UnitedHealthcare® Commercial and Individual Exchange
Medical Policy

Genetic Testing for Cardiac Disease

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➲ Instructions for Use

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Application

UnitedHealthcare Commercial

This Medical Policy applies to all UnitedHealthcare Commercial benefit plans.

UnitedHealthcare Individual Exchange

This Medical Policy applies to Individual Exchange benefit plans in all states except for Colorado.

Coverage Rationale

Pre-test genetic counseling is strongly recommended in order to inform persons being tested about the advantages and limitations of the test as applied to a unique person.

Inherited Arrythmias

Multi-Gene Panel testing for the diagnosis of a hereditary arrhythmia syndrome is proven and medically necessary in individuals with a confirmed or suspected diagnosis of any of the following conditions:

- Brugada syndrome (BrS); or
- Catecholaminergic polymorphic ventricular tachycardia (CPVT); or
- Familial long QT syndrome (LQTS) when acquired causes have been ruled out and one of the following criteria are met:
    - Prolonged QTc [> 460ms] on exercise or ambulatory electrocardiogram (ECG), Holter monitoring or during pharmacologic provocation testing; or
    - T wave abnormalities on ECG suggestive of LQTS (i.e., Torsade de pointes, T wave alternans or notched T wave in 3 leads); or
    - Profound congenital bilateral sensorineural hearing loss and prolonged QTc; or
    - Schwartz Score ≥ 1.5 points
- Short QT syndrome (SQTS)

Inherited Cardiomyopathies

Multi-Gene Panel testing for the diagnosis of a hereditary cardiomyopathy is proven and medically necessary in individuals with a confirmed or suspected diagnosis of any of the following conditions:

- Arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C); or
- Dilated cardiomyopathy (DCM), without an identifiable cause, when one of the following criteria are met:
  - Individual has cardiac conduction disease (first-, second- or third- degree block); or
  - Sudden cardiac death in a First- or Second-Degree Relative at age 45 or younger
- Hypertrophic cardiomyopathy (HCM) without an identifiable cause (e.g., valvular disease, hypertension, infiltrative or neuromuscular disorder)

Inherited Thoracic Aortic Disease

Multi-Gene Panel testing is proven and medically necessary for either of the following:

- Individual has confirmed thoracic aortic disease; or
- Thoracic aortic disease is suspected based on family history of thoracic aortic disease in a First- or Second-Degree relative

Testing Based Only On Family History

Multi-Gene Panel testing for the diagnosis of inherited arrhythmic disorders or cardiomyopathy is proven and medically necessary in asymptomatic individuals who have a First-Degree or Second-Degree Relative with one of the following conditions:

- Arrhythmogenic right ventricular dysplasia/cardiomyopathy (ARVD/C); or
- Brugada syndrome (BrS); or
- Catecholaminergic polymorphic ventricular tachycardia (CPVT); or
- Congenital long QT syndrome (LQTS); or
- Familial dilated cardiomyopathy (DCM); or
- Hypertrophic cardiomyopathy (HCM); or
- Short QT syndrome (SQTS); or
- A First-Degree Relative experienced sudden cardiac death or near sudden death at age 45 or younger

Genetic testing for cardiomyopathies, arrhythmias or aortic vascular disease is unproven and not medically necessary for all other indications due to insufficient evidence of efficacy.

Genetic testing for coronary artery disease (CAD) is unproven and not medically necessary due to insufficient evidence of efficacy. This includes, but is not limited to, the following tests:

- Gene expression tests
- Microarray or other genetic profiles for cardiac disease risk (e.g., Cardiac DNA Insight®, Cardiac Healthy Weight DNA Insight®, Cardio IQ® gene tests and panels)

Documentation Requirements

Benefit coverage for health services is determined by the member specific benefit plan document and applicable laws that may require coverage for a specific service. The documentation requirements outlined below are used to assess whether the member meets the clinical criteria for coverage but do not guarantee coverage of the service requested.

CPT Codes*	Required Clinical Information
Genetic Testing for Cardiac Disease	
0237U 81410 81411 81413 81414 81439 81479	Medical notes documenting the following, when applicable: • Personal history of the condition, if applicable, including age at diagnosis • Complete family history (usually three-generation pedigree) relevant to condition being tested • Genetic testing results of family member, if applicable, and reason for testing • Ethnicity/ancestry (e.g., Ashkenazi Jewish), if reason for testing • Any prior genetic testing results • How clinical management will be impacted based on results of genetic testing • Genetic counseling (if available)

*For code descriptions, refer to the Applicable Codes section.

Definitions

First-Degree Relative: First-Degree Relatives include parents, siblings and offspring (National Comprehensive Cancer Network, 2023).

Multi-Gene Panel: Genetic tests that use next-generation sequencing to test multiple genes simultaneously. Also called multiple gene panel (National Cancer Institute Dictionary of Genetics Terms).

Schwartz Score: A set of diagnostic criteria for long QT syndrome (LQTS). The criteria are divided into three main categories with a maximum score of nine. (Schwartz and Crotti, 2011).

Schwartz Score Calculation		
EKG[1]		**Points**
QTc[2]	≥ 480 ms	3
	460 to 479 ms	2
	450 to 459 ms (in males)	1
QTc fourth minute of recovery from exercise stress test ≥ 480 ms		1
Torsades de pointes[3]		2
T wave alternans		1
Notched T wave in 3 leads		1
Low heart rate for age[4]		0.5
Clinical History		**Points**
Syncope[3]	With stress	2
	Without stress	1
Congenital deafness		0.5
Family History		**Points**
Family members with definite LQTS[5]		1.0
Unexplained sudden cardiac death < 30 years in immediate family[5]		0.5
Total Score		

Scoring: ≤ 1.0 point = low probability of LQTS; 1.5-3.0 points = intermediate probability of LQTS; ≥ 3.5 points = high probability of LQTS:

1. In the absence of medications or disorders known to affect these electrocardiographic features.
2. QTc calculated by Bazett's formula where $QTc = QT/\sqrt{RR}$.
3. Mutually exclusive.
4. Resting heart rate < 2nd percentile for age.
5. The same family member cannot be counted for both criteria.

Scoring: ≤ 1.0 point = low probability of LQTS; 1.5-3.0 points = intermediate probability of LQTS; ≥ 3.5 points = high probability.

Second-Degree Relative: Second-Degree Relatives include half-brothers/sisters, aunts/uncles, grandparents, grandchildren and nieces/nephews affected on the same side of the family (National Comprehensive Cancer Network, 2023).

Applicable Codes

The following list(s) of procedure and/or diagnosis codes is provided for reference purposes only and may not be all inclusive. Listing of a code in this policy does not imply that the service described by the code is a covered or non-covered health service. Benefit coverage for health services is determined by the member specific benefit plan document and applicable laws that may require coverage for a specific service. The inclusion of a code does not imply any right to reimbursement or guarantee claim payment. Other Policies and Guidelines may apply.

CPT Code	Description
0237U	Cardiac ion channelopathies (e.g., Brugada syndrome, long QT syndrome, short QT syndrome, catecholaminergic polymorphic ventricular tachycardia), genomic sequence analysis panel including ANK2, CASQ2, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNQ1, RYR2, and SCN5A, including small sequence changes in exonic and intronic regions, deletions, duplications, mobile element insertions, and variants in non-uniquely mappable regions
0401U	Cardiology (coronary heart disease [CAD]), 9 genes (12 variants), targeted variant genotyping, blood, saliva, or buccal swab, algorithm reported as a genetic risk score for a coronary event
81410	Aortic dysfunction or dilation (e.g., Marfan syndrome, Loeys Dietz syndrome, Ehler Danlos syndrome type IV, arterial tortuosity syndrome); genomic sequence analysis panel, must include sequencing of at least 9 genes, including FBN1, TGFBR1, TGFBR2, COL3A1, MYH11, ACTA2, SLC2A10, SMAD3, and MYLK
81411	Aortic dysfunction or dilation (e.g., Marfan syndrome, Loeys Dietz syndrome, Ehler Danlos syndrome type IV, arterial tortuosity syndrome); duplication/deletion analysis panel, must include analyses for TGFBR1, TGFBR2, MYH11, and COL3A1
81413	Cardiac ion channelopathies (e.g., Brugada syndrome, long QT syndrome, short QT syndrome, catecholaminergic polymorphic ventricular tachycardia); genomic sequence analysis panel, must include sequencing of at least 10 genes, including ANK2, CASQ2, CAV3, KCNE1, KCNE2, KCNH2, KCNJ2, KCNQ1, RYR2, and SCN5A
81414	Cardiac ion channelopathies (e.g., Brugada syndrome, long QT syndrome, short QT syndrome, catecholaminergic polymorphic ventricular tachycardia); duplication/deletion gene analysis panel, must include analysis of at least 2 genes, including KCNH2 and KCNQ1
81439	Hereditary cardiomyopathy (e.g., hypertrophic cardiomyopathy, dilated cardiomyopathy, arrhythmogenic right ventricular cardiomyopathy), genomic sequence analysis panel, must include sequencing of at least 5 cardiomyopathy-related genes (e.g., DSG2, MYBPC3, MYH7, PKP2, TTN)
81479	Unlisted molecular pathology procedure
81493	Coronary artery disease, mRNA, gene expression profiling by real-time RT-PCR of 23 genes, utilizing whole peripheral blood, algorithm reported as a risk score

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Description of Services

Technologies used for genetic testing of cardiac syndromes and coronary artery disease can vary. Tests can include, but are not limited to, those that evaluate variations in the genes, such as chromosome microarray analysis (CMA) and next generation sequencing (NGS), as well as others that assess the gene products, such as gene expression arrays and microRNA analysis. The number of genes evaluated can range from a single gene to the whole exome or genome of an individual. Results of genetic testing may assist individuals and healthcare providers with determining a diagnosis, prognosis and identification of appropriate clinical interventions (Jabbari et al., 2013; Millat et al., 2014; Ladapo et al., 2017). This policy addresses genetic test panels or microarray profiles with five or more genes for cardiac related syndromes and other coronary artery disease risk or monitoring. Cardiomyopathies that present primarily as neuromuscular disorders and related genetic testing are covered in the Medical Policy titled Genetic Testing for Neuromuscular Disorders.

Clinical Evidence

Arrhythmias

Congenital Long QT Syndrome (LQTS)

LQTS is a disorder of the heart's electrical system classified as a channelopathy. This disorder affects the cardiac ion channels and predisposes the individual to irregular heartbeats, syncope and possible sudden cardiac death (SCD). Symptoms may occur in young, otherwise healthy individuals and events such as stress or exercise may cause symptoms (Priori et al., 2004). It is characterized by a QT interval prolongation on an electrocardiogram (ECG) and screening is generally performed by electrocardiography. Clinical features and family history may also be helpful in the diagnosis. An ECG finding of a prolonged QTc interval of > 470 msec (males) or > 480 msec (females) is diagnostic (Ackerman et al., 2011). The Schwartz score has been used as a means of establishing diagnostic criteria which focuses on ECG finding and clinical/family history (Alders et al., 2018). Approximately 10-40% of individuals with LQTS will not demonstrate ECG changes (Ackerman et al., 2011). LQTS can be congenital or may be acquired through other heart conditions or exposure to certain medications or dietary deficiencies (Alders et al., 2018).

