The MOGE(S) system explained

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In a standard textbook of medicine, the first step in the evaluation of cardiomyopathy is to make the distinction between ischaemic heart disease (IHD) as the cause of cardiomyopathy as opposed to nonischaemic causes of cardiomyopathy.

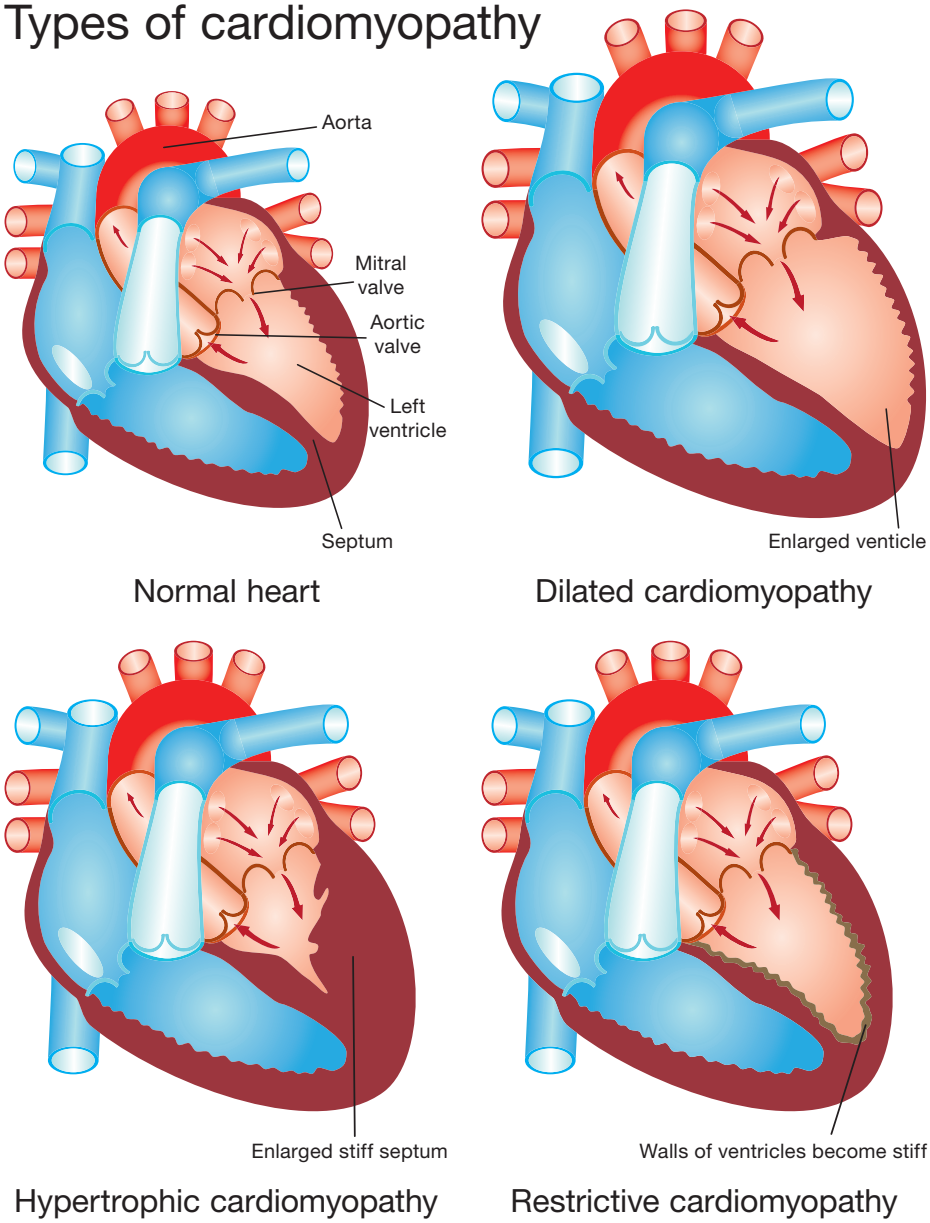
DEFINITION AND CLASSIFICATION

In 2006 cardiomyopathies were defined as diseases of the myocardium associated with mechanical and/or electrical dysfunction, which usually (but not invariably) exhibit inappropriate ventricular hypertrophy or dilatation due to a variety of causes that frequently are genetic, classified as primary (solely confined to heart muscle) or secondary (heart muscle involved as part of a multisystem disorder).

