for that individual. They should be counseled on the presenting signs and symptoms of the specific cardiomyopathy, any associated reduced penetrance and variable expressivity, and the rationale and frequency of the recommended clinical surveillance (reviewed at Guideline 2).

Leveraging Family-based Segregation Information to Impact Variant Analysis

Some variants detected with cardiomyopathy genetic testing will be novel, that is, variants that have not been previously reported in publicly accessible databases, and will meet other usual criteria for pathogenicity. However, even if the variant is of the type that is known to be disease-causing and has occurred in a well-established gene associated with the cardiomyopathy phenotype in the family, such novel variants will often be adjudicated as VUSs because of lack of prior case or family data. In this circumstance, searching for segregation of the variant in question with the cardiomyopathy phenotype in additional family members can provide additional valuable information. Depending upon the size of the pedigree, the number of individuals tested, and the genetic testing results, such information may help reclassify a variant

from VUS to pathogenic or benign. The ClinGen initiative[10] proposes to rectify this issue by aggregating all available disease-associated variants into ClinVar, a publicly accessible database utilizing a standardized curation approach tailored after the ACMG/AMP recommendations,[9] and all professionals with any access to genetic data relevant to the cardiomyopathies are urged to contribute to this important database. However, because of the numbers of genes involved in the cardiomyopathies, many variants in the near term will likely be curated as VUS's. For example, in one HCM study, the cardiomyopathy with the largest disease-specific databases and where ~80% of pathogenic variants can be identified in two genes, *MYPBC3* or *MYH7*, in one recent study 30% and 35% of variants were novel, respectively, for these two genes. In other well established HCM genes 76% of variants were unique.[38]

The corollary of the above is that if the VUS does not segregate with affected family members, the likelihood that the VUS is relevant for the family phenotype is reduced. However, this analysis must encompass the growing reality of bilineal or multi-variant disease, which has been postulated to be more common in DCM[8, 35] and ARVC.[126]

In most clinical situations, sequencing a VUS is not undertaken in family members who have completed clinical screening and have been shown to be free of the phenotype (negative clinical phenotype screening), as genetic information will not inform variant pathogenicity. One important exception to this is parental sequencing to confirm the possibility of *de novo* occurrence of a variant. A second exception to this includes sequencing older unaffected family members, who are highly informative when assessing the penetrance of a variant. Application of this principle depends greatly upon the age of onset of the phenotype in the family (infant, pediatric, early adult, late adult), the clarity and severity of the phenotype, as well as the gene involved and disease mechanisms.

Finally, as noted above, variant calls may change. The most problematic is when a previously called variant, deemed pathogenic or likely pathogenic, is downgraded to a VUS. In this circumstance,

recommendations for the clinical surveillance screening of at-risk family members change. Most importantly, a genotype-negative family member must now be counseled that they remain at risk for the family phenotype, and hence need to re-engage in clinical screening. The proband and any family members who tested positive for the variant, now downgraded to a VUS, must also be counseled that future genetic re-evaluation may be appropriate. All clinicians participating in genetic evaluations must be aware of the implications of changes in variant calls, and the family members should be counseled regarding these possibilities during the initial genetic evaluation and the need for possible future contact. Given the seeming recent increase in downgrading to a VUS, this highly impactful change in variant status carries great potential for unintended clinical errors if not identified and communicated effectively to the relevant family unit.

Guideline 5. Genetic counseling is recommended for all patients with cardiomyopathy and their family members. (Level of Evidence A)

Key Point: Genetic counseling for cardiomyopathy may be offered by board-certified or board-eligible genetic counselors, clinical geneticists, or in the absence of available genetics professionals, by clinicians who have the required background, expertise and training. Genetic counseling for cardiomyopathy includes review of medical records essential for phenotyping, obtaining a pedigree, patient and family education, evaluating genetic testing options, obtaining consent for genetic testing, facilitating family communication, and ordering and interpreting genetic test results while addressing psychosocial issues.

Guideline 5 - Background

Genetic counseling facilitates understanding and adaptation to the impact of a genetic condition at the medical, psychological, and the family level,[127] and is valued positively as an

essential service by both caregivers and patients.[1, 46, 128] This service may be provided by clinical geneticists, genetic counselors, or specially trained nurses. In the United States this is performed mostly by genetic counselors, who are mid-level providers with a Masters level training in gathering, interpreting, and communicating medical genetics information. Their scope of practice also includes psychosocial assessment and support. Genetic counseling conceptualizes the family as the unit of care, with a broadened focus including preventive care for at-risk family members.

Genetic counseling is usually undertaken by genetic counselors and/or clinical geneticists who are knowledgeable of the cardiovascular features of the type of cardiomyopathy in question, or by cardiologists, adult or pediatric, who are expert in the cardiomyopathy in question and are fluent in the content and nature of genetic counseling. Cardiologists with special interest and expertise in genetic cardiomyopathies usually integrate genetic counselors into their practice.

Genetic counseling is an essential component of the evaluation, diagnosis, and management of the cardiomyopathies. Genetic counseling roles include review and gathering of medical records essential for phenotyping, obtaining a family history (Guideline 1), educating the patient and family regarding the disease transmission and family risks, evaluating genetic testing options (Guideline 4), obtaining consent for genetic testing including discussing the implications of positive, negative, or uncertain results, providing key information to other at-risk family members as identified by the index patient, ordering testing, interpreting genetic test results, as well as communicating results and their clinical implications, including screening recommendations for family members (Guideline 2).

Counseling is also aimed to promote informed choices and adaptation to risk or condition while exploring and addressing psychosocial issues, as they emerge. Addressing family dynamics, which could potentially impact dissemination of genetic information to at-risk

family members, is an active area of focus in genetic counseling that may be aided by the use of patient letters, educational materials, or other communication tools.

Guideline 6. Focused cardiovascular phenotyping is recommended when pathogenic or likely pathogenic variants in cardiomyopathy genes, designated for reporting of secondary findings by the ACMG, are identified in an individual.

a. **If a cardiovascular phenotype is identified as would be predicted by currently available knowledge of the gene/variant pair, all usual approaches described in this document for a genetic evaluation, including family-based approaches, are recommended.**

b. **If no cardiovascular disease phenotype is identified in the individual, recommendations for surveillance screening at intervals should be considered.**

c. **If no cardiovascular phenotype is identified in the individual, cascade evaluation of at-risk relatives may be considered, tempered by the strength of evidence supporting the pathogenicity of the variant, the usual age of onset of the gene/variant pair, and pedigree information (e.g., the ages of at-risk family members, other previously known cardiovascular clinical data in the pedigree, and related information).**

Guideline 6 - Background

Across specialties genetic testing is moving towards use of large gene panels, whole exome sequencing, and potentially whole genome sequencing. These tests may be performed for a wide variety of indications and diseases that do not include a cardiac phenotype.

Individuals who undergo genetic testing for a disease that does not involve the heart may have a genetic variant discovered that may predispose that individual to a cardiomyopathy. This discovery may occur in two ways: 1) the gene, known to confer risk from high penetrance variants that are medically actionable, may be ***intentionally analyzed*** as recommended by the American College of Medical Genetics and Genomics. Variants identified from intentional analysis are termed secondary findings. 2) A variant is ***identified incidentally or accidentally*** through the analysis of genes related to the original phenotype for which the test was performed. These are termed incidental findings.

The ACMG has developed guidelines to manage secondary findings, which were first published in 2013[4] and updated in 2016.[5] The ACMG guidance directs the reporting only of Known Pathogenic (KP) or Expected Pathogenic (EP) variants,[5] the former defined as "Sequence variation is previously reported and is a recognized cause of the disorder" and the latter as "Sequence variation is previously unreported and is of the type which is expected to cause the disorder." These definitions were taken from the ACMG 2008 guidance for variant interpretation,[129] which was updated by the ACMG/AMP in 2015[9] with modified nomenclature of "pathogenic" (P) and "likely pathogenic" (LP). The latter attributions (P, LP) are now nearly universally used in clinical genetic testing laboratories in the US. This nomenclature is also used in ClinGen[10, 11], the ClinGen Cardiovascular Clinical Domain Working Group,[130] and this guideline. Despite possible subtle differences of KP/EP and P/LP, since the P and LP attributions are used for the other specific numbered guidelines in this document, for simplicity and parsimony these attributions will also be used in this section.