There are several congenital LQTS. These include Anderson-Tawil syndrome, Jervell and Lange-Nielsen syndrome, Romano-Ward syndrome and Timothy syndrome. All forms of LQTS are estimated to affect at least 1 in 2,500 people (Ackerman et al., 2011). The autosomal dominant Romano-Ward syndrome is the most common; with a prevalence of 1 in 3,000 to 1 in 5,000. Jervell and Lange-Nielsen syndrome is a rare recessive form that is associated with congenital deafness, early clinical manifestations and a poorer prognosis. Congenital LQTS has been associated with mutations in at least 13 genes, many of which are related to the ion channels in the heart. The majority of cases are associated with mutations in three genes: KCNQ1 (30-35%), KCNH2 (25-30%) and SCN5A (5-10%) (Goldenberg and Moss, 2008). As part of the National Heart, Lung and Blood Institute (NHLBI) GO exome sequencing project (ESP) sequence variations of LQTS was reported. In a sample of 5,400 individuals who did not have a diagnosis of heart disease and/or channelopathies (Refsgaard et al., 2012), 33 mutations across the studied genes were identified (all of them being missense variations). There are multiple subtypes that correlate to different genes and some of these genetic subtypes are also associated with non-cardiac abnormalities. For familial testing after a mutation has been identified in an affected family member, other at-risk family members may be identified by testing for the specific mutation and does not require screening a panel of genes (Alders et al., 2018).

Adler et al. (2020) coordinated three, blinded, gene-curation teams to score the level of evidence for 17 genes with strong associations for LQTS. A Clinical Domain Channelopathy Working Group then determined a final classification of the causative LQTS genes after independent assessment by the blinded teams was completed. 3/17 (KCNQ1, KCNH2, SCN5A) were determined to be definitive LQTS genes; 9/17 causative genes (AKAP9, ANK2, CAV3, KCNE1, KCNE2, KCNJ2, KCNJ5, SCN4B, SNTA1) were re-classified as having limited/disputed evidence for being LQTS genes; 4/17 (CALM1, CALM2, CALM3, TRDN) were shown to have strong evidence for atypical LQTS; 1/17 (CACNA1C) demonstrated moderate evidence for LQTS. The evidence in the study revealed that more than 50% of previously reported LQTS causative genes have limited/disputed evidence to support causation. The authors suggested that variants in these genes should not be used for clinical decision-making unless new future genetic evidence is revealed. Furthermore, evidence-based evaluations for disease-causing genes are recommended to ensure appropriate use in precision medicine.

Van Lint et al. (2019) reported on the detection rates for variants of unknown, likely, and certain pathogenicity in cardiac gene panels. 936 arrhythmia panels and 1,970 cardiomyopathy panels were performed. Unknown, likely, and certain variants were detected in 34.8%, 4.2%, and 4.6% of arrhythmia panels, respectively. The cardiomyopathy panel revealed unknown, likely and certain variants in 40.8%, 7.9%, and 12% of patients, respectively. The arrhythmia panel revealed variants in 44% of patients overall, while the cardiomyopathy panels revealed variants in 61% of patients. The authors concluded that “larger gene panels can increase the detection rate of likely pathogenic and pathogenic variants but may increase the frequency of variants of unknown significance.”

Compared with ECG criteria and family history, the positive predictive value of genetic testing for LQTS is 70% to 80% (Modell et al., 2012) and a genetic variant can be identified in approximately 72% to 80% of individuals with a clinical diagnosis of LQTS. However, the clinical criteria for LQTS are neither sensitive nor specific for the syndrome and potential clinical outcomes. Genetic testing may identify more individuals with possible LQTS compared with clinical diagnosis. Hofman et al. (2007) evaluated 513 relatives of 77 LQTS probands who had a known LQTS mutation. Only 41 of 208 carriers were identified with the Schwartz criteria as having a “high probability” of LQTS, which yielded 19% sensitivity for these clinical criteria. The researchers concluded that the use of clinical criteria, while specific, had low sensitivity as compared to genetic testing; and, for families with a known LQTS mutation, genetic testing is the preferred diagnostic approach. Another large study performed by Tester et al. (2006) evaluated the percent of individuals with a clinical diagnosis of LQTS that were found to have a genetic variant. Clinical phenotyping was completed on 541 patients that were referred for evaluation of LQTS and 123 (22.7%) of those had “definite” LQTS defined by clinical criteria. Of the 541 patients, 274 (50.6%) were found to have a LQTS-associated genetic variant and of the 123 clinically diagnosed LQTS patients, 72% (89/123) were found to have a genetic variant. Lieve et al. (2013) examined the diagnostic yield of genetic testing for LQTS in 855 patients. Using NGS, the authors determined that 259 patients had one mutation and 18 patients had two mutations. In comparison with clinical signs, genetic testing had a sensitivity of 72% and a specificity of 49%.

Genetic testing for LQTS to determine prognosis is also performed as different subtypes of LQTS may have varying risks of cardiac events. Several studies have indicated that there are varying rates of cardiovascular events among different subtypes (Priori et al., 2003; Schwartz et al., 2001; Albert et al., 2010; Migdalovich et al., 2011; Costa et al., 2012; Kolder et al., 2015; Amin et al., 2012; Park et al., 2012; Earle et al., 2014; Mullally et al., 2013).

Catecholaminergic Polymorphic Ventricular Tachycardia (CPVT)

CPVT is an inherited channelopathy which can present with either autosomal dominant or autosomal recessive inheritance. CPVT is rare with an estimated prevalence between 1 in 7,000 and 1 in 10,000 persons (Ackerman et al., 2013). This condition typically presents during childhood or adolescence.

The clinical presentation of CPVT is similar to LQTS; however, CPVT is thought to be a more malignant condition. Many patients are asymptomatic before a cardiac event. Individuals with CPVT often present with symptoms such as syncope or cardiac arrest, which are triggered by exercise or stress. Untreated individuals have a mortality rate of 30 to 50 % by age 40 years. ECG studies are usually normal, but exercise stress testing can create arrhythmia in the majority of cases (75-100%) (Napolitano et al., 2022; Perrin and Gollob, 2012). Therefore, evaluation for CPVT includes exercise stress testing, Holter monitoring and genetic screening. The management of individuals with CPVT is usually with beta-blockers or antiarrhythmics if beta-blockers fail to provide complete protection from cardiac events. An ICD may be necessary if there is a recurrence of symptoms. CPVT individuals will also need to commit to lifestyle modification by the avoidance of strenuous exercise.

The autosomal dominant pattern of CPVT is associated with variants in RYR2, CALM1, CALM2, CALM3 or KCNJ2. Variants in CASQ2, TECRL and TRDN are associated with autosomal recessive inheritance. (Napolitano et al., 2022). The majority of cases are represented by RYR2 variants and most of these (90%) are missense mutations (Ackerman et al., 2013). CASQ2 accounts for ~5% and TRDN accounts for < 1% percentage of cases. RYR2 variants have a penetrance of approximately 83%. Approximately 25% of individuals with CPVT have no pathogenic variant identified in any of the known genes mentioned above (Napolitano et al., 2022).

Walsh et al. (2022) conducted an evidence-based reappraisal of genes that have been reported to cause CPVT and short QT syndrome (SQTS). Results related to SQTS are discussed in SQTS section of this policy below. For this evaluation, published evidence for 11 CPVT implicated genes was collected via the ClinGen gene curation framework. An expert panel of 10 individuals with extensive experience in clinical care and/or research related to clinical genetics, CPVT and SQTS performed a comprehensive evaluation and final classification for each gene. Definitive to moderate evidence for disease causation in CPVT was found for seven genes, either with autosomal dominant (RYR2, CALM1, CALM2, CALM3) or autosomal recessive (CASQ2, TRDN, TECRL) inheritance. Four genes for CPVT were disputed; of those, 3 (KCNJ2, PKP2, SCN5A) were determined to be reported for phenotypes that did not represent CPVT and the fourth gene variant (ANK2) was found to be too common in the general population to be causative for disease. This evaluation and reappraisal of the relationships between genes and diseases for CPVT provides evidence-based support regarding which genes may be considered valid, disease-causing genes and therefore included in genetic testing panels. The authors caution that a systematic and evidence-based approach should be performed for assessment of validity for any new gene-disease relationship prior to use in patient care and assert that both genetic and phenotypic data should be subject to careful assessment when exploring any new genetic causes related to CPVT.

In a Clinical Utility Evaluation, Hayes indicated that evidence demonstrating improved health outcomes for individuals who had undergone genetic testing after clinical diagnosis of CPVT was insufficient and recommended additional investigation (Hayes 2018a, updated 2022). For family members of individuals with CPVT, Hayes found probable clinical utility, stating that genetic testing for CPVT can lead to preventative treatment and activity restrictions when family members test positive. The Hayes report also states that genetic testing is most helpful when the familial variant is identified in a clinically diagnosed individual (Hayes 2018b, updated 2022).

Clinical sensitivity has been studied using a three gene CPVT gene card and was estimated to be 50-75% by the manufacturer (Napolitano et al., 2014). The variability in phenotype in ventricular tachycardia syndromes affects the estimated clinical validity and yield of this multi-gene panel. Thus, the specificity of CPVT known pathogenic variants is not certain. A study by the National Heart, Lung and Blood Institute ESP described sequence variations in 6,503 patients without a diagnosis of CPVT (Jabbari et al., 2013). Exome data were reviewed to identify missense variations that are previously associated with CPVT. The researchers identified 11% of the previously described variants in this population resulting in 41 presumed CPVT cases. This study demonstrated that false positive results are likely low (< 0.6%), but the presence of one of these variants may not always translate into the development of CPVT.

Brugada Syndrome (BrS)

BrS is an inherited channelopathy that is described by a characteristic ECG abnormality and an increased risk of syncope, ventricular fibrillation and SCD and is estimated to be responsible for 12% of unexpected SCD cases (Abriel et al., 2013). In an individual with BrS, the heart remains structurally normal. This disorder often presents in adulthood; however, it has been reported at all ages (Huang et al., 2004) and is more common in males than females (8:1 ratio). There is a high clinical suspicion of BrS when the characteristic ECG pattern is present with at least one of the following clinical features: documented ventricular arrhythmia, SCD in a family member < 45 years old, characteristic ECG pattern in a family member, inducible ventricular arrhythmias on EP studies, syncope or nocturnal agonal respirations. In general, management of BrS focuses on ICDs and medication in individuals with syncope or cardiac events. Those who have BrS and are asymptomatic are followed closely.

BrS is usually inherited in an autosomal dominant pattern and has incomplete penetrance. Genetic abnormalities causing BrS have been linked to mutations in 16 different genes; however, 15-30% of cases are associated with the ion channel gene SCN5A (Ackerman et al., 2013). Other genes including SCN10A are minor significance and only account for 5% of cases (Bennett et al., 2013). In individuals with a high clinical suspicion of BrS, testing yields variants in only 25-35% of cases (Brugada et al., 2016). Even though there are eight suspected genes, SCN5A is most commonly identified and identified in 20% of genotype positive cases.

A Hayes Clinical Utility Evaluation suggests insufficient evidence exists to support the use of genetic testing for individuals who have been clinically diagnosed with Brugada syndrome, as no existing studies were found that would indicate improved health outcomes for the affected individual related to such testing (Hayes 2018c, updated 2022). Limited evidence supported the use of genetic testing in family members of individuals with Brugada syndrome (Hayes 2018d, updated 2022).

A Japanese registry trial studied the *SCN5A* variant genotype/phenotype with symptoms of BrS (Yamagata et al., 2017). The researchers studied 415 patients who were previously diagnosed with BrS and evaluated them for *SCN5A* mutations. Those with pathogenic mutations were compared to those without over a period of 72 months. They determined that those individuals with BrS and a *SCN5A* pathogenic variant had significantly more ECG abnormalities and an increased risk for cardiac events.

