

What are cardiomyopathies?

Cardiomyopathies are a group of heart muscle diseases, often genetically determined with different modality of transmission, which can show symptoms that limit the functional capacity of the heart, and that involve complications such as atrial fibrillation, heart failure, stroke and, rarely, malignant ventricular arrhythmias and sudden death. Patients with different types of cardiomyopathy (hypertrophic, dilated, arrhythmogenic right ventricular cardiomyopathy, restrictive) are estimated to be about 3 per thousand of general population, but unfortunately the cardiologist notice them only when serious or deadly events occur.

Are cardiomyopathies inherited?

In developed countries, sudden cardiac death is responsible of more than 5% of total deaths and of more of 50% of mortality for cardiovascular disease. In Italy, it can be estimated, with a good approximation, that the incidence of this phenomenon is about 0.7/1000 inhabitants/ year. Sudden death happens in 20-25% of cases in apparently healthy individuals, as a first manifestation of an unacknowledged underlying pathology. The 5-10% of sudden death cases occur in absence of evident structural cardiac anomalies in structurally normal hearts (sine materia sudden death), in presence of electrophysiological disorder which determines an electric instability responsible of the onset of ventricular arrhythmias, same as the case of long QT syndrome (LQTS), the Brugada syndrome (BS), catecholaminergic polymorphic ventricular tachycardia (CPVT). In a study conducted by British Steering Group, in 32 consecutive cases of sudden arrhythmic death sine materia, not selected by age, the cardiac screening of first-degree relatives has revealed the presence of an inherited heart disease in 22% of examined families, and approximately half of the cases were LQTS.

In a Tan et al. analysis conducted on 43 families in which there was at least a case of sudden death under 40 years of age, in 40% of cases cardiac screening allowed to identify an inherited heart disease (LQTS, CPVT, BS and arrhythmogenic right ventricular cardiomyopathy ARVC). A more recent study conducted in England on 262 relatives (of which 70% of first grade) of 57 families with at least one sudden death case, has documented an inherited heart disease in 53% of the examined families: 17% of cases were about a structural heart disease (ARVC, hypertrophic cardiomyopathy HCM, dilated cardiomyopathy, left ventricular noncompaction). In the remaining 26% the diagnosis was LQTS or BS.

CardioScreen- Cardiomyopathies test

CardioScreen – Cardiomyopathies is a diagnostic test that allows us to do a multiple genetic analysis **to see if there is the presence of mutations associated with inherited cardiomyopathies**. Therefore, the test, allows us to identify patients at genetic risk of potentially mortal cardiac events through the analysis of their DNA.

Whom is CardioScreen-Prevention sudden cardiac arrest test for?

Genetic screening test for inherited cardiomyopathies is recommended for those who know about a case of sudden cardiac death in their family (included sudden infant death), heart failure or transplant, which suggest inherited cardiac pathological substratum. It is useful to inspect also the relatives of accidental death victims

caused by sudden illness, for example during the driving of a vehicle, to see if the event is attributable to a syncopal episode or to a sudden cardiac death. The analysis of the family tree crossed with genetic screening, can provide information about the modality of transmission of inherited heart disease and its level of penetrance in any family members. Genetic screening of mutations associated to inherited cardiomyopathies is useful to arrange prevention strategies so that unexpected serious events do not occur and do not affect members of the same family.

Furthermore is particularly useful as a prevention instrument in case of:

- Professional or amateur agonistic activity, also for individuals with no familiarity
- Young individuals (younger than 40 years) with idiopathic cardiac symptomatology
- Children and teenagers with a suspect clinical picture for QT anomalies or cardiac rhythm

The geneticist, as mutually agreed upon with the cardiologist, upon informed agreement of the person concerned, will suggest whether to proceed or not with the genetic screening.

What are CardioScreen-Cardiomyopathies test benefits?

The possibility to identify an at-risk individual for inherited cardiomyopathies or for sudden cardiac arrest, represents today the best method to express an early diagnosis of a potential pathology, and, therefore, to reduce mortality and related morbidity. Members of inherited high-risk families, and in particular who is affected by an idiopathic cardiac symptomatology, can ask for a genetic consultation and discuss the own genetic-clinical situation with the geneticist.