This was also the first attempt to classify cardiomyopathies by genetic origin (genetic, acquired or mixed).

In 2008 another classification defined cardiomyopathy as a myocardial disorder in which the heart muscle was structurally and functionally abnormal and classified cardiomyopathies based on phenotype as dilated (DCM), hypertrophic (HCM), restrictive (RCM), arrhythmogenic right ventricle cardiomyopathy (ARVC) or unclassified.

Types of cardiomyopathy



Normal heart

Dilated cardiomyopathy

Hypertrophic cardiomyopathy

Restrictive cardiomyopathy

For clinical practice the importance of phenotype preceding genotype was maintained. In all these early efforts to classify the cardiomyopathies, it is important that ischaemic heart disease is excluded as well as hypertensive, valvular and congenital heart disease.

DIAGNOSIS

The morphologic diagnosis of cardiomyopathy has been greatly enhanced with the development of new improved technology used to evaluate cardiac structure and function.

Echocardiography is still the cornerstone of diagnosis, but many other diagnostic modalities have been added such as cardiac magnetic resonance (CMR), cardiac CT, single photon emission CT (SPECT) and positron emission tomography (PET), which can aid in the functional and anatomic imaging of the heart and myocardium and have become valuable in the phenotypic description of cardiomyopathy.

The generic complications of any cardiomyopathy are that of the risk to develop heart failure with its bad prognosis and the ever present danger of sudden cardiac death mainly due to arrhythmias. These diagnostic modalities are increasingly used to evaluate asymptomatic family members of patients with cardiomyopathy with the aim of early treatment.

Substantial progress has also been made in the field of genetics which increased knowledge about the importance of and the role of genetic mutations and abnormalities of genes in the etiology of cardiomyopathies. This knowledge contributed to a better understanding of the complexities of cardiomyopathy and lead to a new classification system.

This better understanding may bring the hope for a more effective approach to therapy one day in the future.

PHENOTYPING

The morphofunctional phenotype-based classification of cardiomyopathies still continues to offer a clinical useful and simple classification which the majority of clinicians can and will use in everyday practice. All current

treatment protocols are also based on the phenotype as well as symptoms and signs.

This phenotype-based classification system defines cardiomyopathies as: DCM, which is the most common type, HCM, RCM, ARVC and left ventricular noncompaction (LVNC). The treatment of heart failure, once it develops, follow current general guidelines on the treatment of heart failure with renin-angiotensin-aldosterone system blockers, beta blockers, intracardiac defibrillators (ICD) and biventricular pacing.

There is also more specific therapy unique to a phenotype for example ablation of ventricular muscle in HCM.

This phenotypic approach describes the major forms of cardiomyopathy but it does not describe their cause.

SUBTYPES

The cardiomyopathies are clinically very heterogeneous diseases and even within subtypes there are differences in age of onset, rate of progression, risk of heart failure and even the possibility of sudden death due to arrhythmias.

In understanding the nature of cardiomyopathy this simple classification is not adequate for complete description although it remains practical.

GENETICS

It has always been known that some cardiomyopathies have a familial nature and the number of such cases have slowly increased as knowledge on the genetic basis of cardiomyopathy has evolved and the methods to investigate the genotype have been developed.

Most cardiomyopathies have an autosomal dominant inheritance but rarely there are also X-linked recessive, autosomal recessive and matrilineal inheritance patterns. The problem is that a family history may not in itself be enough to make a genetic diagnosis.

Linkage analyses, genome-wide association studies, whole-exome sequencing and the like have increased the knowledge of the genetics of cardiomyopathies.

Currently there are more than 100 genes identified in cardiomyopathies.

HCM is caused by at least 100 mutations on nine genes that code for structural and functional proteins of the sarcomere and so affects sarcomeric function. DCM is caused by mutation of genes related to structure and function of nuclear envelope, cytoskeleton, sarcomere and sarcoplasmic reticulum. ARVC is a collection of conditions of mutations of the desmosome and RCM is caused by defects in the genes involved in sarcometric proteins or intermediate filaments (such as desmin).

The problem is that most genes are not linked to a unique phenotype and identical genes may result in different phenotypes. It became clear that a new type of classification system is necessary to account for all the new data and genetic studies in cardiomyopathy.