Behr et al. (2015) evaluated seven candidate genes (SCN10A, HAND1, PLN, CASQ2, TKT, TBX3 and TBX5) among patients negative for SCN5A variants (n = 156) with symptoms indicative of BrS (64%) and/or a family history of sudden death (47%) or BrS (18%). Eighteen patients (11.5%) were found to have variants, most often in SCN10A (12/18; 67%). A study by Hu et al. (2014) analyzed the prevalence of SCN10A variants in 150 probands for BrS. Seventeen SCN10A variants were identified in 25 probands, with a variant detection rate of 16.7% in BrS probands. This study identified SCN10A variant as a major susceptibility gene for BrS. Another genome-wide association study by Bezzina et al. (2013) evaluated 312 individuals with BrS and found two significant variants were identified, one at the SCN10A locus (rs10428132) and another near the HEY2 gene (rs9388451). These findings suggest that there may be more variants associated with BrS.

Short QT Syndrome (SQTS)

SQTS is a rare genetic condition that is characterized by a shortened QT interval on ECG, reflecting a shortened action potential of the heart. This results in an increased risk of ventricular and atrial fibrillation as well as SCD. As approximately only 100 cases of SQTS have been identified, the prevalence and risk of SCD remains unknown (Bennett et al., 2013). The symptomology can range from no clinical symptoms to dizziness and fainting or may include cardiac arrest and SCD. Treatment for SCD includes ICD regardless of diagnosis. While it is unclear if testing results will change management or improve health outcomes, the rarity of SQTS limits the ability to conduct prospective trials to comprehensively evaluate the clinical validity and utility of genetic testing.

Walsh et al. (2022) conducted an evidence-based reappraisal of genes that have been reported to cause CPVT and SQTS. Results related to CPVT are discussed in CPVT section of this policy above. Published evidence for 9 SQTS implicated genes was collected and evaluated by a panel of experts in clinical genetics, CPVT and SQTS. The expert team performed final evaluation and classification of each gene. For SQTS, only one gene (KCNH2) could be classified as definitive. Three other genes (KCNQ1, KCNJ2, SLC4A3) had strong to moderate evidence. Although CACNA1C, CACNB2, and CACNA2D1 are included in most commercial SQTS panels, rare variants in these genes are likely be interpreted as variants of unknown significance (VUS) and would not increase yield of panel but would contribute to increased turnaround time and/or lead to anxiety or uncertainty because of VUS outcome. Notably, most of the evidence for SQTS genes came from very few variants (a total of 5 in KCNJ2, 2 in KCNH2 and 1 in KCNQ1/SLC4A3). This reevaluation of gene-disease relationships for SQTS provides an evidence-based analysis of genes to be considered as valid disease genes and included in multi-gene panels. The researchers recommend that a systematic, evidence-based approach be used to evaluate and assess validity of any reported or new gene-disease relationship before use in clinical care and that both phenotype and genetic data must be carefully reviewed and evaluated when assessing potential genetic cause of SQTS.

Inherited Atrial Fibrillation

Inherited atrial fibrillation (AF) is an abnormality of the heart's rhythm where there are episodes of uncoordinated electrical activity (fibrillation) in the upper chambers causing an irregular, fast heartbeat. Symptoms from genetic-based disease is generally indistinguishable from AF caused by non-genetic reasons. This familial type of AF has an unknown incidence (MedLinePlus, 2017a). There are some genes that have been of focus; however, there has not been sufficient evidence to show that genetic testing improves outcomes.

To investigate the results of genetic testing for early onset AF, Yoneda et al. (2021) conducted a prospective, observational cohort study including 1293 participants. The study participants were enrolled from an academic medical center from November 1999 through June 2015. Each participant had been diagnosed with AF prior to 66 years of age and underwent whole genome sequencing with evaluation of 145 genes commonly included on commercially available cardiomyopathy and arrythmia panels. Sequencing data were evaluated using automation followed by manual review performed by a panel of independent, blinded reviewers. Primary outcome was the classification of rare variants via the American College of Medical Genetics and Genomics criteria including benign, likely benign, VUS, likely pathogenic or pathogenic. The study defined disease-associated variants as pathogenic or likely pathogenic variants in genes associated with autosomal dominant or X-linked dominant disorders. Of the 1293 participants, 10.1% (131) were found to have a disease-associated variant identified by genetic testing performed and 62.8% (812) were found to have a VUS. Heterozygous carriers for autosomal recessive disorders made up 7.1% (92) of the study population and 20% (258) had no suspicious variants reported. Participants diagnosed with AF prior to the age of 30 were most likely to have a disease-associated variant and those diagnosed after the age of 60 were least likely to have a disease-associated variant. Of note, disease-associated variants were more likely to be associated with inherited cardiomyopathy syndromes than inherited arrhythmias. The authors assert that these results support use of genetic testing in the case of early-onset AF. Study limitations included disagreement on ACMG classification for given variants and limited evidence on many of the genes that are typically included on commercial panels for specific cardiac phenotypes. In addition, this study population came from a single center and was primarily made up of people of European ancestry so is not representative of all ethnicities.

Roselli et al. (2018) collaborated with global researchers to study the genetic basis of AF. The researchers compiled data from over 65,000 individuals with AF and identified several new genetic risk factors. Of the nearly 100 genetic regions associated with risk of developing AF, 67 were never before linked to the disease. The study demonstrated that there are methods for genetic testing for AF; however, there will need to be further study to determine the specific genes involved and the role for genetic testing in clinical management.

Clinical Practice Guidelines

American College of Cardiology (ACC)/American Heart Association (AHA)/ Heart Rhythm Society (HRS)

ACC, AHA and HRS guidelines for the management of patients with AF (January et al., 2014) state that routine genetic testing related to AF is not indicated. Individuals with AF and multi-generational family members with AF should be referred for genetic counseling and consideration of specific testing. A 2019 focused update did not address genetic testing (January et al., 2019).

ACC, AHA and HRS published guidelines for management of patients with ventricular arrhythmias and the prevention of SCD (Al-Khatib et al., 2018) which recommended the following general guidelines related to genetic testing:

- The availability of genetic testing for inherited arrhythmia syndromes can provide opportunity to confirm a suspected diagnosis for the proband and offer cascade screening of potentially affected family members when a disease-causing mutation is identified in the proband.

- Genotyping is frequently most useful when a pathogenic mutation is identified in the proband, such that screening can be applied to relatives who are in a preclinical phase, allowing institution of lifestyle changes, therapy, or ongoing monitoring for those who are gene mutation positive.
- In young patients (< 40) without structural heart disease who have unexplained cardiac arrest, unexplained near drowning, or recurrent exertional syncope, genetic testing may be important to identify an inherited arrhythmia syndrome as a likely cause.

European Heart Rhythm Association (EHRA)/Heart Rhythm Society (HRS)/Asia Pacific Heart Rhythm Society (APHRS)/Latin American Heart Rhythm Society (LAHRS)

In an Expert Consensus Statement on genetic testing for cardiac disease, the EHRA, HRS, APHRS and LAHRS (Wilde et al., 2022). provide the following recommendations for genetic testing in arrythmias:

LQTS

- Molecular genetic testing for definitive disease associated genes (currently KCNQ1, KCNH2, SCN5A, CALM1, CALM2, and CALM3) should be offered to all index patients with a high probability diagnosis of LQTS, based on examination of the patient's clinical history, family history, and ECG characteristics obtained at baseline, during ECG Holter recording and exercise stress test (Schwartz Score > or = 3.5).
- Analysis of specific genes should be offered to patients with a specific diagnosis as follows:
  - KCNQ1 and KCNE1 in patients with Jervell and Lange-Nielsen syndrome.
  - CACNA1C in Timothy syndrome.
  - KCNJ2 in Andersen–Tawil syndrome.
  - TRDN in patients suspected to have triadin knockout syndrome.
- An analysis of CACNA1C and KCNE1 may be performed in all index patients in whom a cardiologist has established a diagnosis of LQTS with a high probability, based on examination of the patient's clinical history, family history, and ECG characteristics obtained at baseline, during ECG Holter recording and exercise stress test (Schwartz Score > or = 3.5).
- Variant-specific genetic testing is recommended for family members and appropriate relatives following the identification of the disease-causing variant.
- Predictive genetic testing in related children is recommended from birth onward (any age).

CPVT

- In any patient satisfying the diagnostic criteria for CPVT (such as Class 1 clinical diagnosis or CPVT diagnostic score > 3.5$_b$), molecular genetic testing is recommended for the currently established definite/strong evidence CPVT-susceptibility genes: RYR2, CASQ2, CALM1-3, TRDN, and TECRL.
- In phenotype-positive CPVT patients who are negative for those established CPVT-susceptibility genes, genetic testing may be considered for CPVT phenocopies resulting from pathogenic variants in the KCNJ2, SCN5A, and PKP2 genes.
- In patients with a modest phenotype for CPVT (i.e., CPVT diagnostic score > or = 2 but < 3.5b), genetic testing may be considered for the established definite/strong evidence CPVT-susceptibility genes: RYR2, CASQ2, CALM1-3, TRDN, and TECRL.
- Variant-specific genetic testing is recommended for family members and appropriate relatives following the identification of the disease-causative variant.
- Predictive genetic testing in related children at risk of inheriting a pathogenic (L)/likely pathogenic (LP) variant is recommended from birth onward (any age).

BrS

- Genetic testing with sequencing of *SCN5A* is recommended for an index case diagnosed with BrS with a type I ECG in standard or high precordial leads occurring either (i) spontaneously, or (ii) induced by sodium-channel blockade in presence of supporting clinical features or family history.
- Rare variants in genes with a disputed or refuted gene-disease clinical validity should not be reported routinely for BrS genetic testing in a diagnostic setting.
- Targeted sequencing of variant(s) of unknown significance in *SCN5A* with a population allele frequency < 1 X 10^{-5} identified in an index case can be considered concurrently with phenotyping for family members, following genetic counselling, to assess variant pathogenicity through co-segregation analysis.
- Variant-specific genetic testing is recommended for family members and appropriate relatives following the identification of the disease-causative variant.

- Predictive genetic testing (of pathogenic *SCN5A* variants) in related children is recommended from birth onward (any age).

SQTS

- In any patient satisfying the diagnostic criteria for SQTS (such as Class 1 clinical diagnosis or SQTS diagnostic score > 4), molecular genetic testing is recommended for the definitive disease associated genes (currently KCNH2, KCNQ1).
- Testing of KCNJ2 and SLC4A3 may be performed in all index patients in whom a cardiologist has established with a high probability a diagnosis of SQTS, based on examination of the patient's clinical history, family history, and ECG characteristics obtained at baseline or during ECG Holter recording and exercise stress test (SQTS diagnostic score > or = 4).
- Variant-specific genetic testing is recommended for family members and appropriate relatives following the identification of the disease-causative variant.
- Predictive genetic testing in related children may be considered in specific settings.

Inherited AF

- An analysis of SCN5A, KCNQ1, MYL4 and truncating TTN variants may be performed in all index patients in whom the diagnosis of familial (young = age < 60) AF, is established, based on examination of the patient's clinical history, family history, and ECG characteristics.
- Variant-specific genetic testing may be recommended for family members and appropriate relatives following the identification of the disease-causative variant.
- Predictive genetic testing in related children may be considered in specific settings.

Nielsen et. al (2020) published an expert consensus on behalf of the EHRA, HRS, APHRS and LAHRS addressing risk assessment in cardiac arrythmias. This consensus recommends consideration of genetic testing for inherited arrhythmic disease associated with increased risk of ventricular arrhythmia and SCD and notes that clinically applicable genetic testing is intended to be driven by phenotype. Pre-test probability of specific diagnosis is the determinant for utility of the genetic evaluation. Because of incomplete penetrance of genetic arrythmia syndromes, identification of a genetic variant with known pathogenicity is rarely, if ever, enough to meet diagnostic criteria for a given syndrome. Genetic testing can prove useful for family members of a genotype identified proband but is not recommended without the presence of a diagnostic ECG. In addition, the document notes that searching for common genetic variants associated with AF risk has not been found to be useful in the clinical setting and further studies are required to assess whether genetic information improves ability to predict AF in conjunction with clinical variables.