This evaluation will be able to promote the genetic test to verify if the patient is carrier of a mutation associated to an inherited cardiomyopathy and sudden cardiac arrest. If the test is positive, the examination will be extended to patient's relatives to identify at-risk individuals of the nuclear family.

The information obtained from the genetic test can generate remarkable **benefits**, such us:

1. The identification of family members at **high risk of inherited cardiomyopathy**;
2. The organisation of an adequate **medical examination program** reserved for high risk individuals so to facilitate the adoption of **the most effective preventive measures** (for example implantable defibrillators or antiarrhythmic pharmacologic therapies);
3. The knowing of the possibility of **transmission of genetic mutation** to the progeny and the identification of individuals children with germinal genic mutations at high risk.

How is CardioScreen-Cardiomyopathies test done?

CardioScreen test is done through the taking of a haematic sample. By means of a complex laboratory analysis, the DNA is isolated from nucleated cells and **amplified by C-reactive protein (CRP) technique**. Later, thanks to an innovative technological process of **massive parallel sequencing (MPS)**, which employs **Next Generation Sequencing (NGS)** techniques using **ILLUMINA** sequencers, they completely sequence at an elevated in – depth reading, **46 genes** (exons and adjacent intragenic regions, ± 5 nucleotides) connected to inherited cardiomyopathies (see Table).

Genetic sequences obtained are analysed through an advanced **bioinformatics** analysis to determine the presence of potential mutations on genes taken under exam.

Achievable result with CardioScreen-Cardiomyopathies test

“POSITIVE”- Presence of one or more mutations: it indicates the test has revealed one or more mutations of one (or more) genes related to inherited cardiomyopathies. Our geneticist, during genetic counselling, will explain in a detailed way the meaning of the test result. A positive result doesn't mean that the patient to whom the mutation has been found will have a serious pathological cardiac event, but it means that the patient has a mutation related to inherited cardiomyopathies, that is a greater risk compared with a person who doesn't have that specific mutation. In a suspect situation, the test is useful for confirming diagnostic hypothesis that has to be verified. As a matter of fact, not all people who carry a mutation undergo to gravely pathological heart events; although these mutations considerably increase the risk that a sudden cardiac event may occur during life or during cardiac stress like a sports performance. The identification of a predisposing mutation allows to establish a protocol of clinical controls and to evaluate the opportunity of preventive interventions like implantable defibrillators or antiarrhythmic drug therapies. The positive test result also allows you to extend screening to other family members at risk who wish to do it. In the latter, the analysis has a predictive value, because allows distinguishing, within these families, carriers of potentially dangerous mutations from noncarriers, by precisely identifying high-risk individuals and those whose risk is comparable to that of the general population. In this way, the first can be started in a targeted manner to specific surveillance or prophylactic programs, while the seconds can be directed to the controls planned for the general population.

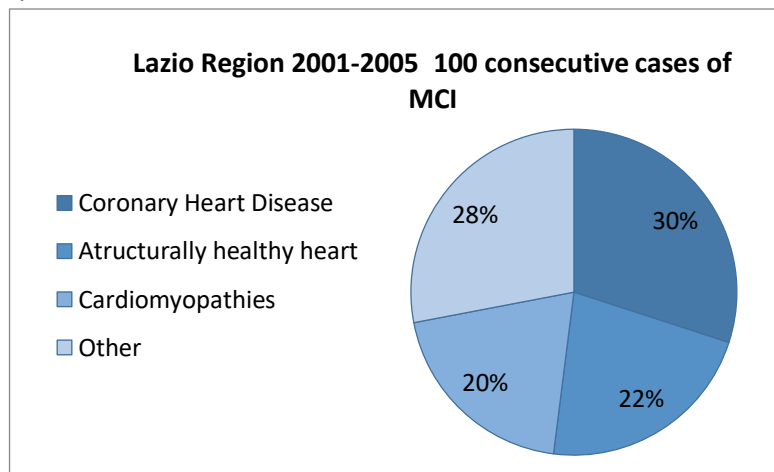
Mutations observed through **CardioScreen-Cardiomyopathies** test can be included in the following prognostic categories:

- **Known pathological meaning;**
- **Benign meaning,** since they can be found in normal individuals and they are pathologically meaningless
- **Pathological uncertain meaning,** since they aren't known or characterized from the scientific-medical community. In this case, further investigation can be necessary to clarify the variation meaning.