MOGE(S) CLASSIFICATION

This new system describes cardiomyopathies by integrating a morphofunctional phenotype-based description together with the extra-cardiac involvement in cases of cardiomyopathy as well as the pattern of inheritance and the genetic aspects in familial disease and it can also describe sporadic cases of cardiomyopathy.
A recent review of this new system is described in this article.

MORPHO-FUNCTIONAL PHENOTYPE

M provides the clinical description: DCM, HCM, LVNC, RCM and ARVC: It is notated MD, MH etc. M provides red flags such as short PR (PR) e.g. MD (PR) and other arrhythmias can be flagged.

M can also describe nonspecific phenotypes e.g. hypertrabeculation when criteria for LVNC are not fulfilled: MD (PR) (NS).

The M notation is therefore very flexible and any clinical phenotype or new aspect or uncertain type of cardiomyopathy can be added.

ORGANS INVOLVED

If the heart alone is involved it is notated as: O (H). If the heart and skeletal muscle are involved: O (H+M). If the heart and nervous system are involved: O (H+N) etc.

This involvement of organs other than the heart and the description with this O notation also makes it easier to recognise syndromes.

GENETIC INHERITANCE

This description is for the inheritance pattern according to the family history. This notation reads G (AD) when there is an autosomal dominant inheritance if the inheritance is autosomal recessive it will be notated as: G (AR) etc. G (S) would be the notation for a sporadic case.

ETIOLOGY

In a known genetic mutation it is notated as: E (G) implying a genetic cause as Etiology and then the gene and its mutation are added: E (G-MYH) as it will be notated for HCM. In non-genetic etiologies of cardiomyopathies it is notated as: E (V-EBV) which implies that the cause is a virus (V) and EBV is the Ebstein-Barr virus involved. A myocarditis will be notated as: E (M-Sarcoid): This notation means the Etiology is a myocarditis and the cause of the myocarditis is Sarcoidosis.

FUNCTIONAL STATUS

This notation has two sub-types: One for the description of the stage of heart failure (A,B,C,D) and one for the New York Heart Association description of symptoms in Class 1 to 4.
S (A-1): This notation implies that the patient is in Stage A of heart failure and has Class 1 NYHA (no symptoms. The S notation is optional but it can be useful in the description of early cardiomyopathy.

CONCLUSIONS

The enormous increase in the knowledge of the genetic basis of cardiomyopathy makes it necessary to develop a new way to view and classify cardiomyopathies incorporating not only the genetic aspects but also other components.

The MOGE(S) system is a very flexible system and additions to this system and expansions can be made without any problems. This system can capture an enormous amount of data that could be lost if it is not systematically captured as in this system.

The MOGE(S) system forces one to describe all the results obtained in all the diagnostic steps that were taken in the evaluation of the presenting patient.

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1	One of the first steps in the evaluation of cardiomyopathy is to exclude ischaemic as well as hypertensive, valvular and congenital heart disease.	T	F
2	For clinical practice the importance of phenotype preceding genotype was scrapped.	T	F
3	The morphologic diagnosis of cardiomyopathy has been greatly enhanced with the development of new improved technology used to evaluate cardiac structure and function.	T	F
4	Cardiac magnetic resonance imaging is the cornerstone of diagnosis.	T	F
5	The generic complications of any cardiomyopathy are that of the risk to develop heart failure with its bad prognosis and the ever present danger of sudden cardiac death mainly due to arrhythmias.	T	F
6	Some current treatment protocols are based on the phenotype as well as symptoms and signs.	T	F
7	Most cardiomyopathies have an autosomal dominant inheritance but there are also rarely X-linked recessive, autosomal recessive and matrilineal inheritance patterns.	T	F
8	ARVC is a collection of conditions of mutations of the desmosome and RCM is caused by defects in the genes involved in sarcometric proteins or intermediate filaments (such as desmin).	T	F
9	The new MOGE(S) classification describes cardiomyopathies by integrating a morphofunctional phenotype-based description together with the extra-cardiac involvement in cases of cardiomyopathy as well as the pattern of inheritance and the genetic aspects in familial disease. It can also describe sporadic cases of cardiomyopathy.	T	F
10	The MOGE(S) system forces one to describe all the results obtained in all the diagnostic steps that were taken in the evaluation of the presenting patient..	T	F

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