Cardiomyopathies

Hypertrophic Cardiomyopathy (HCM)

HCM is the most common genetic cardiovascular condition and is associated with thickening of the heart wall surrounding the left ventricle (also called left ventricular hypertrophy or LVH) (Bos et al., 2009; Cirino and Ho, 2021). Clinical diagnosis can be demonstrated by a non-dilated left ventricle with a wall thickness of 13-15mm or more in adults (McKenna et al., 1997; Maron et al., 2003; Cirino and Ho, 2021). LVH can be determined by echocardiogram or magnetic resonance imaging (MRI). There are also other conditions that can lead to LVH and must be ruled out to diagnose HCM (Cirino and Ho, 2021). HCM has a phenotypic prevalence of approximately 1 in 500 adults (0.2%) and is the most common cause of SCD in young adults, including athletes (Ramaraj, 2008; Alcalai et al., 2008). Overall, the death rate for HCM patients is estimated to be 1% per year in the adult population (Marian, 2008; Roberts and Sigwart, 2005).

Symptoms range from asymptomatic to heart failure to SCD (Bos et al., 2009; Cirino and Ho, 2021). Even in family members that present with the same variant, and symptoms may be different due to variations in the environment or the influence of other genes. It is thought that the majority of HCM patients are asymptomatic or have few symptoms. However, some patients have significant symptoms that may lead to heart failure or SCD (Maron et al., 2003). Patient management includes treating any cardiac comorbidities, avoiding therapies that may worsen obstructive symptoms and treating symptoms with medications and surgery.

In a 2022 systematic review and meta-analysis, Cirino et al. summarized data regarding the use of genetic counseling and testing for individuals with HCM and their at-risk family members and the impact of counseling and testing on patient reported outcomes (PROs). A total of 48 studies (47 observational, 1 randomized) were included. The uptake of genetic testing in probands was 57% (95% confidence interval [CI]: 40, 73) and the uptake of cascade testing for family members with risk was

61% (95% CI: 45, 75) for genetic testing, 58% for cardiac screening (e.g. echocardiography) (95% CI: 40, 73), and 69% for either/both approaches (95% CI: 43, 87). Family members of probands with positive results were substantially more likely to proceed with cascade screening in comparison to family members of probands whose results were negative (odds ratio = 3.17, 95% CI: 2.12, 4.76). The range of uptake of genetic counseling for both probands and their family members ranged from 37% to 84%. Several studies found the difference in PROs between those individuals receiving positive versus negative results was minimal, but some studies showed worse psychological outcomes in participants that had positive test results. Genetic counseling was related to high levels of satisfaction, an increase in perceived personal control and sense of empowerment and a decrease in anxiety. The authors concluded that PROs after genetic testing varied, but genetic counseling showed an association with high satisfaction and increased PROs. They encourage study around the decision-making process for probands, new methods for promotion of cascade screening, factors impacting psychological outcomes after genetic testing and counseling and collaboration among cardiovascular genetic teams to ensure systematic assembly of outcomes with consistent variable definition and standardized reporting.

Christian et al. (2022) published the results of a systematic review and meta-analysis summarizing the diagnostic validity and clinical utility of genetic testing for individuals diagnosed with HCM and their relatives who may be at risk. In all, 132 articles from inception through March 2020 (span of 25 years in total) met inclusion criteria for the study. Of these, 80 reported on detection rate, 44 described genotype-phenotype associations and 51 addressed penetrance estimates. Sensitivity analyses and subgroup were prespecified for individual sarcomere genes, pediatric and adult cohorts, family history, inclusion of probands, presence/absence of pathogenic variants and variant classification method. The review found significantly higher detection rate of pathogenic variants in pediatric cohorts than in adult cohorts (56% vs 42%; $p = 0.01$) and in adults with a family history compared with sporadic cases (59% vs 33%; $p = 0.005$). In studies using current, improved variation interpretation standards, detection rate decreased significantly from 42% to 33% ($p = 0.0001$) since fewer variants met the criteria to be considered pathogenic. Age of onset in adults differed significantly for genotype-positive vs genotype-negative cohorts (mean difference 8.3 years; $p < 0.0001$). *MYH7* vs *MYBPC2* cohorts and individuals with multiple variants also had a significant difference in age of onset (8.2 years; $p < 0.0001$ and 7.0 years; $p < 0.0002$, respectively). Disease penetrance in adult cohorts was 62% overall, but significant differences were seen based on whether probands were included or excluded (73% vs 55%; $p = 0.003$). This analysis collectively quantified historical understandings of rate of detection, disease penetrance and genotype-phenotype associations for HCM and confirmed some previously established trends and associations, serving as to bridge to further understanding of the clinical utility of genetic testing for HCM. The authors point out the variabilities in study design and outcome reporting that limited the analysis but stress the importance of the large volume of data analyzed that will help provide answers regarding detection rates and genotype-phenotype correlations. Key areas for further study include expansion of genotype-phenotype associations and disease penetration estimates across varying populations. Authors Mazzarotto (2019), Restrepo-Cordova (2017), Murphy (2016), Rubattu (2016), Alfares (2015), Loar (2015), Gruner (2013), Ingles (2013), Zou (2013), Michels (2009), Olivotto (2008), Richard (2003), Van Driest (2003), Niimura (1998), Charron (1997), and Watkins (1995), which were previously cited in this policy, are included in the Christian (2022) systematic review.

Hathaway et al. (2021) studied the diagnostic yield of genetic testing in persons with a suspected diagnosis of HCM who were referred for testing to multiple, world-wide centers. The authors performed a retrospective review of these patients who had testing performed by Blueprint Genetics. Variants categorized as P/LP were determined to be diagnostic. 369/1,376 samples (26.8%) were diagnostic; 373 P or LP variants were reported. Sarcomeric genes (85%) comprised the majority of diagnostic variants; 4.3% of diagnostic variants were reported in RASopathy genes; cardiomyopathy genes other than HCM/arrhythmia were identified in 2%. An increased likelihood of identifying a diagnostic variant was associated with earlier age of diagnosis ($p < 0.0001$), a higher maximum wall thickness ($p < 0.0001$), a positive family history ($p < 0.0001$), absence of hypertension ($p = 0.0002$), and the presence of an ICD ($p = 0.0004$). While the reported diagnostic yield was lower in this cohort compared to other patient cohorts, the authors concluded that the spectrum of genes implicated illustrates the necessity of pre-and post-test counseling when performing genetic testing to a broad-based HCM population.

The genetic component of HCM includes a defect in the cardiac sarcomere, which is the basic contractile unit of cardiac myocytes (Keren et al., 2008). While other non-sarcomeric genes have been assessed, Walsh et al. (2010) determined that the majority of these genes were not associated with the condition. Multiple genes and individual mutations have been identified as genetic components of HCM (Maron et al., 2012; Cirino and Ho, 2021; Ghosh and Haddad, 2011). Pathogenic variants in *MYH7* and *MYBPC3* account for approximately 80% of all cases for which a molecular diagnosis is determined (Teekakirikul et al., 2013). Generally, these defects are inherited in an autosomal dominant pattern. In approximately 60% of patients with clinical HCM, a genetic abnormality can be identified (Elliott and McKenna, 2004). The researchers also determined that the number of mutations correlated with severity of disease. The screening of at-risk family members is an important consideration in the management of HCM. Many guidelines recommend this screening with physical examination, ECG and echocardiography (Maron et al., 2012).

A pediatric study sought to add to the literature more information on the genotype-phenotype association in pediatric patients with HCM (Ellepola et al., 2018). The researchers performed a retrospective review of 70 individuals with HCM who had a mean age at presentation of 5.48 years. Genetic testing was positive in 54/70 patients (77%). Of the 23 patients with a positive family history, 13 had mutations (57%).

Manrai et al. (2016) evaluated publicly available data and identified variants that had previously been considered causal for HCM that were overrepresented in the general population. The researchers found that a number of patients, all of African or unspecified ethnicity, had variants that were misclassified as pathogenic based on the understanding at the time. However, all of these variants were now categorized as benign. Furthermore, these reclassified variants were more common among black Americans than white Americans. This study that was funded by the National Institutes of Health concluded that there is a need to sequence genomes of varying populations to determine the pathogenicity of a variant.

A study in 2016 used whole exome sequencing (WES) for HCM genes (Nomura et al.). This study evaluated seven relatives from a family with inherited HCM. Five relatives were clinically affected. The WES detected 60,020 rare variants in this group and of those, 3,439 were missense, nonsense, splice-site or frameshift variants. After analysis was completed linking the genotype-phenotype, 13 pathogenic variants remained. In addition, one variant in MYL3 was shared with the five affected relatives. A larger cohort study by Gómez et al. (2014), used next generation sequencing NGS in 136 patients with HCM. First, the researchers amplified the exons of MYH7, MYBPC3, TNNT2, TNNI3, ACTC1, TNNC1, MYL2, MYL3 and TPM1 and then performed NGS. In the validation cohort of 60 patients, Sanger sequencing was performed for nine genes as well as NGS. The NGS method was found to have a specificity of 97% for single nucleotide variants, sensitivity of 100% and specificity of 80% for insertion/deletion variants compared with Sanger sequencing. Next, 76 cases in a discovery cohort were analyzed. A total of 19 mutations were discovered in this cohort, which led the researchers to conclude that NGS is valuable in screening large cohorts of HCM patients.

The analytic sensitivity for HCM mutation detection has been demonstrated to be high regardless of technology used, either Sanger sequencing or NGS. The available information on specificity of genetic testing for HCM, mainly from series of patients without a personal or family history of HCM, suggests that false-positive results for known pathologic mutations using Sanger sequencing are uncommon. A study by Oliveira et al. (2015) compared HCM variant detection by NGS with Sanger sequencing. The researchers found a maximum 96.7% sensitivity for single-nucleotide variants and a positive predictive value above 95% for the NGS panels. NGS may have a higher yield of VUS, which may impact the positive and negative predictive value of the test.

Arrhythmogenic Cardiomyopathy (ACM)

ACM is a cardiac condition that is characterized by progressive fibro-fatty replacement of the myocardium. This creates the risk of ventricular dysfunction and arrythmias. The structural alterations present with ACM can impact left, right or both ventricles leading to three recognized phenotypes: the most common, dominant-right (arrhythmogenic right ventricular cardiomyopathy (ARVC), the biventricular variant (BivACM), and the dominant-left (arrhythmogenic left ventricular cardiomyopathy (ALVC). Identification of a LP/P variant is a major diagnostic criterion for each of these types and can actually be a requirement for diagnosis of the ALVC variant (Wilde et. al, 2022).

Diagnostic criteria for arrhythmogenic right ventricular cardiomyopathy/dysplasia ARVC/D were established by an international task force (ITF) in 1994 and modified in 2010 (McKenna et al.,1994; Marcus et al., 2010). Often a patient will present with an arrhythmia. The ITF criteria combine results of ECG and signal averaged ECGs, imaging studies that include 2D echocardiography, cardiac MRI or RV angiography, and arrhythmia presence documented by telemetric monitoring, genetic testing and family history to determine if criteria are met for a diagnosis. The management of individuals with ARVC/D is complicated. Most affected individuals can live a normal lifestyle; however, some must avoid activity that will strain the right side of the heart. Some individuals with a higher risk of cardiac events or SDS are treated with anti-arrhythmic medications or may be considered for an ICD.