Thus, variants in the ACMG-listed cardiomyopathy genes (Table 3) that have been identified as secondary findings and adjudicated as P or LP are considered medically actionable. In those cases, cardiac phenotyping should be conducted in the individuals who carry those variants, assuming that the individual has not opted out of notification.

Greater difficulty in determining whether a variant is medically actionable may occur for incidental findings reported by the diagnostic laboratory that fall outside the ACMG guidelines. Incidental findings may be classified as pathogenic, likely pathogenic, variants of uncertain significance, likely benign or benign, with specific criteria for the strength of assertion.[9]

The single most important analysis for determining if a specific incidental finding is actionable rests on the strength of evidence for disease causality of the gene/variant pair. Identifying a variant in a gene previously observed in multiple cases or families, including at times functional data confirming a damaging effect, can have substantial evidentiary strength, and such variants may be able to be classified as pathogenic or likely pathogenic. Such evidence forms the basis of the ACMG recommendations and informs sections a, b, and c of this guideline. For HCM, where 80% of genetic cause, when found, is within two genes (*MYBPC3, MYH7*), a greater likelihood exists that prior case data may be available. However, in contrast to HCM, the gene ontology for DCM is much more extensive, as most genes contribute only a small fraction to the totality of known genetic cause, and many reported variants remain private. The number of genes considered relevant for ARVC is smaller than either DCM or HCM, but because it is much less common than HCM or DCM, many ARVC variants will also remain private. Overall it is likely that most cardiomyopathy variants identified as incidental findings, even those for HCM, will remain VUSs because of lack of prior data, or lack of the requisite genetic data to assess segregation in large and well phenotyped families with multiple affected individuals.

Item C of this guideline suggests thoughtful and cautiously implemented, cascade clinical (phenotype) screening of putatively at-risk family members may be considered, even if the clinical phenotype screening was negative in the individual (proband) who completed genetic analysis. This statement recognizes the possibility that the proband may be younger than the usual age of onset of the cardiovascular phenotype. It also recognizes the utility and necessity of gathering clinical phenotype data in an extended family to help interpret the genetic

information in cascade testing if phenotypes are encountered in the family members predicted by the gene/variant pair.

We also recognize that at times a novel variant will be identified in an established, well-curated[131] gene known to have other variants of high risk, and the variant will be recognized as the type that is expected to be pathogenic, but because it is novel it may be appropriately adjudicated as a VUS. In select situations within the context of expert evaluation described above (Guideline 3) and known limitations summing the integrated risk derived from molecular genetics and clinical knowledge of the gene/variant pair (Guideline 4), a personal and family history, pedigree analysis and phenotyping of the individual harboring such a VUS may be considered. The rationale for this comment results directly from the significant risk of morbidity and mortality noted above that may devolve from such cardiomyopathy genes and variants. If phenotype evidence is found to support a disease association in the individual, the remainder of these guidelines would become operative, including consideration of pedigree expansion to help establish or refute the pathogenicity of the variant, and to better discern the overall risk incurred to the individual and the family.

A distinct limitation is that we are unaware of published outcomes data to support, validate, or refute the above guidance, which can only be considered as expert opinion. This emphasizes the need for well-designed rigorous studies examining outcomes of phenotyping and family studies following secondary or incidental findings of variants relevant for the cardiomyopathies.

Therapy Based on Genetic Evaluation and Cardiac Phenotype

The clinical characteristics associated with variants in some disease genes, when integrated with pedigree data, may directly influence the overall assessment and clinical recommendations for a patient or family.

One gene with substantial evidence fitting this situation is *LMNA*, which commonly presents with nonsyndromic cardiomyopathy in adult cardiology practice and is well known for progressive conduction system disease (first-, second-, or third-degree heart block), usually with supraventricular and/or ventricular arrhythmias prior to, during or soon thereafter. All of this may occur prior to or contemporaneously with early DCM. Because in the US the use of ICDs is not recommended until the left ventricular ejection fraction (LVEF) falls to less than 35%, patients with *LMNA* cardiomyopathy may have inadequate protection from life-threatening ventricular arrhythmias if the LVEF remains >35%.[78, 132] For this reason a specific guideline was created for the 2009 HFSA guideline[1] and has been preserved (Guideline 9). Other DCM genes (e.g., *DES* or *SCN5A*, *FLNC* and other genes not yet identified) may also have prominent risk of lethal arrhythmia and may also benefit from earlier ICD use.[133] As noted above, arrhythmia or sudden cardiac death, may precede the development of cardiomyopathy, and may be the presenting feature.

Other genes with mutations causing syndromic diseases involving cardiomyopathy that have clear therapeutic indications include *GLA*, which encodes alpha-galactosidase A, and *GAA*, encoding alpha-glucosidase. Deficiencies of these enzymes cause Fabry or Pompe disease, respectively. Both have protein replacement treatments that have been shown to be efficacious.[134, 135]

The rationale for conducting genetic evaluations for the cardiomyopathies rests on the concept that in most cases treatment interventions once clinical disease has been recognized can forestall progressive disease and/or anticipate and prevent complications of disease progression. Each cardiomyopathy type has its own considerations that exceed the scope of this genetics oriented document. However, even surveillance for common complications (e.g., sudden cardiac death, either from brady- or tachy arrhythmias in progressive *LMNA* cardiomyopathy; atrial fibrillation in long standing HCM; onset of heart failure in previously

asymptomatic but progressive DCM) can trigger appropriate interventions with drugs and/or devices to prevent or ameliorate disease, as reviewed below.

The role and risks of exercise in cardiomyopathy, and questions regarding exercise limitation, are frequently raised by patients and families. These have been addressed in other guideline statements.[136]

7. Medical therapy based on cardiac phenotype is recommended as outlined in consensus guidelines. Level of Evidence = A.

Guidelines for the evaluation and management of patients with cardiomyopathy have been published for HCM,[137, 138] DCM,[6, 139-141] and ARVC.[142] These guidelines provide comprehensive guidance for care of those who are presymptomatic (stage B heart failure) or have had the onset of symptoms (stage C or D heart failure). Guidelines for the clinical care of patients with RCM are not yet available. Controversy continues whether LVNC represents an anatomical phenotype or distinct cardiomyopathy, and even when observed no specific treatment is indicated other than for associated cardiovascular phenotypes, as reviewed above. A multi-society (ACC/AHA/HFSA) guideline update for management of patients with heart failure has recently been published.[140]

8. Device therapies for arrhythmia and conduction system disease based on cardiac phenotype are recommended as outlined in consensus guidelines. Level of Evidence = B.

In brief, ICDs are indicated for secondary prevention of ventricular tachycardia or ventricular fibrillation regardless of the type of cardiomyopathy or degree of ventricular dysfunction. The indications for ICDs for primary prevention of sudden cardiac death in patients with nonischemic cardiomyopathy with reduced ejection fraction of any etiology are summarized

in guideline statements,[6, 139, 143-145] even though some ICD trials excluded individuals with familial cardiomyopathy associated with sudden death.[146] Device therapy for arrhythmia should not rely exclusively on the presence of a P or LP gene variant but must be integrated into overall attributable risk. For DCM, ICD therapy is indicated in patients who have a left ventricular ejection fraction less than or equal to 35% and who are in NYHA functional Class II or III (class I, level of evidence B). Additional class II and III guideline recommendations[144] are provided in Supplementary Table 3.

9. In patients with cardiomyopathy and significant arrhythmia or known risk of arrhythmia an ICD may be considered before the left ventricular ejection fraction falls below 35%. Level of Evidence = C.