“NEGATIVE” - Absence of mutations: it indicates the test didn't detect the presence of mutations in the analysed genes. However is important to underline that a negative result doesn't mean the patient has zero risk to meet with a potentially serious cardiac event or to develop a cardiomyopathy in the own lifetime. The risk for this people is the same as for the general population, this because not all forms of cardiomyopathy and sudden cardiac arrest has to be connected to genetic causes.

CLINICAL RECORDS IN LITERATURE

In a study conducted on 100 consecutive cases of sudden deaths in young people (up to 40 years), occurring in the Lazio Region between 2001 and 2005, the autopsy allowed to identify coronary artery disease in 30% of cases, (mostly atherosclerotic) and cardiomyopathy in 22% of cases. Among cardiomyopathies, the most recurring is the arrhythmogenic right ventricular cardiomyopathy (AVRC, 12%) followed by hypertrophic cardiomyopathy (HCM, 4%). Myocarditis was observed in 2% of cases and mitral valve prolapse in 3%. Finally, in 20% of cases the heart resulted structurally normal during autopsy while in the remaining 28% the causes of death were not closely related to heart disease.



There is an English perspectival study conducted by Behr et al. in England on adult subjects, that is focused only on unexpected cardiac death with negative autopsy (defined sudden arrhythmic death syndrome SADS) some of which can be attributed to inherited arrhythmic syndromes. In this study was observed an SADS annual incidence of 0.16 cases on 100 000 per year (500 cases per year), with a predominance in young man. In absence of structural heart disease, the pathophysiological substratum of sudden death is represented by inherited primitive electrophysiological disorders, represented by ion channels diseases, mainly LQTS, BS and CPVT. The study also identify a 18% prevalence of a positive family history for other cases of sudden or unexplained accidental deaths, suggesting the possibility of an underlying inherited heart cause.

In SADS study conducted by British Steering Group, in 32 consecutive cases of sudden arrhythmic death sine materia, not selected by age, cardiac screening of first-degree relatives has revealed the presence of an inherited heart disease in the 22% of examined families; approximately half of the cases were about LQTS.

Parameters employed to report genetic variants

The analysis is focused exclusively to genes listed in Table 1. It will be reported only the mutations classified as “known pathogenetics meaning” or with “uncertain meaning”, based on the scientific literature data and the classification included in the reference database Human Gene Mutation Database (HGMD), updated to the date of the sample. Furthermore, following the indications of American College of Medical Genetics (ACMG), it has been considered as pathogenetics or alleged pathogenetics, only the mutations with a value of Minor Allele Frequency (MAF) <5% (1000 Genomes Project), that can be attributed as the frequency of recurrence of the less common allele within the population.

Target Coverage

For Target Coverage it is meant the average number of readings obtained from the sequencing for each nucleotide base that constitutes the gene. The variants with a reading depth (number of reads) lower than 30X, are not highlighted by the bioinformatics analysis algorithm.

Accuracy of CardioScreen- Cardiomyopathies test

Current DNA sequencing techniques produce results with an accuracy superior to 99%. Although this test is very accurate it is always necessary to consider the exam limits, shown below.

CardioScreen- Cardiomyopathies test limits

This exam evaluates only genetic diseases and the genes listed in the Table 1.

The test does not highlight other genetic diseases or genes not specifically investigated.

Furthermore, the exam is not able to highlight:

- Mutations localised in intragenic regions over ± 5 nucleotides from breakpoints;
- Deletions, inversions or duplications superior than 20bp;
- Germinal line mosaicisms (that are mutations present only in gametes).

A “**NEGATIVE**” result – **Absence of mutations** for investigated genes do not exclude the possibility of being carrier of a mutation localised in a genome region that wasn’t investigated during the exam.

