

Genetic Factors Contributing to the Development of Hypertrophic Cardiomyopathy

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Introduction

Hypertrophic Cardio Myopathy (HCM) is a hereditary heart disease characterized by abnormal thickening of the heart muscle, particularly the left ventricle. This condition can lead to various complications, including heart failure, arrhythmias and, in some cases, sudden cardiac death. HCM is considered one of the most common genetic heart diseases, affecting a significant portion of the population, often without showing symptoms until later stages. While environmental factors and lifestyle choices may influence the progression of the disease, the primary driver of HCM is genetic mutations. The underlying genetic factors responsible for HCM primarily involve mutations in genes encoding sarcomeric proteins, which are essential for muscle contraction.

These mutations disrupt the normal functioning of the heart, leading to the thickening of the heart muscle and impaired cardiac function. This article will explore the genetic mutations associated with hypertrophic cardiomyopathy, focusing on their role in the disease's development, inheritance patterns and the clinical implications of genetic findings. Understanding these genetic factors is critical not only for diagnosing and managing the disease but also for advancing potential treatments tailored to the genetic makeup of individuals affected by HCM [1].

Description

Hypertrophic cardiomyopathy manifests as the thickening of the left ventricular wall, often affecting the interventricular septum and is commonly accompanied by disorganized myocardial fibers and fibrosis. These changes impair the heart's ability to pump blood efficiently and can lead to symptoms such as chest pain, shortness of breath and fatigue. The condition can also cause arrhythmias, which increase the risk of sudden cardiac death, particularly in younger individuals. The heart's inability to relax properly, a condition known as diastolic dysfunction, is also commonly observed in HCM. At the molecular level, the primary cause of HCM is mutations in genes encoding the proteins of the sarcomere, the fundamental contractile unit of muscle cells. The majority of HCM cases are linked to mutations in genes that code for proteins such as Myosin Heavy Chain (MYH7), Cardiac MYosin-Binding Protein C (MYBPC3) and Troponin T (TNNT2). These sarcomeric proteins are essential for muscle contraction and mutations disrupt their normal function, leading to the hypertrophic changes observed in the heart muscle [2].

For example, the MYH7 gene encodes the beta-myosin heavy chain, one of the key components of the sarcomere responsible for generating

force during contraction. Mutations in this gene are among the most common causes of HCM, leading to altered myosin function and impaired contractile force. Similarly, MYBPC3, which encodes cardiac myosin-binding protein C, also plays a crucial role in muscle contraction and mutations in this gene lead to misalignment of the sarcomeric structure. The TNNT2 gene, responsible for encoding troponin T, a protein that regulates muscle contraction by controlling calcium sensitivity, is also frequently mutated in HCM cases. These mutations affect the function of the sarcomere, leading to abnormal thickening of the heart muscle and subsequent development of the disease.

Hypertrophic cardiomyopathy follows an autosomal dominant inheritance pattern, meaning that an individual only needs one copy of the mutated gene from either parent to develop the disease. This inheritance pattern makes family members of affected individuals at higher risk of carrying the genetic mutation. Genetic testing can help identify family members who may carry the mutation, even if they are asymptomatic, allowing for early intervention and management. Early detection can help prevent complications such as arrhythmias and sudden cardiac death, which are often seen in individuals with untreated HCM [3].

While genetic mutations are the primary cause of HCM, the disease's expression can vary significantly among individuals with the same mutation, suggesting that additional factors, such as gene-environment interactions, may influence disease severity. Environmental factors such as exercise, stress and other lifestyle elements can modify the expression of the genetic mutations and contribute to the progression of the disease. These interactions complicate the clinical presentation of HCM and emphasize the importance of personalized care for individuals with the disease.

One of the key challenges in managing HCM is the variability in clinical presentation. Some individuals with mutations may remain asymptomatic for most of their lives, while others may develop severe forms of the disease with pronounced hypertrophy, impaired cardiac function and arrhythmias. Even among family members carrying the same mutation, there can be significant differences in disease severity, making individualized monitoring and management essential. Moreover, advances in genetic testing have improved the accuracy of diagnosing HCM and identifying at-risk individuals. Genetic screening is especially beneficial for family members of individuals with HCM, as early identification allows for proactive monitoring and treatment [4].

Despite these advances, genetic counseling and testing in HCM present ethical and psychological challenges. The discovery of a genetic mutation in an asymptomatic individual can raise concerns about the implications for their health, future prognosis and reproductive decisions. Additionally, incidental findings related to other genetic conditions may further complicate counseling and decision-making. It is essential that individuals undergo genetic counseling before and after testing to fully understand the potential consequences of the results.

Advancements in research are also driving the development of potential therapies aimed at correcting the genetic mutations that cause HCM. Gene therapy holds promise as a future treatment option, where healthy versions of the mutated genes are delivered into the heart to correct the underlying genetic defect. Another exciting avenue involves the use of CRISPR-Cas9 technology, which has shown potential in editing the specific genetic mutations responsible for HCM. While these therapies are still in the experimental phase, they offer the possibility of a long-term solution for individuals with

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HCM, potentially halting or reversing the disease's progression [5].

Conclusion

Hypertrophic cardiomyopathy is a genetic heart disease with a significant impact on patient health and genetic factors are central to its development. Mutations in key sarcomeric proteins, such as MYH7, MYBPC3 and TNNT2, disrupt the normal function of the heart muscle, leading to thickening of the heart walls and impaired cardiac function. The autosomal dominant inheritance pattern of HCM means that family members of affected individuals are at risk of inheriting the mutations, making early detection through genetic testing crucial for managing the disease.

The variability in clinical presentation of HCM underscores the complexity of the disease, with environmental and lifestyle factors contributing to the severity of symptoms. Genetic testing and screening have become essential tools in diagnosing and managing HCM, allowing for earlier intervention and more personalized treatment plans. While challenges remain in the application of genetic testing and counseling, the potential for advancements in genetic therapies, including gene editing and CRISPR technology, holds promise for more effective treatments in the future.

As research into the genetic underpinnings of hypertrophic cardiomyopathy continues to evolve, the goal is to develop targeted therapies that address the root cause of the disease, potentially providing long-term benefits and improving outcomes for affected individuals. By understanding the genetic basis of HCM, healthcare providers can offer better care, risk stratification and personalized treatment plans, ultimately improving the quality of life for patients with this challenging condition.

References

1. Cirino, Allison L., Neal K. Lakdawala, Barbara McDonough and Lauren Conner, et al. "A comparison of whole genome sequencing to multigene panel testing in hypertrophic cardiomyopathy patients." *Circ Cardiovasc Genet* 10 (2017): e001768.
2. Bagnall, Richard D., Jodie Ingles, Marcel E. Dinger and Mark J. Cowley, et al. "Whole genome sequencing improves outcomes of genetic testing in patients with hypertrophic cardiomyopathy." *Am Coll Cardiol* 72 (2018): 419-429.
3. Chaffin, Mark, Irinna Papangeli, Bridget Simonson and Amer-Denis Akkad, et al. "Single-nucleus profiling of human dilated and hypertrophic cardiomyopathy." *Nature* 608 (2022): 174-180.
4. Jiang, Jianming, Hiroko Wakimoto, J. G. Seidman and Christine E. Seidman. "Allele-specific silencing of mutant Myh6 transcripts in mice suppresses hypertrophic cardiomyopathy." *Science* 342 (2013): 111-114.
5. Ingles, Jodie and Christopher Semsarian. "Conveying a probabilistic genetic test result to families with an inherited heart disease." *Heart Rhythm* 11 (2014): 1073-1078.

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