Electrophysiological disease can be considered broadly as conduction system disease and arrhythmia. Please see the discussion above regarding *LMNA* cardiomyopathy, however this guideline applies to any genetic cardiomyopathy that presents or progresses to lethal arrhythmia or heart block prior to advanced LV dysfunction. Examples of other conditions include the myotonic dystrophies.[58] Conventional guidelines apply for symptomatic or pre-symptomatic conduction system disease regardless of other aspects of the patient's clinical situation.[144] Pacemakers are indicated for symptomatic bradycardia, high grade AV block regardless of symptoms, or for any other symptomatic conduction system disease. Pacemakers may also be considered to allow for the institution of disease-modifying therapy (e.g., beta-blockers) when limited by bradycardia or along with AV junction ablation to treat refractory atrial fibrillation with rapid ventricular response. In the setting of *LMNA* cardiomyopathy and other genetic conditions with similar risk profiles requiring pacemaker placement, the use of an ICD rather than a pacemaker has been previously recommended[1] and is supported by extensive literature documenting the risks of sudden cardiac death concurrent with conduction system

disease requiring pacemaker placement.[76, 78, 99, 100, 147-150] For a patient with reduced ejection fraction that is likely to require chronic ventricular pacing, placement of a cardiac resynchronization therapy device (e.g., CRT-D) should be considered.

References

1. Hershberger RE, Lindenfeld J, Mestroni L, Seidman CE, Taylor MR, Towbin JA. Genetic evaluation of cardiomyopathy--a Heart Failure Society of America practice guideline. J Card Fail 2009;15:83-97.
2. Mital S, Musunuru K, Garg V, Russell MW, Lanfear DE, Gupta RM, et al. Enhancing Literacy in Cardiovascular Genetics: A Scientific Statement From the American Heart Association. Circ Cardiovasc Genet 2016;9:448-467.
3. Furqan A, Arscott P, Girolami F, Cirino AL, Michels M, Day SM, et al. Care in Specialized Centers and Data Sharing Increase Agreement in Hypertrophic Cardiomyopathy Genetic Test Interpretation. Circ Cardiovasc Genet 2017;10.
4. Green RC, Berg JS, Grody WW, Kalia SS, Korf BR, Martin CL, et al. ACMG recommendations for reporting of incidental findings in clinical exome and genome sequencing. Genet Med 2013;15:565-74.
5. Kalia SS, Adelman K, Bale SJ, Chung WK, Eng C, Evans JP, et al. Recommendations for reporting of secondary findings in clinical exome and genome sequencing, 2016 update (ACMG SF v2.0): a policy statement of the American College of Medical Genetics and Genomics. Genet Med 2016;19:249-255.
6. Yancy CW, Jessup M, Bozkurt B, Butler J, Casey DE, Jr., Drazner MH, et al. 2013 ACCF/AHA Guideline for the Management of Heart Failure: A Report of the American College of Cardiology Foundation/American Heart Association Task Force on Practice Guidelines. Circulation 2013;128:1810-52.
7. Bennette CS, Gallego CJ, Burke W, Jarvik GP, Veenstra DL. The cost-effectiveness of returning incidental findings from next-generation genomic sequencing. Genet Med 2015;17:587-95.
8. Hershberger RE, Hedges DJ, Morales A. Dilated cardiomyopathy: the complexity of a diverse genetic architecture. Nat Rev Cardiol 2013;10:531-47.

9. Richards S, Aziz N, Bale S, Bick D, Das S, Gastier-Foster J, et al. Standards and guidelines for the interpretation of sequence variants: a joint consensus recommendation of the American College of Medical Genetics and Genomics and the Association for Molecular Pathology. Genet Med 2015;17:405-23.

10. Rehm HL, Berg JS, Brooks LD, Bustamante CD, Evans JP, Landrum MJ, et al. ClinGen--the Clinical Genome Resource. N Engl J Med 2015;372:2235-42.

11. *ClinGen - Clinical Genome Resource*. Available from: http://clinicalgenome.org/.

12. Japp AG, Gulati A, Cook SA, Cowie MR, Prasad SK. The Diagnosis and Evaluation of Dilated Cardiomyopathy. J Am Coll Cardiol 2016;67:2996-3010.

13. Maron BJ, Towbin JA, Thiene G, Antzelevitch C, Corrado D, Arnett D, et al. Contemporary definitions and classification of the cardiomyopathies: an American Heart Association Scientific Statement from the Council on Clinical Cardiology, Heart Failure and Transplantation Committee; Quality of Care and Outcomes Research and Functional Genomics and Translational Biology Interdisciplinary Working Groups; and Council on Epidemiology and Prevention. Circulation 2006;113:1807-16.

14. Teekakirikul P, Kelly MA, Rehm HL, Lakdawala NK, Funke BH. Inherited Cardiomyopathies: Molecular Genetics and Clinical Genetic Testing in the Postgenomic Era. J Mol Diagn 2012;15:158-170.

15. Burke MA, Cook SA, Seidman JG, Seidman CE. Clinical and Mechanistic Insights Into the Genetics of Cardiomyopathy. J Am Coll Cardiol 2016;68:2871-2886.

16. Arbustini E, Weidemann F, Hall JL. Left ventricular noncompaction: a distinct cardiomyopathy or a trait shared by different cardiac diseases? J Am Coll Cardiol 2014;64:1840-50.

17. Oechslin E, Jenni R. Nosology of Noncompaction Cardiomyopathy: The Emperor Still Wears Clothes! Can J Cardiol 2017;33:701-704.

18. Anderson RH, Jensen B, Mohun TJ, Petersen SE, Aung N, Zemrak F, et al. Key Questions Relating to Left Ventricular Noncompaction Cardiomyopathy: Is the Emperor Still Wearing Any Clothes? Can J Cardiol 2017;33:747-757.

19. Kawel N, Nacif M, Arai AE, Gomes AS, Hundley WG, Johnson WC, et al. Trabeculated (noncompacted) and compact myocardium in adults: the multi-ethnic study of atherosclerosis. Circ Cardiovasc Imaging 2012;5:357-66.

20. Weir-McCall JR, Yeap PM, Papagiorcopulo C, Fitzgerald K, Gandy SJ, Lambert M, et al. Left Ventricular Noncompaction: Anatomical Phenotype or Distinct Cardiomyopathy? J Am Coll Cardiol 2016;68:2157-2165.

21. Gati S, Chandra N, Bennett RL, Reed M, Kervio G, Panoulas VF, et al. Increased left ventricular trabeculation in highly trained athletes: do we need more stringent criteria for the diagnosis of left ventricular non-compaction in athletes? Heart 2013;99:401-8.

22. Caselli S, Attenhofer Jost CH, Jenni R, Pelliccia A. Left Ventricular Noncompaction Diagnosis and Management Relevant to Pre-participation Screening of Athletes. Am J Cardiol 2015;116:801-8.

23. Gati S, Papadakis M, Papamichael ND, Zaidi A, Sheikh N, Reed M, et al. Reversible de novo left ventricular trabeculations in pregnant women: implications for the diagnosis of left ventricular noncompaction in low-risk populations. Circulation 2014;130:475-83.

24. Hershberger RE, Givertz MM, Ho CY, Judge DP, Kantor P, McBride KL, et al. Genetic Evaluation of Cardiomyopathy - An American College of Medical Genetics and Genomics (ACMG) Practice Resource on behalf of the Professional Practice and Guideline Committee. Genet Med 2017;(pending).

25. Recommendations from the EGAPP Working Group: testing for cytochrome P450 polymorphisms in adults with nonpsychotic depression treated with selective serotonin reuptake inhibitors. Genet Med 2007;9:819-25.

26. Kohler J, Turbitt E, Lewis KL, Wilfond BS, Jamal L, Peay HL, et al. Defining personal utility in genomics: A Delphi study. Clin Genet 2017.

27. Executive summary: HFSA 2006 Comprehensive Heart Failure Practice Guideline. J Card Fail 2006;12:10-38.

28. Morales A, Cowan J, Dagua J, Hershberger RE. Family history: an essential tool for cardiovascular genetic medicine. Congest Heart Fail 2008;14:37-45.

29. Kaski JP, Syrris P, Burch M, Tome-Esteban MT, Fenton M, Christiansen M, et al. Idiopathic restrictive cardiomyopathy in children is caused by mutations in cardiac sarcomere protein genes. Heart 2008;94:1478-84.

30. Morita H, Rehm HL, Menesses A, McDonough B, Roberts AE, Kucherlapati R, et al. Shared genetic causes of cardiac hypertrophy in children and adults. N Engl J Med 2008;358:1899-908.