It is possible that some areas of our own DNA can’t be sequenced, or that have a lower coverage than the limits set by the GENOMA Group experts to ensure an accurate analysis of the variants. These regions will not be included in the analysis in case they do not pass qualitative standard requested. In some cases, the genomic analysis result can reveal a DNA variation or mutation with a clinical meaning uncertain or determinable, on the basis of the current scientific-medical knowledge.

The interpretation of genetic variation is based on the most recent available knowledge at the time the analysis is done. This interpretation could change in the future with the acquisition of new scientific and medical information on genome structure and could influence on the same evaluation of variations.

Some pathologies can be caused or regulated by more than one variant in the DNA in one or more genes. Some of these variants may not yet be identified or validated by the scientific community and therefore not reported as pathogenetics at the time of the analysis.

The intrinsic limit of NGS methodology used is the lack of coverage homogeneity for each analysed region. This limitation translates in the possibility, inherited in NGS methods, that specific mutations of selected genes may not have been detected by the test.

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List of the analysed genes and investigated genetic diseases

Table 1: CardioScreen- Cardiomyopathies

	DISEASE NAME	PhenoMIM	GENE
1	Atrial fibrillation, familial, 12	614050	ABCC9
2	Atrial septal defect 5	612794	ACTC1
3	Dilated cardiomyopathy 1AA	612158	ACTN2
4	Ventricular tachycardia, catecholaminergic polymorphic, 2	611938	CASQ2
5	Cardiomyopathy, familial hypertrophic	192600	CAV3
6	Cardiomyopathy, dilated, 1II	615184	CRYAB
7	Cardiomyopathy, dilated, 1M	607482	CSRP3
8	Cardiomyopathy, dilated, 1I	604765	DES
9	Arrhythmogenic right ventricular dysplasia 11	610476	DSC2
10	Arrhythmogenic right ventricular dysplasia 10	610193	DSG2
11	Arrhythmogenic right ventricular dysplasia 8	607450	DSP
12	Left ventricular noncompaction 1, with or without congenital heart defects	604169	DTNA
13	Emery-Dreifuss muscular dystrophy 1, X-linked	310300	EMD
14	Fabry disease, cardiac variant	301500	GLA
15	Arrhythmogenic right ventricular dysplasia 12	611528	JUP
16	Cardiomyopathy, dilated, 1JJ	615235	LAMA4
17	Danon disease	300257	LAMP2
18	Cardiomyopathy, dilated, 1C, with or without LVNC	601493	LDB3
19	Cardiomyopathy, dilated, 1A	115200	LMNA
20	Cardiomyopathy, dilated, 1MM	615396	MYBPC3
21	Atrial septal defect 3	614089	MYH6
22	Cardiomyopathy, dilated, 1S	613426	MYH7
23	Cardiomyopathy, hypertrophic, 10	608758	MYL2
24	Cardiomyopathy, hypertrophic, 8	608751	MYL3
25	Cardiomyopathy, hypertrophic, 1, digenic	192600	MYLK2
26	Cardiomyopathy, hypertrophic, 16	613838	MYOZ2
27	Cardiomyopathy, dilated, 1CC	613122	NEXN
28	Arrhythmogenic right ventricular dysplasia 9	609040	PKP2
29	Cardiomyopathy, dilated, 1P	609909	PLN
30	Cardiomyopathy, hypertrophic 6	600858	PRKAG2
31	Cardiomyopathy, dilated, 1DD	613172	RBM20
32	Arrhythmogenic right ventricular dysplasia 2	600996	RYR2
33	Cardiomyopathy, dilated, 1L	606685	SGCD
34	Barth syndrome	302060	TAZ
35	Cardiomyopathy, hypertrophic, 25	607487	TCAP

36	Arrhythmogenic right ventricular dysplasia 5	604400	TMEM43
37	Cardiomyopathy, dilated, 1Z	611879	TNNC1
38	Cardiomyopathy, dilated, 2A	611880	TNNI3
39	Cardiomyopathy, dilated, 1D	601494	TNNT2
40	Cardiomyopathy, dilated, 1Y	611878	TPM1
41	Cardiomyopathy, dilated, 1G	604145	TTN
42	Amyloidosis, hereditary, transthyretin-related	105210	TTR
43	Cardiomyopathy, dilated, 1W	611407	VCL