ARVC/D prevalence is thought to be 1 case per 10,000 and an autosomal dominant inheritance pattern has been demonstrated. However, there is variable penetrance and around half of the cases are new mutations and do not have a family history of disease. There are several genes that are more commonly associated with ARVC/D and include: DSC2, DSG2, DSP, JUP, PKP2 and TMEM43. Other genes that have been implicated include: CTNNA3, DES, LMNA, PLN, RYR2, TGFB3 and TTN

(McNally et al., 2017). Even with this genetic knowledge, a high number of cases have been reported with no known genetic loci (50%) (Corrado et al., 2000).

Bariani et al. (2022) published findings from a systematic review evaluating the understanding of the genetic background and clinical features of ALVC. Overall, 31 studies were included in the review. The DSP gene had the highest representation in the literature and was the gene in focus for about half of the published studies. FLNC had the second-highest representation in the literature. Abnormalities in ECG results was reported in 58% of individuals. In 26% of included cases, major ventricular arrhythmias were found and an ICD was implanted in 29%. Heart failure symptoms were seen in 6% of individuals and 15% of the individuals had myocarditis-like episodes. In addition, assessment of the reported clinical features of individuals with ALVC indicated electrical instability that often led to implantation of an ICD.

Deshpande et al. (2016) reviewed 16 pediatric cases of ARVC/D that were diagnosed through modified diagnostic criteria, genetic testing and pathology. Only two patients had a previously described gene mutation, and another patient had a novel mutation. For pediatric cases, the authors note that pathology and clinical findings alone may be sufficient for diagnosis.

A study by te Riele et al. (2016) aimed to determine the predictors of ARVC/D and optimize risk stratification for at-risk family members. Data from 274 first-degree relatives of 138 ARVC/D probands was analyzed. Of the 274 relatives, 96 (35%) were diagnosed with ARVC/D by using the ITF criteria. Siblings had a three-fold increased risk compared to parents and children. Similarly, Sen-Chowdhry et al. (2007) noted that while genetic studies have provided information in regarding the role of genetics in ARVC/D, there is not enough insight into genotyping yet. These researchers state that the key clinical application of genetic testing in ARVC/D is for confirmatory testing of index cases to facilitate interpretation of borderline investigations and cascade screening of families.

Familial Dilated Cardiomyopathy (DCM)

DCM occurs when the cardiac muscle becomes thin and weakened resulting in an enlarged heart (MedLinePlus, 2017b). Symptoms of DCM may include arrhythmia, shortness of breath, fatigue, swelling of the legs and feet, syncope and an increased risk of SCD. DCM is a leading cause of heart transplantation (Mestroni and Taylor, 2013). For many years, the cause of DCM was unknown, possibly viral or autoimmune. However, some cases are hereditary (30-50%) (Mestroni and Taylor, 2013). Familial DCM may be inherited as an X-linked, autosomal recessive, or autosomal dominant condition. Genetic testing identifies a mutation in 22–50% of cases (Roncarati et al., 2013). Over 30 gene mutations have been identified, including mutations in *DES, LMNA* and *SCN5A*. Mutations in one gene, *TTN*, account for approximately 20% of familial DCM cases (Begay et al., 2015).

In a 2022 systematic review, Peters et al. focused on a review of phenotypes, functional effects, natural history and treatment outcomes of DCM-associated rare variants specific to the *SCN5A* gene. The researchers identified 18 *SCN5A* rare variants in 173 affected individuals from 29 families. Eleven of the variants had undergone evaluation and 7 of these had a consistent phenotype that was characterized by frequent multifocal narrow and broad complex ventricular premature beats (VPB; 72% of affected relatives), atrial arrhythmias (32%), ventricular arrhythmias (33%), DCM (56%) and SCD (13%). The VPD variant was not seen either with variants that increased late sodium current or with variants that reduced peak current density/had mixed effects. In the absence of arrhythmias, DCM did not occur for any variant. Of note, 12 studies with a total of 23 patients reported success with the use of sodium channel-blockers for the VPB-predominant cardiomyopathy. The authors concluded that *SCN5A* can present with varied primary arrhythmic features, with the majority of DCM-associated variants causing a multifocal VPD-predominant cardiomyopathy (reversible with sodium channel-blocking therapy). They assert that early recognition of the distinctive phenotype associated with this variant and associated genetic testing is very important for management of *SCN5A* variants in DCM patients.

Rangaraju and Dalal (2021) laid out the following genetic testing recommendations for cardiomyopathies and channelopathies and broadly summarized genetic testing recommendations from the ACGM, ACC and EHRA as follows:

- Genetic testing is recommended as a Class I indication in probands with a confirmed diagnosis of cardiomyopathies and channelopathies.
- Genetic testing is recommended in at-risk family members of the proband.
- Testing is recommended in presymptomatic individuals with a strong family history of cardiac disorders.

- Genetic testing is recommended even in diagnosed patients with no family history of inherited cardiac disease or sudden death, as this may reflect incomplete information of family history and screening, incomplete penetrance, or a de novo mutation in the proband.

Mazzarotto et al. (2020) studied the largest genetically characterized cohort of DCM patients to-date to determine the frequency of rare variation in 2,538 DCM patients for 56 commonly tested genes. In order to increase accuracy and reduce uncertainty for DCM clinical genetic testing, the authors also sought to provide evidence for curation efforts for the ClinGen initiative to validate DCM disease genes and to validate gene/variant classes. The results compared 912 confirmed healthy controls and a reference population of 60,706 to identify clinically interpretable genes that are definitively associated with dominant monogenic DCM. Using the TruSight Cardio sequencing panel, 12 strong-association genes were identified. Truncating variants in TTN and DSP were associated with DCM in all comparisons; MYH7, LMNA, BAG3,TNNT2, TNNC1, PLN, ACTC1, NEXN, TPM1, and VCL were significantly enriched in certain patient subsets; TPM1 and VCL contributed primarily to early-onset forms of DCM. The authors stated that burden of rare variation comparison showed that most genes associated with DCM do not have a significant enrichment or rare variants in cases making them unlikely to be causative. They should, therefore, be evaluated further to determine their clinical validity for DCM. The authors also stated that they were able to evaluate the basis of DCM genetics and revealed variants that were particularly associated with early onset disease.

Predictive genetic testing is described as appropriate for an asymptomatic at-risk individual with a first- or second-degree blood relative in whom a mutation has been identified. This testing can aid in planning for appropriate surveillance including diagnostics like lab testing and ECGs. Early treatment is not indicated for individual with a pathogenic mutation; however, close monitoring would be appropriate. In patients with lamin A/C gene mutations (LMNA), ICD placement may be indicated (Meune et al., 2006). McNally and Mestroni (2017) provided two options for genetic testing including cascade screening and clinical genetic testing. Cascade testing is recommended for first-degree relatives of probands. The authors suggest that this first line of screening in cascade should be ECG and echocardiography. Genetic testing is recommended in patients with familial DCM when there is a specific mutation to be tested.

Familial screening can identify DCM patients at an earlier stage of disease. Moretti et al. (2010) aimed to compare long-term prognosis of familial DCM and sporadic forms. The study enrolled 637 DCM patients and of these 130 had familial DCM. This group of patients included 82 proband and 48 non-proband familial patients. The researchers then compared the 48 non-proband patients with a cohort of sporadic DCM patients. They determined that the non-proband patients were younger, less symptomatic, had a higher left ventricular ejection fraction and were less intensively treated with drugs than the sporadic DCM group. The study concluded that family screening should be recommended for all DCM patients.

Clinical Practice Guidelines

American College of Cardiology (ACC)/American Heart Association (AHA)

The 2020 AHA/ACC Guideline for HCM published the following key perspectives regarding genetic testing (Ommen et al., 2020):

- Genetic testing should be offered to individuals with HCM. For individuals with variants of unknown significance, serial re-evaluation of test results is recommended to assess variant reclassification. The usefulness of clinical genetic testing of phenotype-negative relatives for the purpose of variant reclassification is uncertain. If a proband has a pathogenic or likely pathogenic variant on genetic testing, cascade genetic testing should be offered.
- When individuals with HCM have undergone genetic testing and were found to have no pathogenic variants (i.e., harbor only benign/likely benign variants), cascade genetic testing of the family is not useful.

American College of Cardiology (ACC)/American Heart Association (AHA)/Heart Failure Society of America (HFSA)

The 2022, the AHA/ACC/HFSA (Heidenreich et al.) published updated heart failure guidelines which advise that genetic screening and counseling is recommended to detect cardiac disease and prompt consideration of treatments to decrease HF progression and sudden death in first degree relatives of select individuals with genetic or inherited cardiomyopathies.

American Heart Association (AHA)

The AHA Council on Genomic and Precision Medicine; Council on Arteriosclerosis, Thrombosis and Vascular Biology; Council on Cardiovascular and Stroke Nursing; Council on Clinical Cardiology (Musunuru et al., 2020) published a scientific statement recommending that:

- Genetic testing should be reserved for patients with a confirmed or suspected diagnosis of an inherited cardiovascular disease, or for persons at high a priori risk resulting from a previously identified familial pathogenic variant.
- Disease-appropriate phenotyping with a three generation family history should be performed.
- If genetic testing is performed, the clinician should choose the appropriate testing which ranges from targeted sequencing of a single or few genes, to large panels that include limited evidence genes, to unbiased exome or genome sequencing.

European Heart Rhythm Association (EHRA)/Heart Rhythm Society (HRS)/Asia Pacific Heart Rhythm Society (APHRS)/Latin American Heart Rhythm Society (LAHRS)

In an Expert Consensus Statement on genetic testing for cardiac disease, the EHRA, HRS, APHRS and LAHRS (Wilde et al., 2022). provide the following recommendations for genetic testing in cardiomyopathies:

HCM

- For genetic testing in a proband with HCM (including those cases diagnosed post-mortem), the initial tier of genes tested should include genes with definitive or strong evidence of pathogenicity (currently MYH7, MYBPC3, TNNI3, TPM1, MYL2, MYL3, ACTC1, and TNNT2).
- For genetic testing in a proband with HCM, the initial tier of genes tested may include genes with moderate evidence of pathogenicity (CSRP3, TNNC1, JPH2).
- In patients with HCM, genetic testing is recommended for identification of family members at risk of developing HCM.
- In patients with atypical clinical presentation of HCM, or when another genetic condition associated with unexplained hypertrophy is suspected (e.g., HCM phenocopy) genetic testing is recommended.
- Predictive genetic testing in related children is recommended in those aged > 10–12 years.
- In patients with HCM who harbor a variant of uncertain significance, the usefulness of genetic testing of phenotype-negative relatives for the purpose of variant reclassification is uncertain.
- Predictive genetic testing in related children aged below 10–12 years may be considered, especially where there is a family history of early-onset disease.
- In patients with HCM who harbor a variant of uncertain significance, testing of affected family members for the purpose of variant classification may be considered.
- For patients with HCM in whom genetic testing found no LP/P variants, cascade genetic testing of family relatives is not recommended.
- Ongoing clinical screening is not recommended in genotype-negative relatives in most families with genotype-positive HCM.

ACM

- Comprehensive genetic testing is recommended for all patients with consistent phenotypic features of ACM, including those cases diagnosed post-mortem, whatever familial context.
- Genetic testing of first tier definitive disease-associated genes (currently PKP2, DSP, DSG2, DSC2, JUP, TMEM43, PLN, FLNC, DES, LMNA) is recommended.
- Owing to the possibility of complex genotypes, in families with multiple affected members, the case with the more severe and/or earlier phenotype may be considered the ‘genetic proband’ and be tested first.
- In patients with a borderline ACM phenotype, comprehensive genetic testing may be considered. The identification of a LP/P genetic variant would be useful to confirm the diagnosis.
- Variant-specific genetic testing is recommended for family members and appropriate relatives following the identification of the disease-causative variant.
- Predictive genetic testing in related children is recommended in those aged > 10–12 years.
- Predictive genetic testing in related children aged below 10–12 years may be considered, especially where there is a family history of early-onset disease.