31. Van Driest SL, Vasile VC, Ommen SR, Will ML, Tajik AJ, Gersh BJ, et al. Myosin binding protein C mutations and compound heterozygosity in hypertrophic cardiomyopathy. J Am Coll Cardiol 2004;44:1903-10.

32. Richard P, Charron P, Carrier L, Ledeuil C, Cheav T, Pichereau C, et al. Hypertrophic cardiomyopathy: distribution of disease genes, spectrum of mutations, and implications for a molecular diagnosis strategy. Circulation 2003;107:2227-32.

33. Ingles J, Doolan A, Chiu C, Seidman J, Seidman C, Semsarian C. Compound and double mutations in patients with hypertrophic cardiomyopathy: implications for genetic testing and counselling. J Med Genet 2005;42:e59.

34. Fourey D, Care M, Siminovitch KA, Weissler-Snir A, Hindieh W, Chan RH, et al. Prevalence and Clinical Implication of Double Mutations in Hypertrophic Cardiomyopathy: Revisiting the Gene-Dose Effect. Circ Cardiovasc Genet 2017;10.

35. Haas J, Frese KS, Peil B, Kloos W, Keller A, Nietsch R, et al. Atlas of the clinical genetics of human dilated cardiomyopathy. Eur Heart J 2015;36:1123-35a.

36. Schaffer AA. Digenic inheritance in medical genetics. J Med Genet 2013;50:641-52.

37. Waddell-Smith KE, Donoghue T, Oates S, Graham A, Crawford J, Stiles MK, et al. Inpatient detection of cardiac-inherited disease: the impact of improving family history taking. Open Heart 2016;3:e000329.

38. Ross SB, Bagnall RD, Ingles J, Van Tintelen JP, Semsarian C. Burden of Recurrent and Ancestral Mutations in Families With Hypertrophic Cardiomyopathy. Circ Cardiovasc Genet 2017;10.

39. Maron BJ, Seidman JG, Seidman CE. Proposal for contemporary screening strategies in families with hypertrophic cardiomyopathy. J Am Coll Cardiol 2004;44:2125-32.

40. Dalal D, Nasir K, Bomma C, Prakasa K, Tandri H, Piccini J, et al. Arrhythmogenic right ventricular dysplasia: a United States experience. Circulation 2005;112:3823-32.

41. Sen-Chowdhry S, Prasad SK, Syrris P, Wage R, Ward D, Merrifield R, et al. Cardiovascular magnetic resonance in arrhythmogenic right ventricular cardiomyopathy revisited: comparison with task force criteria and genotype. J Am Coll Cardiol 2006;48:2132-40.

42. Murphy RT, Thaman R, Blanes JG, Ward D, Sevdalis E, Papra E, et al. Natural history and familial characteristics of isolated left ventricular non-compaction. Eur Heart J 2005;26:187-92.

43. Bhatia NL, Tajik AJ, Wilansky S, Steidley DE, Mookadam F. Isolated noncompaction of the left ventricular myocardium in adults: a systematic overview. J Card Fail 2011;17:771-8.

44. Hoedemaekers YM, Caliskan K, Michels M, Frohn-Mulder I, van der Smagt JJ, Phefferkorn JE, et al. The importance of genetic counseling, DNA diagnostics, and cardiologic family screening in left ventricular noncompaction cardiomyopathy. Circ Cardiovasc Genet 2010;3:232-9.

45. Korngiebel DM, Fullerton SM, Burke W. Patient safety in genomic medicine: an exploratory study. Genet Med 2016;18:1136-1142.

46. Ingles J, Zodgekar PR, Yeates L, Macciocca I, Semsarian C, Fatkin D, et al. Guidelines for genetic testing of inherited cardiac disorders. Heart Lung Circ 2011;20:681-7.

47. Priori SG, Wilde AA, Horie M, Cho Y, Behr ER, Berul C, et al. HRS/EHRA/APHRS expert consensus statement on the diagnosis and management of patients with inherited primary arrhythmia syndromes: document endorsed by HRS, EHRA, and APHRS in May 2013 and by ACCF, AHA, PACES, and AEPC in June 2013. Heart Rhythm 2013;10:1932-63.

48. Hilgart JS, Hayward JA, Coles B, Iredale R. Telegenetics: a systematic review of telemedicine in genetics services. Genet Med 2012;14:765-76.

49. Kindel SJ, Miller EM, Gupta R, Cripe LH, Hinton RB, Spicer RL, et al. Pediatric cardiomyopathy: importance of genetic and metabolic evaluation. J Card Fail 2012;18:396-403.

50. Cox GF, Sleeper LA, Lowe AM, Towbin JA, Colan SD, Orav EJ, et al. Factors associated with establishing a causal diagnosis for children with cardiomyopathy. Pediatrics 2006;118:1519-31.

51. Moretti M, Merlo M, Barbati G, Di Lenarda A, Brun F, Pinamonti B, et al. Prognostic impact of familial screening in dilated cardiomyopathy. Eur J Heart Fail 2010;12:922-7.

52. Dani C, Bertini G, Simone P, Rubaltelli FF. Hypertrophic cardiomyopathy in preterm infants treated with methylprednisolone for bronchopulmonary dysplasia. Pediatrics 2006;117:1866-7.

53. Werner JC, Sicard RE, Hansen TW, Solomon E, Cowett RM, Oh W. Hypertrophic cardiomyopathy associated with dexamethasone therapy for bronchopulmonary dysplasia. J Pediatr 1992;120:286-91.

54. Gutgesell HP, Speer ME, Rosenberg HS. Characterization of the cardiomyopathy in infants of diabetic mothers. Circulation 1980;61:441-50.

55. Prendiville TW, Gauvreau K, Tworog-Dube E, Patkin L, Kucherlapati RS, Roberts AE, et al. Cardiovascular disease in Noonan syndrome. Arch Dis Child 2014;99:629-34.

56. Wilkinson JD, Lowe AM, Salbert BA, Sleeper LA, Colan SD, Cox GF, et al. Outcomes in children with Noonan syndrome and hypertrophic cardiomyopathy: a study from the Pediatric Cardiomyopathy Registry. Am Heart J 2012;164:442-8.

57. Colquitt JL, Noonan JA. Cardiac findings in Noonan syndrome on long-term follow-up. Congenit Heart Dis 2014;9:144-50.

58. Elliott P. Myotonic dystrophy: time for evidence-based therapy. Eur Heart J 2014;35:2135-7.

59. Kang SL, Forsey J, Dudley D, Steward CG, Tsai-Goodman B. Clinical Characteristics and Outcomes of Cardiomyopathy in Barth Syndrome: The UK Experience. Pediatr Cardiol 2016;37:167-76.

60. Scaglia F, Towbin JA, Craigen WJ, Belmont JW, Smith EO, Neish SR, et al. Clinical spectrum, morbidity, and mortality in 113 pediatric patients with mitochondrial disease. Pediatrics 2004;114:925-31.

61. Boucek D, Jirikowic J, Taylor M. Natural history of Danon disease. Genet Med 2011;13:563-8.

62. Porto AG, Brun F, Severini GM, Losurdo P, Fabris E, Taylor MR, et al. Clinical Spectrum of PRKAG2 Syndrome. Circ Arrhythm Electrophysiol 2016;9:e003121.

63. Hsu TR, Hung SC, Chang FP, Yu WC, Sung SH, Hsu CL, et al. Later Onset Fabry Disease, Cardiac Damage Progress in Silence: Experience With a Highly Prevalent Mutation. J Am Coll Cardiol 2016;68:2554-2563.

64. Miller EM, Wang Y, Ware SM. Uptake of cardiac screening and genetic testing among hypertrophic and dilated cardiomyopathy families. J Genet Couns 2013;22:258-67.

65. The SOLVD Investigators. Effect of enalapril on mortality and the development of heart failure in asymptomatic patients with reduced left ventricular ejection fractions. N Engl J Med 1992;327:685-691.

66. Colucci WS, Kolias TJ, Adams KF, Armstrong WF, Ghali JK, Gottlieb SS, et al. Metoprolol reverses left ventricular remodeling in patients with asymptomatic systolic dysfunction: the REversal of VEntricular Remodeling with Toprol-XL (REVERT) trial. Circulation 2007;116:49-56.

67. Ho CY, Lakdawala NK, Cirino AL, Lipshultz SE, Sparks E, Abbasi SA, et al. Diltiazem treatment for pre-clinical hypertrophic cardiomyopathy sarcomere mutation carriers: a pilot randomized trial to modify disease expression. JACC Heart Fail 2015;3:180-8.

68. Ingles J, McGaughran J, Scuffham PA, Atherton J, Semsarian C. A cost-effectiveness model of genetic testing for the evaluation of families with hypertrophic cardiomyopathy. Heart 2012;98:625-30.

69. Alfares AA, Kelly MA, McDermott G, Funke BH, Lebo MS, Baxter SB, et al. Results of clinical genetic testing of 2,912 probands with hypertrophic cardiomyopathy: expanded panels offer limited additional sensitivity. Genet Med 2015;17:880-8.

70. Aggarwal V, Dobrolet N, Fishberger S, Zablah J, Jayakar P, Ammous Z. PRKAG2 mutation: An easily missed cardiac specific non-lysosomal glycogenosis. Ann Pediatr Cardiol 2015;8:153-6.

71. Thevenon J, Laurent G, Ader F, Laforet P, Klug D, Duva Pentiah A, et al. High prevalence of arrhythmic and myocardial complications in patients with cardiac glycogenosis due to PRKAG2 mutations. Europace 2017;19:651-659.

72. van Velzen HG, Vriesendorp PA, Oldenburg RA, van Slegtenhorst MA, van der Velden J, Schinkel AFL, et al. Value of Genetic Testing for the Prediction of Long-Term Outcome in Patients With Hypertrophic Cardiomyopathy. Am J Cardiol 2016;118:881-887.

73. Li Q, Gruner C, Chan RH, Care M, Siminovitch K, Williams L, et al. Genotype-positive status in patients with hypertrophic cardiomyopathy is associated with higher rates of heart failure events. Circ Cardiovasc Genet 2014;7:416-22.

74. van Rijsingen IA, van der Zwaag PA, Groeneweg JA, Nannenberg EA, Jongbloed JD, Zwinderman AH, et al. Outcome in phospholamban R14del carriers: results of a large multicentre cohort study. Circ Cardiovasc Genet 2014;7:455-65.

75. Ortiz-Genga MF, Cuenca S, Dal Ferro M, Zorio E, Salgado-Aranda R, Climent V, et al. Truncating FLNC Mutations Are Associated With High-Risk Dilated and Arrhythmogenic Cardiomyopathies. J Am Coll Cardiol 2016;68:2440-2451.

76. van Rijsingen IA, Arbustini E, Elliott PM, Mogensen J, Hermans-van Ast JF, van der Kooi AJ, et al. Risk factors for malignant ventricular arrhythmias in lamin a/c mutation carriers a European cohort study. J Am Coll Cardiol 2012;59:493-500.

77. Kayvanpour E, Sedaghat-Hamedani F, Amr A, Lai A, Haas J, Holzer DB, et al. Genotype-phenotype associations in dilated cardiomyopathy: meta-analysis on more than 8000 individuals. Clin Res Cardiol 2017;106:127-139.

78. Meune C, Van Berlo JH, Anselme F, Bonne G, Pinto YM, Duboc D. Primary prevention of sudden death in patients with lamin A/C gene mutations. N Engl J Med 2006;354:209-10.

79. Hodgkinson KA, Howes AJ, Boland P, Shen XS, Stuckless S, Young TL, et al. Long-Term Clinical Outcome of Arrhythmogenic Right Ventricular Cardiomyopathy in Individuals With a p.S358L Mutation in TMEM43 Following Implantable Cardioverter Defibrillator Therapy. Circ Arrhythm Electrophysiol 2016;9.

80. Wilson KD, Shen P, Fung E, Karakikes I, Zhang A, InanlooRahatloo K, et al. A Rapid, High-Quality, Cost-Effective, Comprehensive and Expandable Targeted Next-Generation Sequencing Assay for Inherited Heart Diseases. Circ Res 2015;117:603-11.

81. Ceyhan-Birsoy O, Pugh TJ, Bowser MJ, Hynes E, Frisella AL, Mahanta LM, et al. Next generation sequencing-based copy number analysis reveals low prevalence of deletions and duplications in 46 genes associated with genetic cardiomyopathies. Mol Genet Genomic Med 2016;4:143-51.

82. Golbus JR, Puckelwartz MJ, Fahrenbach JP, Dellefave-Castillo LM, Wolfgeher D, McNally EM. Population-Based Variation in Cardiomyopathy Genes. Circ Cardiovasc Genet 2012;5:391-399.

83. Herman DS, Lam L, Taylor MR, Wang L, Teekakirikul P, Christodoulou D, et al. Truncations of titin causing dilated cardiomyopathy. N Engl J Med 2012;366:619-28.

84. Walsh R, Thomson KL, Ware JS, Funke BH, Woodley J, McGuire KJ, et al. Reassessment of Mendelian gene pathogenicity using 7,855 cardiomyopathy cases and 60,706 reference samples. Genet Med 2016;19:192-203.

85. Ingles J, Semsarian C. Conveying a probabilistic genetic test result to families with an inherited heart disease. Heart Rhythm 2014;11:1073-8.

86. Arad M, Maron BJ, Gorham JM, Johnson WH, Jr., Saul JP, Perez-Atayde AR, et al. Glycogen storage diseases presenting as hypertrophic cardiomyopathy. N Engl J Med 2005;352:362-72.

87. Long PA, Evans JM, Olson TM. Exome sequencing establishes diagnosis of Alstrom syndrome in an infant presenting with non-syndromic dilated cardiomyopathy. Am J Med Genet A 2015;167A:886-90.

88. Ingles J, Sarina T, Yeates L, Hunt L, Macciocca I, McCormack L, et al. Clinical predictors of genetic testing outcomes in hypertrophic cardiomyopathy. Genet Med 2013;15:972-7.

89. Pan S, Caleshu CA, Dunn KE, Foti MJ, Moran MK, Soyinka O, et al. Cardiac structural and sarcomere genes associated with cardiomyopathy exhibit marked intolerance of genetic variation. Circ Cardiovasc Genet 2012;5:602-10.

90. Teekakirikul P, Kelly MA, Rehm HL, Lakdawala NK, Funke BH. Inherited cardiomyopathies: molecular genetics and clinical genetic testing in the postgenomic era. J Mol Diagn 2013;15:158-70.

91. Walsh R, Buchan R, Wilk A, John S, Felkin LE, Thomson KL, et al. Defining the genetic architecture of hypertrophic cardiomyopathy: re-evaluating the role of non-sarcomeric genes. Eur Heart J 2017.

92. Ware SM. Evaluation of genetic causes of cardiomyopathy in childhood. Cardiol Young 2015;25 Suppl 2:43-50.

93. Lakdawala NK, Funke BH, Baxter S, Cirino AL, Roberts AE, Judge DP, et al. Genetic testing for dilated cardiomyopathy in clinical practice. J Card Fail 2012;18:296-303.

94. Pugh TJ, Kelly MA, Gowrisankar S, Hynes E, Seidman MA, Baxter SM, et al. The landscape of genetic variation in dilated cardiomyopathy as surveyed by clinical DNA sequencing. Genet Med 2014;16:601-8.

95. Morales A, Hershberger RE. The Rationale and Timing of Molecular Genetic Testing for Dilated Cardiomyopathy. Can J Cardiol 2015;31:1309-12.

96. Roberts AM, Ware JS, Herman DS, Schafer S, Baksi J, Bick AG, et al. Integrated allelic, transcriptional, and phenomic dissection of the cardiac effects of titin truncations in health and disease. Sci Transl Med 2015;7:270ra6.

97. Schafer S, de Marvao A, Adami E, Fiedler LR, Ng B, Khin E, et al. Titin-truncating variants affect heart function in disease cohorts and the general population. Nat Genet 2017;49:46-53.

98. Norton N, Li D, Rampersaud E, Morales A, Martin ER, Zuchner S, et al. Exome Sequencing and Genome-Wide Linkage Analysis in 17 Families Illustrates the Complex Contribution of TTN Truncating Variants to Dilated Cardiomyopathy. Circ Cardiovasc Genet 2013;6:144-153.