DCM

- Genetic testing is recommended for probands with DCM and family history of DCM, and the initial tier of genes tested should include genes with definitive or strong evidence of pathogenicity (currently BAG3, DES, FLNC, LMNA, MYH7, PLN, RBM20, SCN5A, TNNC1, TNNT2, TTN, DSP).
- For genetic testing in a proband with DCM, the initial tier of genes tested may include genes with moderate evidence of pathogenicity (ACTC1, ACTN2, JPH2, NEXN, TNNI3,TPM1, VCL).
- Genetic testing is recommended for patients with DCM and family history of premature unexpected sudden death or in a DCM patient with clinical features suggestive of a particular/rare genetic disease (such as atrioventricular block or sinus dysfunction or creatine phosphokinase elevation).
- Genetic testing can be useful for patients with apparently sporadic DCM, particularly in the presence of either severe systolic dysfunction (left ventricular ejection fraction < 35%), or a malignant arrhythmia phenotype (e.g., sustained ventricular tachycardia/fibrillation), or particularly at a younger age.
- Genetic testing may be considered for patients with DCM related to an acquired or environmental cause that may overlap with a genetic cause (such as peripartum or alcoholic cardiomyopathy).
- Genetic testing is useful for patients with DCM to improve risk stratification and guide therapy.
- Variant-specific genetic testing is recommended for family members and appropriate relatives following the identification of the disease-causative variant.
- Predictive genetic testing in related children is recommended in those aged > 10–12 years.
- Predictive genetic testing in related children aged below 10–12 years may be considered, especially where there is a family history of early-onset disease.

Heart Failure Society of America (HFSA)/American College of Medical Genetics (ACMG)

In 2018, the HFSA updated their guideline addressing the genetic evaluation of cardiomyopathy in collaboration with the ACMG (Hershberger et al., 2018). This document, written by cardiologists and genetics professionals with expertise in both adult and pediatric cardiomyopathy, provides the following directives:

- Obtaining a family history of at least 3 generations, including the creation of a pedigree, is recommended for all patients with a primary cardiomyopathy.
- Clinical (phenotypic) screening for cardiomyopathy in at-risk first-degree relatives is recommended.
- Referral of patients with genetic, familial or other unexplained forms of cardiomyopathy to expert centers is recommended.
- Genetic testing is recommended for patients with cardiomyopathy.
  - Genetic testing is recommended for the most clearly affected family member.
  - Cascade genetic testing of at-risk family members is recommended for pathogenic and likely pathogenic variants.
  - In addition to routine newborn screening tests, specialized evaluation of infants with cardiomyopathy is recommended, and genetic testing should be considered.
- Genetic counseling is recommended for all patients with cardiomyopathy and their family members. (Level of Evidence A).
- 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.
  - 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.
  - If no cardiovascular disease phenotype is identified in the individual, recommendations for surveillance screening at intervals should be considered.
  - 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).
- Medical therapy based on cardiac phenotype is recommended, as outlined in consensus guidelines. (Level of Evidence A)
- Device therapies for arrhythmia and conduction system disease based on cardiac phenotype are recommended, as outlined in consensus guidelines. (Level of Evidence B)
- 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)

Levels of Evidence:

- A – Genetic evaluation or testing has a high correlation with the cardiomyopathic disease of interest in studies with a moderate or large sample size.

- B – Genetic evaluation or testing has a high correlation with the cardiomyopathic disease of interest in smaller or single-center studies.
- C – Genetic evaluation or testing correlates with the cardiomyopathic disease of interest in case reports.

Inherited Thoracic Aortic Disease

Aortic diseases are the 18th most common cause of death worldwide, and about 20% are genetic, but this could be an underestimate as genetic testing is not frequently used in the clinical setting. Thoracic aortic aneurysm refers to a permanent dilation of the thoracic aorta and may involve different segments of the aorta. Overtime, an aneurysm can weaken as it gets bigger, resulting in blood leaking through a tear in the wall, called a dissection. Some dissections are acute and have a high rate of mortality, while others can be chronic and less likely to be fatal. Most heritable thoracic aortic diseases (HTADs) are inherited in an autosomal dominant fashion with high penetrance, so getting a clear family history as part of any workup is important. Some cases may occur as de novo mutations. The four most common HTADs are Marfan syndrome, caused by mutations in the FBN1 gene, Loeys-Dietz syndrome, caused by mutations in TGFBR1, TGFBR2, SMAD3, TGFB2 and TGFB3, Ehlers-Danlos Syndrome, caused by mutations in COL3A1 and Familial thoracic aortic disease (TAAD). Familial TAAD represents a group of non-syndromic disorders that presents with isolated aortopathy and no other characteristic features. Genes that have been implicated in the latter group include ACTA2, MYH11, TGFBR2, MYLK, PRKG1, LOX, MAT2A and more. About 70% of non-syndromic HTADs do not yet have an identifiable genetic cause. In recent reviews, it is recommended to target testing based on clinical features. If an individual has characteristics of Marfan syndrome, test for FBN1, otherwise due to the clinical overlap between other syndromes, consider a panel of 15-16 genes associated with HTAD (Milewicz and Regaldo, 2017).

Genetic factors have been proposed as a very important mechanism for ascending aortic dilatation (AAD) involving both the aortic root and the tubular segment. Ma et al. (2021) sought to investigate the rare genetic variants that contribute to the pathogenesis of aortic roots in individuals affected with bicuspid aortic valve (BAV). In this study, aortic root or ascending aorta with diameter greater than or equal to 40mm was considered AAD. In a cohort of 96 unrelated individuals with BAV including 34 with AAD, a custom-designed testing panel of 13 BAV-associated genes was performed using targeted next-generation sequencing. Rare variants with allele frequency < 0.05% were selected and evaluated, compared with the Exome aggregation consortium (ExAC) (Karczewski et al., 2020) and evaluated for pathogenicity of variants according to ACMG guidelines. Ultimately, 27 rare nonsynonymous coding variants involving 9 different genes were identified in 25 participants. Variants in GATA5, GATA6, and NOTCH1 had significant associations with BAV. Detection rate of rare variants was higher in the group of individuals with root dilatation (71.4%) than in the group with normal aorta (29.0%) and the group with tubular dilatation (29.6%). The authors concluded that although a broad genetic spectrum was identified in individuals with BAV, rare variants of BAV genes contribute most significantly to root-type phenotypes. They recommend further study on rare variants associated with BAV including long-term follow up to assess potential pathogenicity of rare genetic variants.

Using the ClinGen Aortopathy Working Group, Renard et al. (2018) attempted to identify hereditary thoracic aortic aneurysm and dissection (HTAAD) predisposition genes. This curation research was intended to aid and inform clinical laboratories in the development, interpretation, and establish subsequent clinical implications of clinical testing for aortic disease. Presumed gene-disease relationships between 53 candidate genes and HTAAD were explored. Genes were chosen based on published data and those tested in clinical aortopathy gene panels; six genes were added based on newly published literature and seven were added because they were offered on diagnostic panels for aortic disease. 37/53 genes were autosomal dominant; 4/53 were x-linked recessive; 1/53 were x-linked dominant; 11/53 were autosomal recessive. Gene-disease causations were evaluated by a pre-defined curator-expert pair and reviewed by an expert panel. Causative genes were determined for HTAAD if they were associated with isolated thoracic aortic disease and were clinically actionable, triggering routine aortic surveillance, intervention and family cascade testing. 9/53 genes (ACTA2, COL3A1, FBN1, MYH11, MYLK, SMAD3, TGFB2, TGFBR1, TGFBR2) were categorized as having definitive causation; 2/53 (PRKG1, LOX) strong; 4/53 moderate; 15/53 limited; 23/53 no evidence. The authors concluded that the ClinGen framework is useful when semi-quantitatively determining the strength of gene-disease relationships for HTAAD.

Overwater et al. (2018) described the clinical validity of a panel of genes associated with inherited TAAD in 810 TAAD patients at the VU University Medical Center in the Netherlands. The genes included ACTA2, COL3A1, EFEMP2, ELN, FBN1, FBN2, MYH11, MYLK, NOTCH1, PLOD1, PRKG1, SCARF2, SKI, SLC2A10, SMAD2, SMAD3, SMAD4, TGFB2, TGFB3, TGFBR1 and TGFBR2. A pathogenic or likely pathogenic variant was found in 66 patients (8%). Of these, six were copy number variants not detectable by NGS, but through additional studies. The authors noted that the prevalence of mutations in this study was lower than found in other studies that had detection rates up to 35% and felt that this was because other studies required a family history or other indicator of a familial form of TAAD prior to testing. In the Netherlands, it is common to test all individuals with TAAD, which may explain the lower yield.

Yang et al. (2016) developed a panel of 15 genes associated with aortopathies in the Chinese population, which included genes for Marfan syndrome (MFS), Loeys-Dietz syndrome (LDS), Ehlers-Danlos syndrome, vascular type (vEDS) and various genes associated with other thoracic aortic aneurysms. Between February 2014 and April 2016, patients referred to the vascular surgery center of Fuwai hospital were informed of the study, and 248 consented to enroll. Of the 248 individuals, all had various stages of aortopathy and were suspected to have MFS (117), LDS (10) or were not categorized and were likely non-syndromic (121). The results identified a pathogenic or likely pathogenic variant in 92 (37%) of individuals. The vast majority were FBN1 mutations (82), consistent with the suspected diagnosis of MFS. Mutations were additionally identified in ACTA2 (2), COLA3A1 (1), MYH11 (1), SLC2A10 (1) and TGFBR1 (2) and TGFBR2 (1). The authors noted that variant analysis and classification was challenging due to a deficient variant database for the Chinese population, so novel variants were difficult to classify.

The diagnostic yield of a seven-gene NGS panel for TAAD was examined by Campens et al. (2015) in 264 patients. Patients represented consecutive cases referred to a genetic testing lab for analysis. Patients that were reported to have Marfan syndrome features were tested first for common FBN1 variants and were included in this study only if the result was negative. Thoracic aneurysm was present in 233 patients, and of these, 27% had a positive family history, and 33% had syndromic features. The 31 non-TAD patients included 23 with a dissection with either a positive family history or syndromic features. Eight patients had only a positive family history or other syndromic features, but no evidence of TAAD. A causal mutation was found in 13% of patients including 12 FBN1 (35.3%), one TGFBR1 (2.9%), two TGFBR2 (5.9%), three TGFB2 (8.8%), nine SMAD3 (26.5%), three COL3A1 (8.8%) and four ACTA2 (11.8%) mutations. The authors noted that the turnaround time for traditional Sanger sequencing is about 12 weeks, but the NGS test was completed in 8 weeks. For this reason, the authors suggest that even those who have a high likelihood of having a FBN1 mutation based on their clinical phenotype be tested with panel approach.

Clinical Practice Guidelines

American College of Cardiology (ACC)/American Heart Association (AHA)

The 2022 ACC/AHA Guideline for the Diagnosis and Management of Aortic Disease (Isselbacher et al.) states that up to 20% of individuals with a thoracic aortic aneurysm (TAA) or aortic dissection have a family history of thoracic aortic disease (TAD), with at least 1 affected first-degree relative. The guideline provides the following recommendations related to genetic testing and screening of family members for TAD:

- For individuals with aortic root/ascending aortic aneurysms or aortic dissection, obtain a multigenerational family history of thoracic aortic disease (TAD), unexplained sudden deaths, and peripheral and intracranial aneurysms.
- For individuals with aortic root/ascending aortic aneurysms or aortic dissection and risk factors for HTAD, genetic testing to identify pathogenic/likely pathogenic variants should be performed.
- For individuals with an established pathogenic or likely pathogenic variant in a gene predisposing to HTAD, genetic counseling should be provided and the individual's clinical management should be guided by the specific gene and variant in the gene.
- For individuals with TAD who have a pathogenic/likely pathogenic variant, genetic testing of at-risk biological relatives (i.e., cascade testing) should be performed.