99. Arbustini E, Pilotto A, Repetto A, Grasso M, Negri A, Diegoli M, et al. Autosomal dominant dilated cardiomyopathy with atrioventricular block: a lamin A/C defect-related disease. J Am Coll Cardiol 2002;39:981-90.

100. Parks SB, Kushner JD, Nauman D, Burgess D, Ludwigsen S, Peterson A, et al. Lamin A/C mutation analysis in a cohort of 324 unrelated patients with idiopathic or familial dilated cardiomyopathy. Am Heart J 2008;156:161-9.

101. Norton N, Li D, Reider MJ, Siegfried JD, Rampersaud E, Zuchner S, et al. Genome-wide studies of copy number variation and exome sequencing identify rare variants in *BAG3* as a cause of dilated cardiomyopathy. Am J Hum Genet 2011;88:273-282.

102. Brauch KM, Karst ML, Herron KJ, de Andrade M, Pellikka PA, Rodeheffer RJ, et al. Mutations in ribonucleic acid binding protein gene cause familial dilated cardiomyopathy. J Am Coll Cardiol 2009;54:930-41.

103. McCaffrey T, Guglieri M, Murphy AP, Bushby K, Johnson A, Bourke JP. Cardiac involvement in female carriers of duchenne or becker muscular dystrophy. Muscle Nerve 2016;55:810-818.

104. Awad MM, Calkins H, Judge DP. Mechanisms of disease: molecular genetics of arrhythmogenic right ventricular dysplasia/cardiomyopathy. Nat Clin Pract Cardiovasc Med 2008;5:258-67.

105. Groeneweg JA, Bhonsale A, James CA, te Riele AS, Dooijes D, Tichnell C, et al. Clinical Presentation, Long-Term Follow-Up, and Outcomes of 1001 Arrhythmogenic Right Ventricular Dysplasia/Cardiomyopathy Patients and Family Members. Circ Cardiovasc Genet 2015;8:437-46.

106. Quarta G, Muir A, Pantazis A, Syrris P, Gehmlich K, Garcia-Pavia P, et al. Familial evaluation in arrhythmogenic right ventricular cardiomyopathy: impact of genetics and revised task force criteria. Circulation 2011;123:2701-9.

107. Saffitz JE. Arrhythmogenic cardiomyopathy: advances in diagnosis and disease pathogenesis. Circulation 2011;124:e390-2.

108. Elliott P, O'Mahony C, Syrris P, Evans A, Rivera Sorensen C, Sheppard MN, et al. Prevalence of desmosomal protein gene mutations in patients with dilated cardiomyopathy. Circ Cardiovasc Genet 2010;3:314-22.

109. James CA, Bhonsale A, Tichnell C, Murray B, Russell SD, Tandri H, et al. Exercise increases age-related penetrance and arrhythmic risk in arrhythmogenic right ventricular dysplasia/cardiomyopathy-associated desmosomal mutation carriers. J Am Coll Cardiol 2013;62:1290-7.

110. Gallego-Delgado M, Delgado JF, Brossa-Loidi V, Palomo J, Marzoa-Rivas R, Perez-Villa F, et al. Idiopathic Restrictive Cardiomyopathy Is Primarily a Genetic Disease. J Am Coll Cardiol 2016;67:3021-3.

111. Rapezzi C, Lorenzini M, Longhi S, Milandri A, Gagliardi C, Bartolomei I, et al. Cardiac amyloidosis: the great pretender. Heart Fail Rev 2015;20:117-24.

112. Ton VK, Mukherjee M, Judge DP. Transthyretin cardiac amyloidosis: pathogenesis, treatments, and emerging role in heart failure with preserved ejection fraction. Clin Med Insights Cardiol 2014;8:39-44.

113. Buxbaum JN, Ruberg FL. Transthyretin V122I (pV142I)* cardiac amyloidosis: an age-dependent autosomal dominant cardiomyopathy too common to be overlooked as a cause of significant heart disease in elderly African Americans. Genet Med 2017;19:733-742.

114. Maurer MS, Elliott P, Comenzo R, Semigran M, Rapezzi C. Addressing Common Questions Encountered in the Diagnosis and Management of Cardiac Amyloidosis. Circulation 2017;135:1357-1377.

115. Fleming RE, Ponka P. Iron overload in human disease. N Engl J Med 2012;366:348-59.

116. Probst S, Oechslin E, Schuler P, Greutmann M, Boye P, Knirsch W, et al. Sarcomere gene mutations in isolated left ventricular noncompaction cardiomyopathy do not predict clinical phenotype. Circ Cardiovasc Genet 2011;4:367-74.

117. Miller EM, Hinton RB, Czosek R, Lorts A, Parroc A, Shikany A, et al. Genetic Testing in Pediatric Left Ventricular Noncompaction. Circ Cardiovasc Genet 2017;10:e001735.

118. Morales A, Painter T, Li R, Siegfried JD, Li D, Norton N, et al. Rare variant mutations in pregnancy-associated or peripartum cardiomyopathy. Circulation 2010;121:2176-82.

119. van Spaendonck-Zwarts KY, van Tintelen JP, van Veldhuisen DJ, van der Werf R, Jongbloed JD, Paulus WJ, et al. Peripartum cardiomyopathy as a part of familial dilated cardiomyopathy. Circulation 2010;121:2169-75.

120. Ware JS, Li J, Mazaika E, Yasso CM, DeSouza T, Cappola TP, et al. Shared Genetic Predisposition in Peripartum and Dilated Cardiomyopathies. N Engl J Med 2016;374:233-41.

121. Cann F, Corbett M, O'Sullivan D, Tennant S, Hailey H, Grieve JH, et al. Phenotype-driven molecular autopsy for sudden cardiac death. Clin Genet 2017;91:22-29.

122. Semsarian C, Ingles J, Wilde AA. Sudden cardiac death in the young: the molecular autopsy and a practical approach to surviving relatives. Eur Heart J 2015;36:1290-6.

123. Tsuchiya KD, Shaffer LG, Aradhya S, Gastier-Foster JM, Patel A, Rudd MK, et al. Variability in interpreting and reporting copy number changes detected by array-based technology in clinical laboratories. Genet Med 2009;11:866-73.

124. Van Driest SL, Wells QS, Stallings S, Bush WS, Gordon A, Nickerson DA, et al. Association of Arrhythmia-Related Genetic Variants With Phenotypes Documented in Electronic Medical Records. JAMA 2016;315:47-57.

125. Xu T, Yang Z, Vatta M, Rampazzo A, Beffagna G, Pilichou K, et al. Compound and digenic heterozygosity contributes to arrhythmogenic right ventricular cardiomyopathy. J Am Coll Cardiol 2010;55:587-97.

126. Bauce B, Nava A, Beffagna G, Basso C, Lorenzon A, Smaniotto G, et al. Multiple mutations in desmosomal proteins encoding genes in arrhythmogenic right ventricular cardiomyopathy/dysplasia. Heart Rhythm 2010;7:22-9.

127. Resta RG. Defining and redefining the scope and goals of genetic counseling. Am J Med Genet C Semin Med Genet 2006;142C:269-75.

128. van Engelen K, Baars MJ, Felix JP, Postma AV, Mulder BJ, Smets EM. The value of the clinical geneticist caring for adults with congenital heart disease: diagnostic yield and patients' perspective. Am J Med Genet A 2013;161A:1628-37.

129. Richards CS, Bale S, Bellissimo DB, Das S, Grody WW, Hegde MR, et al. ACMG recommendations for standards for interpretation and reporting of sequence variations: Revisions 2007. Genet Med 2008;10:294-300.

130. *ClinGen Cardiovascular Domain Working Group*. Available from: https://www.clinicalgenome.org/working-groups/clinical-domain/sub-groups/cardiovascular/.

131. Strande NT, Riggs ER, Buchanan AH, Ceyhan-Birsoy O, DiStefano M, Dwight SS, et al. Evaluating the Clinical Validity of Gene-Disease Associations: An Evidence-Based Framework Developed by the Clinical Genome Resource. Am J Hum Genet 2017;100:895-906.