At the time of publication of the 2022 ACC/AHA guideline, existing HTAD genetic testing panels included eleven genes that have confirmed association with highly penetrant risk for TAD. These include: FBN1, LOX, COL3A1, TGFBR1, TGFBR2, SMAD3, TGFB2, ACTA2, MYH11, MYLK, and PRKG1. The panels typically also include genes that increase risk for TAD or that may lead to systemic features overlapping with Loeys-Dietz syndrome, Marfan syndrome or vascular Ehler-Danlos syndrome.

American College of Cardiology (ACC)/American Heart Association (AHA)/American Association for Thoracic Surgery (AATS)/American College of Radiology (ACR)/American Stroke Association (ASA)/Society of Cardiovascular Anesthesiologists (SCA)/Society for Cardiovascular Angiography and Interventions (SCAI)/Society of Interventional Radiology (SIR)/Society of Thoracic Surgeons (STS)/Society for Vascular Medicine (SVM)/North American Society for Cardiovascular Imaging (NASCI)

Hiratzka et al. (2010) published the consensus guidelines of multiple professional societies involved in the care of individuals who have, or are at risk for, a TAAD. The guidelines note that identification of a genetic mutation as the underlying cause of a TAAD is important in providing care for the individual and at-risk family members. For example, if a patient harbors a mutation in a FBN1, TGFBR1, TGFBR2, COL3A1, ACTA2 or MYH11 gene, first-degree relatives should have genetic counseling and testing. Only family members with an inherited genetic mutation should have aortic imaging (Level of Evidence C). Genetic testing to verify the underlying disorder can help identify the best treatment plan. For example, patients with LDS or a confirmed TGFRB1 or TGFBR2 mutation should have yearly MRI from the cerebrovascular circulation to the pelvis (Level of Evidence B) and if there is an aortic diameter 4.2 cm or greater by ultrasound, surgical repair should be considered (Level of Evidence C). Sequencing of the ACTA2 gene in individuals with a family history of TAAD is reasonable, and sequencing of TGFBR1, TGFBR2, and MYH11 in individuals with a family and clinical history consistent with disease can be considered (Level of Evidence B). The authors note that inherited TAAD is often asymptomatic until a life-threatening event occurs, so evaluating at risk family members can save lives.

Levels of Evidence:

- A – Multiple populations evaluated; data derived from multiple randomized clinical trials or meta-analyses.
- B – Limited populations evaluated; data derived from a single randomized trial or nonrandomized studies.
- C – Very limited populations evaluated; consensus opinion, case studies or standard of care.

American Heart Association (AHA)

In a 2020 scientific statement from the AHA, Musunuru et al. highlight 11 genes with strong or definitive evidence supporting association with penetrant heritable thoracic aortic aneurysms or dissections (HTADs) with or without syndromic features (ACTA2, COL3A1, FBN1, MYH11, SMAD3, TGFB2, TGFBR1, TGFBR2, MYLK, LOX, PRKG1) and 8 additional genes with significant evidence for risk associated with HTADs (EFEMP2, ELN, FBN2, FLNA, NOTCH1, SLC2A10, SMAD4, SKI) as per the ClinGen Aortopathy Working Group (Renard et. al., 2018). Identification of the causal gene can provide information allowing providers to take clinical action related to aortic disease presentation, associated clinical disorders, risk for dissection with or without aortic dilation and risk for other vascular diseases. Of note, genetic testing is negative for 70% of families with HTADS who do not present with systemic features, so it is clear that additional genes associated with HTADs have not yet been identified. In these cases, referral to research studies should be considered.

Coronary Artery Disease (CAD)

The evidence is insufficient to support the use of genomic risk scores or gene expression testing for coronary artery disease. Further studies with a larger number of patients and longer follow-up are needed to determine if these tests provide clinical utility in cardiac patients.

Genetic Profiles for Cardiac Disease Risk

Boccanelli and Scardovi (2023) reported on findings from the PRE-DETERMINE cohort study, the objective of which is to determine whether biomarkers and electrocardiogram can be used to determine whether individuals are more likely to experience SD. In the study, the utility of the genome-wide polygenic scores for coronary artery disease (GPSCAD) for the stratification of risk in a population of individuals with intermediate-risk and stable CAD without severe systolic dysfunction and/or an indication for an implantable cardioverter defibrillator for prevention. Individuals were followed for a mean of 8 years. Individuals in the top decile of GPSCAD were found to have a higher absolute (8.0% vs. 4.8%; $p < 0.005$) and relative (29% vs. 16%; $p < 0.0003$) risk of SD related to the remainder of the cohort. There was no association found between the highest decile of GPSCAD and other causes of death, both cardiac and non-cardiac. The authors conclude that these data can be used only for a theoretical estimate on potential effectiveness of implantable defibrillator in the group of individuals with chronic CAD and moderately depressed left ventricular function as the number needed to treat and potential reduction of mortality for individuals at high risk (defined as the top decile of GPSCAD). They advise that further research is needed in the coming years.

Sun et al. (2021) sought to explore the clinical utility of polygenic risk scores (PRSs) in cardiovascular disease (CVD) focusing on coronary heart disease (CHD) and stroke outcomes as opposed to CHD only. Clinical implications of guideline-recommended intervention were also studied. The incremental predictive gain of PRSs over conventional risk factors was determined using data from the UK Biobank which included 306,654 persons without a history of CVD and not on lipid-lowering treatments. Population health implications of statin therapy were then modeled as recommended by current guidelines from 2.1 million persons from the Clinical Practice Research Datalink. Conventional risk prediction with PRSs data increased the C-index and enhanced risk stratification of cases and non-cases. The C-index, a measure of risk discrimination, was 0.710 (95% CI

0.703-0.717) for a CVD prediction model containing conventional risk predictors alone. The C-index was increased by 0.012 (95% CI 0.009-0.015) with the addition of information on PRSs and resulted in continuous reclassification improvements of 10% and 12% in cases and non-cases, respectively. The authors reported that “if a PRS were assessed in the entire UK primary care population aged 40-75 years, assuming that statin therapy would be initiated in accordance with the UK National Institute for Health and Care Excellence guidelines (i.e., for persons with a predicted risk of ≥ 10% and for those with certain other risk factors, such as diabetes, irrespective of their 10-year predicted risk), then it could help prevent 1 additional CVD event for approximately every 5,750 individuals screened. However, targeted assessment in persons at intermediate (i.e., 5% to < 10%) 10-year CVD risk could help prevent 1 additional CVD event for approximately every 340 individuals screened.” The authors added, further, that a targeted strategy could help prevent 7% more CVD events than conventional risk prediction alone. Potential gains from the assessment of PRSs in addition to conventional risk factors would result in a 1.5-fold increase over those provided by assessment of C-reactive protein, a plasma biomarker included in some risk prediction guidelines. The participants included in this study were all middle-aged individuals from the UK with European ancestry, however, so ability to generalize results is limited. The researchers recommend further studies to evaluate a range of different CVD screening strategies and include participants from differing ethnic groups and countries, as well as including health economic evaluation and investigation of potential psychological harms of using genetic information to predict CVD risk.

A retrospective cohort study was performed by Mosley et al. (2020) to determine whether PRS improved CHD event prediction compared to guideline-recommended clinical risk equations. The accuracy of previously validated PRS among 4,847 white European adults participating in the Atherosclerosis Risk in Communities (ARIC- mean age 62.9 [5.6 SD]) study and 2,390 individuals from the Multi-Ethnic Study of Atherosclerosis (MESA-mean age 61.8 [9.6 SD] was reported. PRS performance data from 1996 to 2015 was compared to data taken from the 2013 American College of Cardiology/American Heart Association pooled cohort equations. Each individual’s genetic risk was calculated by adding the product of weights (international genome-wide association study) and allele dosage for 6,630,149 SNPs. A 10-year initial CHD event prediction was assessed using model discrimination, calibration, and net reclassification improvement. CHD events occurred in 14.4% (n = 696 ARIC participants) and 9.5% (n = 227 MESA participants) over a median follow-up period of 15.5 years. PRS was significantly associated with a 10-year CHD occurrence in ARIC with hazard ratios per standard deviation increments of 1.24 (95% CI, 1.15-1.34) and in MESA, 1.38 (95% CI, 2.21-1.58). From the two cohort study, the PRS was associated with incident CHD events but did not significantly improve discrimination, calibration, or risk reclassification compared with conventional predictors. The authors concluded that based on their findings, a PRS may not enhance risk prediction in the general, white middle-aged population.

Dikilitas et al. (2020) researched the associations of restricted and genome-wide PRSs with CHD in three major US ethic and racial groups. The eMERGE cohort (US based cohort with 99,185 participant DNA samples linked to EHR data to enable large-scale high-throughput genomic studies) included 45,645 European ancestry (EA), 7,597 African ancestry (AA), and 2,493 Hispanic ethnicity (HE) participants. Two restricted PRSs ($\text{PRS}_{\text{Tikkanen}}$ and $\text{PRS}_{\text{Tada;}}$ 28 and 50 variants, respectively) and two genome-wide PRSs ($\text{PRS}_{\text{metaGRS}}$ and $\text{PRS}_{\text{LDPred;}}$ 1.7M and 6.6M variants, respectively), were assessed from EA cohorts. The strength of associations of available PRSs with CHD in EA, AA, and HE adults was quantified by using a high-density genotype dataset linked to electronic health record data from the electronic health records and genomics (eMERGE) network. Within a median 11.1-year follow-up, 2,652 CHD incidents occurred. Hazard and odds ratios for the association of PRSs with CHD were similar in EA and HE groups, but lower in AA. Genome-wide PRSs exhibited a stronger association with CHD than restricted PRSs. $\text{PRS}_{\text{metaGRS}}$ performed the strongest in all three groups. Hazard ratios (95% CI) per 1 SD increase were 1.53(1.46-1.60), 1.53 (1.23-1.90), and 1.27 (1.13-1.43) for CHD incidents in EA, HE and AA persons, respectively. Hazard ratios were comparable in EA and HE cohorts ($p_{\text{interaction}} = 0.77$), but lower in AA individuals ($p_{\text{interaction}} = 2.9\text{x}10^{-3}$. The authors replicated previous reports of PRS association with CHD in EA individuals which were similar to HE individuals, but the associations were significantly lower in AA individuals. The authors concluded that genome-wide PRSs were more strongly associated with CHD than restricted PRSs and $\text{PRS}_{\text{metaGRS}}$ had the strongest association with CHD in all three groups; however, the frequency of variants and the genetic architecture of the traits of interest in such groups limited the generalizability of PRS across ancestral and ethnic groups. The potential clinical utility of PRSs for CHD in the clinical setting was emphasized by the authors, however they explained that until ancestry and ethnic-specific PRSs become available, a genome-wide PRS could be adopted for use in AA individuals.
Most genomic cardiac risk profile studies have focused on Caucasian Europeans. To explore the value of genomic profiles in different populations, Iribarren et al. (2018) examined the clinical utility of using multi-locus genomic profiling and risk scores in individuals of Latino (n = 4349), East Asian (n = 4804) and African (n = 2089) ancestry. They utilized available data from the Genetic Epidemiology Resource in Adult Health and Aging (GERA) cohort of 110,266 adult male and female Kaiser Permanente of Northern California (KPNC) members. Two genomic profiles, one with 12 single-nucleotide polymorphisms (SNPs) and another with 51 SNPs, and the Framingham Risk score were utilized to estimate the 10 year coronary heart disease (CHD) risk. The median years of follow-up available were 8.7, and in the cohort overall there were 450 CHD events. In this subset, the CHD

events included 95 in African, 316 in Latino and 39 in East Asian ancestry. After modeling and adjusting for principal components and risk factors, the 12 SNP genomic risk score was strongly associated with CHD independent of other risk factors and self-reported family history, and when the risk score included the Framingham risk score, the risk in the top tertile of patients was more strongly associated with outcome, particularly in African Americans. In the 51-SNP genomic risk score analysis, there was an independent statistical association only in Latinos. Including the Framingham risk score improved the risk categorization only a small percentage across groups. The authors concluded that universal use of DNA tests for determining cardiovascular risk is not recommended at this time, consistent with guidelines. They argue, however, that their data shows that the value of genomic risk scores demonstrated in European populations applies to other ethnic groups, particularly African American, Latino and to some degree East Asians. Intermediate risk groups who could benefit from more aggressive interventions may benefit from further risk assessments using genomic risk scores.