132. Kumar S, Baldinger SH, Gandjbakhch E, Maury P, Sellal JM, Androulakis AF, et al. Long-Term Arrhythmic and Nonarrhythmic Outcomes of Lamin A/C Mutation Carriers. J Am Coll Cardiol 2016;68:2299-2307.

133. Ackerman MJ, Priori SG, Willems S, Berul C, Brugada R, Calkins H, et al. HRS/EHRA Expert Consensus Statement on the State of Genetic Testing for the Channelopathies and Cardiomyopathies This document was developed as a partnership between the Heart Rhythm Society (HRS) and the European Heart Rhythm Association (EHRA). Heart Rhythm 2011;8:1308-39.

134. Desnick RJ, Brady R, Barranger J, Collins AJ, Germain DP, Goldman M, et al. Fabry disease, an under-recognized multisystemic disorder: expert recommendations for diagnosis, management, and enzyme replacement therapy. Ann Intern Med 2003;138:338-46.

135. Byrne BJ, Falk DJ, Pacak CA, Nayak S, Herzog RW, Elder ME, et al. Pompe disease gene therapy. Hum Mol Genet 2011;20:R61-8.

136. Maron BJ, Udelson JE, Bonow RO, Nishimura RA, Ackerman MJ, Estes NA, 3rd, et al. Eligibility and Disqualification Recommendations for Competitive Athletes With Cardiovascular Abnormalities: Task Force 3: Hypertrophic Cardiomyopathy, Arrhythmogenic Right Ventricular Cardiomyopathy and Other Cardiomyopathies, and Myocarditis: A Scientific Statement From the American Heart Association and American College of Cardiology. J Am Coll Cardiol 2015;66:2362-71.

137. Gersh BJ, Maron BJ, Bonow RO, Dearani JA, Fifer MA, Link MS, et al. 2011 ACCF/AHA Guideline for the Diagnosis and Treatment of Hypertrophic Cardiomyopathy: Executive Summary: A Report of the American College of Cardiology Foundation/American Heart Association Task Force on Practice Guidelines. Circulation 2011;124:2761-96.

138. Elliott PM, Anastasakis A, Borger MA, Borggrefe M, Cecchi F, Charron P, et al. 2014 ESC Guidelines on diagnosis and management of hypertrophic cardiomyopathy: the Task Force for the Diagnosis and Management of Hypertrophic Cardiomyopathy of the European Society of Cardiology (ESC). Eur Heart J 2014;35:2733-79.

139. Heart Failure Society of A, Lindenfeld J, Albert NM, Boehmer JP, Collins SP, Ezekowitz JA, et al. HFSA 2010 Comprehensive Heart Failure Practice Guideline. J Card Fail 2010;16:e1-194.

140. Yancy CW, Jessup M, Bozkurt B, Butler J, Casey DE, Jr., Colvin MM, et al. 2016 ACC/AHA/HFSA Focused Update on New Pharmacological Therapy for Heart Failure: An Update of the 2013 ACCF/AHA Guideline for the Management of Heart Failure: A

Report of the American College of Cardiology/American Heart Association Task Force on Clinical Practice Guidelines and the Heart Failure Society of America. J Am Coll Cardiol 2016;68:1476-88.

141. Ponikowski P, Voors AA, Anker SD, Bueno H, Cleland JG, Coats AJ, et al. 2016 ESC Guidelines for the diagnosis and treatment of acute and chronic heart failure: The Task Force for the diagnosis and treatment of acute and chronic heart failure of the European Society of Cardiology (ESC)Developed with the special contribution of the Heart Failure Association (HFA) of the ESC. Eur Heart J 2016;37:2129-200.

142. Corrado D, Wichter T, Link MS, Hauer RN, Marchlinski FE, Anastasakis A, et al. Treatment of Arrhythmogenic Right Ventricular Cardiomyopathy/Dysplasia: An International Task Force Consensus Statement. Circulation 2015;132:441-53.

143. Kusumoto FM, Calkins H, Boehmer J, Buxton AE, Chung MK, Gold MR, et al. HRS/ACC/AHA expert consensus statement on the use of implantable cardioverter-defibrillator therapy in patients who are not included or not well represented in clinical trials. Circulation 2014;130:94-125.

144. Epstein AE, DiMarco JP, Ellenbogen KA, Estes NA, 3rd, Freedman RA, Gettes LS, et al. 2012 ACCF/AHA/HRS focused update incorporated into the ACCF/AHA/HRS 2008 guidelines for device-based therapy of cardiac rhythm abnormalities: a report of the American College of Cardiology Foundation/American Heart Association Task Force on Practice Guidelines and the Heart Rhythm Society. J Am Coll Cardiol 2013;61:e6-75.

145. Russo AM, Stainback RF, Bailey SR, Epstein AE, Heidenreich PA, Jessup M, et al. ACCF/HRS/AHA/ASE/HFSA/SCAI/SCCT/SCMR 2013 appropriate use criteria for implantable cardioverter-defibrillators and cardiac resynchronization therapy: a report of the American College of Cardiology Foundation appropriate use criteria task force, Heart Rhythm Society, American Heart Association, American Society of Echocardiography, Heart Failure Society of America, Society for Cardiovascular Angiography and

Interventions, Society of Cardiovascular Computed Tomography, and Society for Cardiovascular Magnetic Resonance. Heart Rhythm 2013;10:e11-58.

146. Kadish A, Dyer A, Daubert JP, Quigg R, Estes NA, Anderson KP, et al. Prophylactic defibrillator implantation in patients with nonischemic dilated cardiomyopathy. N Engl J Med 2004;350:2151-8.

147. Taylor MR, Fain PR, Sinagra G, Robinson ML, Robertson AD, Carniel E, et al. Natural history of dilated cardiomyopathy due to lamin A/C gene mutations. J Am Coll Cardiol 2003;41:771-80.

148. Pasotti M, Klersy C, Pilotto A, Marziliano N, Rapezzi C, Serio A, et al. Long-term outcome and risk stratification in dilated cardiolaminopathies. J Am Coll Cardiol 2008;52:1250-60.

149. Brodt C, Siegfried JD, Hofmeyer M, Martel J, Rampersaud E, Li D, et al. Temporal relationship of conduction system disease and ventricular dysfunction in LMNA cardiomyopathy. J Card Fail 2013;19:233-9.

150. Anselme F, Moubarak G, Savoure A, Godin B, Borz B, Drouin-Garraud V, et al. Implantable cardioverter-defibrillators in lamin A/C mutation carriers with cardiac conduction disorders. Heart Rhythm 2013;10:1492-8.

151. Towbin JA, Lorts A, Jefferies JL. Left ventricular non-compaction cardiomyopathy. Lancet 2015;386:813-25.

152. Kohli SK, Pantazis AA, Shah JS, Adeyemi B, Jackson G, McKenna WJ, et al. Diagnosis of left-ventricular non-compaction in patients with left-ventricular systolic dysfunction: time for a reappraisal of diagnostic criteria? Eur Heart J 2008;29:89-95.

153. Agarwal A, Khandheria BK, Paterick TE, Treiber SC, Bush M, Tajik AJ. Left ventricular noncompaction in patients with bicuspid aortic valve. J Am Soc Echocardiogr 2013;26:1306-13.

154. Ryan TD, Ware SM, Lucky AW, Towbin JA, Jefferies JL, Hinton RB. Left ventricular noncompaction cardiomyopathy and aortopathy in a patient with recessive dystrophic epidermolysis bullosa. Circ Heart Fail 2012;5:e81-2.

155. Postma AV, van Engelen K, van de Meerakker J, Rahman T, Probst S, Baars MJ, et al. Mutations in the sarcomere gene MYH7 in Ebstein anomaly. Circ Cardiovasc Genet 2011;4:43-50.

156. Wessels MW, Willems PJ. Mutations in sarcomeric protein genes not only lead to cardiomyopathy but also to congenital cardiovascular malformations. Clin Genet 2008;74:16-9.

157. Luxan G, Casanova JC, Martinez-Poveda B, Prados B, D'Amato G, MacGrogan D, et al. Mutations in the NOTCH pathway regulator MIB1 cause left ventricular noncompaction cardiomyopathy. Nat Med 2013;19:193-201.