In a scientific statement, the AHA summarizes the emergence and state of the science of several transformational technologies for the refinement of cardiovascular disease mechanisms. Technologies such as epigenomics, transcriptomics, proteomics and metabolomics, are now making it possible to address the contributions of the expressed genome to cardiovascular disorders. The statement also identifies issues that need to be addressed to enable the use of the expressed genome for diagnosis and prediction in the clinical setting. Each of the approaches remains a work in progress, and many of the initial findings are still awaiting systematic replication in independent studies (Musunuru et al., 2017).

In a separate AHA scientific statement, Mital et al. (2016) affirm that advances in genomics are enhancing the understanding of the genetic basis of cardiovascular diseases, both congenital and acquired, and stroke. These advances include finding genes that cause or increase the risk for childhood and adult-onset diseases, finding genes that influence how patients respond to medications, and the development of genetics-guided therapies for diseases. The AHA recommends that cardiovascular and stroke clinicians develop a set of core competencies in genetics so that they can systematically and effectively integrate genetics into clinical practice.

Iribarren et al. (2016) examined the clinical utility of genomic risk scores for cardiac disease in a study of 51,954 individuals of European ancestry. They utilized available data from the GERA cohort of 110,266 adult male and female KPNC members. Four different genomic profiles using between 8-51 SNPs were developed using known genetic variants. The mean follow-up was 5.9 years. There were 1864 CHD events in this group, and all four models were linearly associated with CHD events. The hazard ratios, respectively for the 8, 12, 36 and 51 SNP panels were 1.21, 1.20, 1.23 and 1.23. Adding the genomic risk score improved the overall classification of risk in this group by 5% for SNP profiles on 8, 12 and 36 SNPs, and 4% for 51 SNPs. When using the SNP profiling only in those who were intermediate risk by the Framingham score, the net reclassification improvement was 9% for SNP profiles 8 and 12, and 7% for SNP profiles 36 and 51. Using the latter approach, to prevent 1 CHD you would treat 36 individuals with statins in the high risk 8 SNP and 12 SNP groups, 41 in the 36 SNP group and 43 in the 51 SNP group.

Cardiac disease is caused by a combination of genomic and lifestyle factors. To study the extent that a healthy lifestyle can influence genetic risk, Khera et al. (2016) combined the results of four studies of 55,685 white participants that looked at lifestyle factors in the context of genetic risk. The four studies included Atherosclerosis Risk in Communities (ARIC) study, the Women’s Genome Health Study (WGHS), the Malmö Diet and Cancer Study (MDCS) and the BioImage Study. All are described in detail elsewhere. The sub-cohort of each group that was selected for this study resulted in a final study group that had an average age of 58, 75% female, 42% with hypertension at baseline, 6.5% with diabetes mellitus, 25% with a family history positive for CHD, and an average BMI of 26. Additional risk factors related to lipid levels and use of lipid lowering medications were reported in detail for each group. Healthy lifestyle factors such as exercise, non-smoking and a healthy diet were combined into a healthy lifestyle score per group. A genomic panel of up to 50 SNPs was utilized to derive a genomic risk score for participants. Individual participant scores were created by adding up the number of risk alleles at each SNP and then multiplying the sum by the literature-based effect size. The genomic risk score was highly predictive of CHD events, and the relative risk was 91% higher in those at high genetic risk than among those at low genetic risk. A family history of CHD was also strongly associated with CHD events, but not as tightly as the genomic risk score. Levels of LDL cholesterol were also modestly associated with CHD events. Genetic risk categories were not associated with other cardiometabolic risk factors or risk modelling provided by the ACC. As expected, unfavorable lifestyle risk factors were strongly correlated with CHD events. When lifestyle risk factors were analyzed in the context of genomic risk scores, those with a favorable lifestyle had a 45% lower risk of a CHD in the low genomic risk group, a 47% lower risk in the intermediate genomic risk group and a 46% lower risk in the high genomic risk group. The inverse was true as well; an unfavorable lifestyle was strongly correlated with an adverse CHD event even in the low genomic risk group. When an adjustment was made for traditional risk factors, the decreased risk for those with a favorable lifestyle remained statistically significant across all groups. In conclusion, regardless of genetic risk, adherence to a healthy lifestyle substantially reduces the risk of coronary artery disease.

The Sixth Joint Task Force of the European Society of Cardiology and Other Societies on Cardiovascular Disease Prevention in Clinical Practice reviewed the available evidence on the use of genomic risk scores in identifying individuals at risk for coronary artery disease, and preventing subsequent disease (Piepoli et al., 2016). The joint task force concluded that while there is strong pressure to use genomic testing, there is no consensus on what genetic markers should be included, how genomic risk scores should be calculated and how to use the information to prevent cardiac disease. Therefore, use of genetic markers in the prediction of CHD is not recommended.

Gene Expression Testing

Gene expression is the process by which the coded information of a gene is translated into the structures present and operating in the cell (either proteins or ribonucleic acids (RNA). Gene expression profiling (GEP) studies the patterns of many genes in a tissue sample at the same time to assess which ones are turned on (producing RNA and proteins) or off (not producing RNA or proteins). By simultaneously measuring the levels of RNA of thousands of genes, GEP creates a snapshot of the rate at which those genes are expressed in a tissue sample.

Assimes and Roberts (2016) summarized the evolution and discovery of genetic risk variants for coronary artery disease (CAD) and their current and future clinical applications. In order to maximize the clinical utility of the current knowledge gained, the authors propose future tasks which include the identification of the remaining susceptibility loci for CAD, proving the clinical utility of genetic data in the prevention of CAD, and acquiring a solid appreciation of the cellular and/or extracellular mechanisms responsible for genetic associations observed at the population level. They conclude that extremely large sample sizes are needed for additional discoveries, given the distribution of effect sizes observed to date for both common and rare variants, as well as the estimated proportion of the heritability of CAD explained by these variants to date. In the coming years, the authors suggest that this need could be fulfilled by mega-biobanks to assist in the determination of the clinical utility of genetic risk scores, and to conduct additional, well-powered MR studies to complement studies published to date.

Using a series of microarray and real-time polymerase chain reaction (RT-PCR) data sets, comprising more than 1000 patients, Elashoff et al. (2011) developed a blood-based gene expression algorithm for assessing obstructive CAD in non-diabetic patients. The algorithm consists of the expression levels of 23 genes, sex and age.

Wingrove et al. (2008) performed a microarray analysis on 41 patients with angiographically significant CAD and 14 controls without coronary stenosis to identify genes expressed in peripheral blood that may be sensitive to the presence of CAD. A multistep approach was used, starting with gene discovery from microarrays, followed by real-time polymerase chain reaction (RT-PCR) replication. The authors observed that gene expression scores based on 14 genes, independently associated with the presence or absence of CAD, were proportional to the extent of disease burden. This study is limited by its size and retrospective nature. Larger, prospective studies are needed to confirm these initial results.

The U.S. Preventive Services Task Force (USPSTF) recommendations on the use of nontraditional risk factors in coronary heart disease risk assessment do not address genetic/genomic markers (USPSTF, 2018).

Clinical Practice Guidelines

American College of Cardiology (ACC)

ACC guidelines do not address gene expression profiling for predicting the likelihood of obstructive coronary artery disease.

European Heart Rhythm Association (EHRA)/Heart Rhythm Society (HRS)/Asia Pacific Heart Rhythm Society (APHRS)/Latin American Heart Rhythm Society (LAHRS)

In an Expert Consensus Statement on genetic testing for cardiac disease, the EHRA, HRS, APHRS and LAHRS (Wilde et al., 2022) address the state of genetic testing for CAD. The major genes associated with prediction of CAD are APOB, LDLR and PCSK9. In recent decades, widespread contribution of polygenic risk has been shown to contribute to CAD susceptibility and novel genetic mechanisms such as clonal hematopoiesis of indeterminate potential (somatic rather than germline) have also been shown to play a role. Research has indicated that genetic predisposition may prove useful for risk prediction related to

CAD, but the predictive utility of PRS for CAD are widely debated and as such, are not commonly used in clinical practice today.

U.S. Food and Drug Administration (FDA)

This section is to be used for informational purposes only. FDA approval alone is not a basis for coverage.

Laboratories that perform genetic tests for cardiac disease are regulated under the Clinical Laboratory Improvement Amendments (CLIA) Act of 1988. More information is available at: http://www.fda.gov/medicaldevices/deviceregulationandguidance/ivdregulatoryassistance/ucm124105.htm. (Accessed April 27, 2023)

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Policy History/Revision Information

Date	Summary of Changes
10/01/2023	**Application** ***Individual Exchange Plans*** • Removed language indicating this Medical Policy does not apply to Individual Exchange benefit plans in the states of Massachusetts, Nevada, and New York **Coverage Rationale** • Added language to indicate pre-test genetic counseling is strongly recommended in order to inform persons being tested about the advantages and limitations of the test as applied to a unique person

Date	Summary of Changes
	Inherited Thoracic Aortic Disease • Revised language to indicate Multi-Gene Panel testing is proven and medically necessary for either of the following: ○ Individual has confirmed thoracic aortic disease ○ Thoracic aortic disease is suspected based on family history of thoracic aortic disease in a First- or Second-Degree Relative ***Testing Based Only on Family History*** • Replaced reference to "*close blood* relative" with "*First-Degree or Second-Degree* Relative" **Definitions** • Added definition of: ○ First-Degree Relative ○ Second-Degree Relative • Removed definition of "Close Blood Relatives" • Updated definition of "Schwartz Score" **Supporting Information** • Updated *Description of Services*, *Clinical Evidence*, and *References* sections to reflect the most current information • Archived previous policy version 2023T0552T

Instructions for Use

This Medical Policy provides assistance in interpreting UnitedHealthcare standard benefit plans. When deciding coverage, the member specific benefit plan document must be referenced as the terms of the member specific benefit plan may differ from the standard plan. In the event of a conflict, the member specific benefit plan document governs. Before using this policy, please check the member specific benefit plan document and any applicable federal or state mandates. UnitedHealthcare reserves the right to modify its Policies and Guidelines as necessary. This Medical Policy is provided for informational purposes. It does not constitute medical advice.

This Medical Policy may also be applied to Medicare Advantage plans in certain instances. In the absence of a Medicare National Coverage Determination (NCD), Local Coverage Determination (LCD), or other Medicare coverage guidance, CMS allows a Medicare Advantage Organization (MAO) to create its own coverage determinations, using objective evidence-based rationale relying on authoritative evidence (Medicare IOM Pub. No. 100-16, Ch. 4, §90.5).

UnitedHealthcare may also use tools developed by third parties, such as the InterQual® criteria, to assist us in administering health benefits. UnitedHealthcare Medical Policies are intended to be used in connection with the independent professional medical judgment of a qualified health care provider and do not constitute the practice of medicine or medical advice.