158. Zhang W, Chen H, Qu X, Chang CP, Shou W. Molecular mechanism of ventricular trabeculation/compaction and the pathogenesis of the left ventricular noncompaction cardiomyopathy (LVNC). Am J Med Genet C Semin Med Genet 2013;163C:144-56.

159. Chen H, Zhang W, Sun X, Yoshimoto M, Chen Z, Zhu W, et al. Fkbp1a controls ventricular myocardium trabeculation and compaction by regulating endocardial Notch1 activity. Development 2013;140:1946-57.

160. Klaassen S, Probst S, Oechslin E, Gerull B, Krings G, Schuler P, et al. Mutations in sarcomere protein genes in left ventricular noncompaction. Circulation 2008;117:2893-901.

161. Piccolo P, Attanasio S, Secco I, Sangermano R, Strisciuglio C, Limongelli G, et al. MIB2 variants altering NOTCH signalling result in left ventricle hypertrabeculation/non-compaction and are associated with Menetrier-like gastropathy. Hum Mol Genet 2016;26:33-43.

162. Barth PG, Valianpour F, Bowen VM, Lam J, Duran M, Vaz FM, et al. X-linked cardioskeletal myopathy and neutropenia (Barth syndrome): an update. Am J Med Genet A 2004;126A:349-54.

163. Saleeb SF, Margossian R, Spencer CT, Alexander ME, Smoot LB, Dorfman AL, et al. Reproducibility of echocardiographic diagnosis of left ventricular noncompaction. J Am Soc Echocardiogr 2012;25:194-202.

Table 1. Studies Recommended in Baseline Clinical Phenotyping.

Study	DCM	HCM	ARVC	LVNC	RCM
CK-MM[1]	X			X	
ECG	X	X	X	X	X
ETT[2]		X			X[3]
Holter monitoring		X	X		X
CMR[4]	X	X	X	X	X
Metabolic dis-ease screening[5]	X	X		X	X

[1]CK-MM is the MM band (skeletal muscle) fraction of creatine kinase and should be completed if syndromic or neuromuscular disease is suspected. [2]ETT, exercise treadmill testing. [3]In children. [4]Cardiac magnetic resonance imaging (CMR) is recommended if echocardiography is insufficient to define the phenotype; this is relevant to assess the cardiac morphology and function for all of the cardiomyopathies, and the presence and degree of fibrosis inferred from gadolinium uptake. [5]Additional screening tests are indicated for pediatric onset and select adult onset presentations, see Guideline 3.

Table 2. Suggested Clinical Phenotype Screening Intervals by Age and Cardiomyopathy for Unaffected First-Degree Family Members of Affected Individuals

Cardiomyopathy	0-5 years[2]	6-12 years	13-19 years	20-50 years	>50 years
DCM	Annually with positive FDR[1]	1-2 years with positive FDR[1]	1-3 years	2-3 years	5 years
HCM	Annually with positive FDR[1]	1-2 years with positive FDR[1]	2-3 years	5 years	5 years
ARVC	Consider once with positive FDR[1]	5 years	1-3 years	2-3 years	3 years
RCM	Annually with positive FDR[1]	1-2 years with positive FDR[1]	2-3 years	3 years	5 years

[1]Positive FDR means that the unaffected but at-risk family member has a first-degree relative with the phenotype of interest. These screening intervals apply to at-risk family members when genetic testing: has not been performed or is uninformative in the proband, or when it has identified a likely pathogenic or pathogenic variant in the at-risk family member.

[2]Although most DCM is adult-onset and most HCM is adolescent- or adult-onset, both occur in neonates and young children. ARVC is early adult- to adult-onset. Data are limited for RCM.

Table 3. Selected Genes in Association with Cardiomyopathy

	Core genes[1]	Estimates of genetic testing diagnostic yield	ACMG Secondary Findings Gene List		Metabolic Causes of Cardio-myopathty	Examples of Genetic Syndromes
HCM	*MYH7, MYBPC3, TNNT2, TNNC1, TNNI3, TPM1, MYL2, MYL3, ACTC1, ACTN2, CSRP3, PLN, TTR, PRKAG2, LAMP2, GLA*	30-60%	*MYBPC3, MYH7, TNNT2, TNNI3, TPM1, MYL3, ACTC1, PRKAG2, GLA, MYL2, LMNA*		*GAA* (Pompe); Mitochondrial disease genes	RASopathies (e.g., Noonan syndrome, others); Friedreich ataxia
DCM	*TTN*[2]*, LMNA, MYH7, TNNT2, BAG3, RBM20, TNNC1, TNNI3, TPM1, SCN5A, PLN.* For testing, all HCM, ARVC genes are recommended to be included.	10-40%			Mitochondrial disease genes	Muscular dystrophies; Alström syndrome
ARVC	*DES, DSC2, DSG2, DSP, JUP, LMNA, PKP2, PLN, RYR2, SCN5A, TMEM43, TTN*[2]; consider full DCM panel	10-50%	PKP2, DSP, DSC2, TMEM43, DSG2, RYR2 SCN5A			Naxos syndrome; Carvajal syndrome
RCM	Consider HCM or DCM gene panel	10-60%				
LVNC	Use the gene panel for the cardiomyopathy identified in association with the LVNC phenotype	Unknown			Mitochondrial disease genes including *TAZ* in Barth syndrome	1p36 deletion syndrome; RASopathies

[1]Core gene lists represent genes with the highest diagnostic yield and/or strongest evidence of the gene in association with the listed phenotype; the genes listed are not exhaustive and should be considered illustrative for the type of cardiomyopathy. Considerable overlap of genes between cardiomyopathy phenotypes is well established. Genes known to cause metabolic disease or genetic syndromes are often included in testing panels, but vary depending on the clinical laboratory. Gene lists therefore need to be reviewed carefully before ordering testing. Metabolic and genetic syndrome columns provide examples only and are not intended to be comprehensive. [2]Only *TTN* truncating variants are thought relevant for cardiomyopathy.

Appendix. Author Relationships with Industry and Other Entities

Committee Member	Employment	Consultant	Speakers Bureau	Ownership/ Partnership / Principal	Personal Research	Institutional, Organizational, or Other Financial Benefit	Expert Witness
Ray Hershberger	The Ohio State University College of Medicine and Wexner Medical Center, Columbus, OH	Array Biopharma	None	None	None	None	None
Michael M. Givertz	Brigham and Women's Hospital, Harvard Medical School, Boston, MA	None	None	None	None	None	None
Carolyn Ho	Brigham and Women's Hospital, Harvard Medical School, Boston, MA	MyoKardia	None	None	None	MyoKardia	None
Daniel P. Judge	Johns Hopkins University School of Medicine	Array Biopharma, Eidos Therapeutics, Glaxo Smith Kline, Invitae, MyoKardia, and Pfizer.	None	None	Pfizer	None	None
Paul F. Kantor	University of Alberta, Stollery Children's Hospital, Edmonton, AB. CANADA.	None	None	None	None	None	None
Kim L McBride	Nationwide Children's Hospital and College of Medicine, Ohio State University, Columbus	None	None	None	None	None	None

	OH						
Ana Morales	The Ohio State University College of Medicine and Wexner Medical Center, Columbus, OH	None	None	None	None	None	None
Matt Taylor	University of Colorado Denver	Array Biopharma, Guidepoint Global, Wellpoint Inc	GeneDx	None	None	None	None
Matteo Vatta	Indiana University, Indianapolis, IN and Invitae Corporation, San Francisco, CA	None	None	Invitae Corporation, San Francisco, CA	None	Invitae Corporation, San Francisco, CA	None
Stephanie M. Ware	Indiana University School of Medicine, Indianapolis, IN	None	None	None	None	None	None

This table represents the relationships of committee members with industry and other entities that were determined to be possibly relevant to this document. These relationships were reviewed and updated in conjunction with meetings and/or conference calls of the writing committee during the document development process. A person is deemed to have a significant interest in a business if the interest represents ownership of ≥5% of the voting stock or share of the business entity, or ownership of ≥$5,000 of the fair market value of the business entity, or if funds received by the person from the business entity exceed 5% of the person's gross income for the previous year. Relationships that exist with no financial benefit are also included for the purpose of transparency. Relationships in this table are modest unless otherwise noted.