

# 7<sup>th</sup> Advances in Heart Failure 2024

10 e 11 de Outubro

FACULDADE DE MEDICINA DA UNIVERSIDADE DO PORTO

## Fatores de risco não modificáveis para a IC: Que caminho para uma abordagem personalizada e precoce? GENÉTICA

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Health Research Network  
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## Introduction

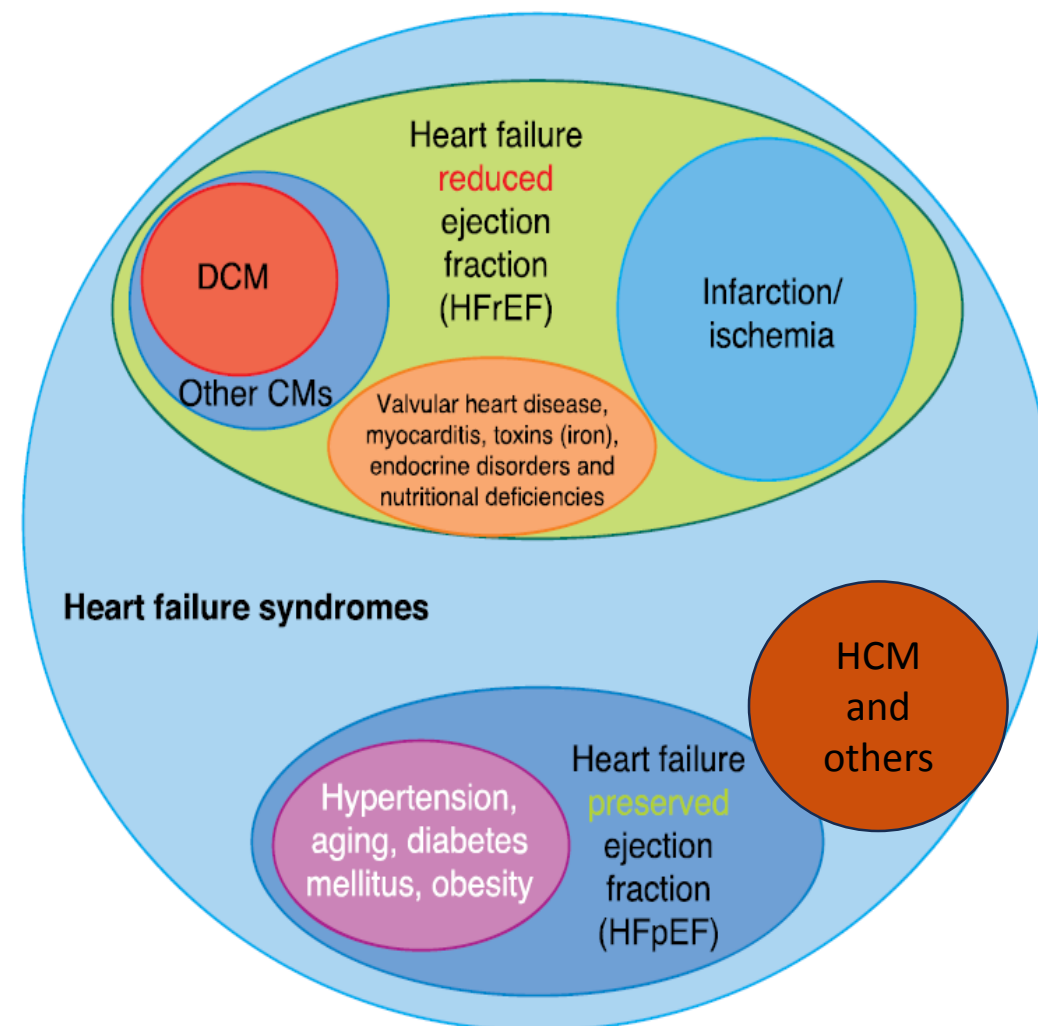
- **Heart failure (HF)** affects globally 40 million people and is a major cause of mortality worldwide.
- In Europe:
  - Incidence: 30/10 000 person-years in all age-groups; 50/10 000 person-years in adults
  - Prevalence: 1–3% of adults
- In Portugal:
  - Prevalence: 16.54% in adults over 50 years
- **High disease burden and costs**

McDonagh TA, Eur Heart J 2021

Borlaug BA, JACC 2023

Kittleson MM, JACC 2023

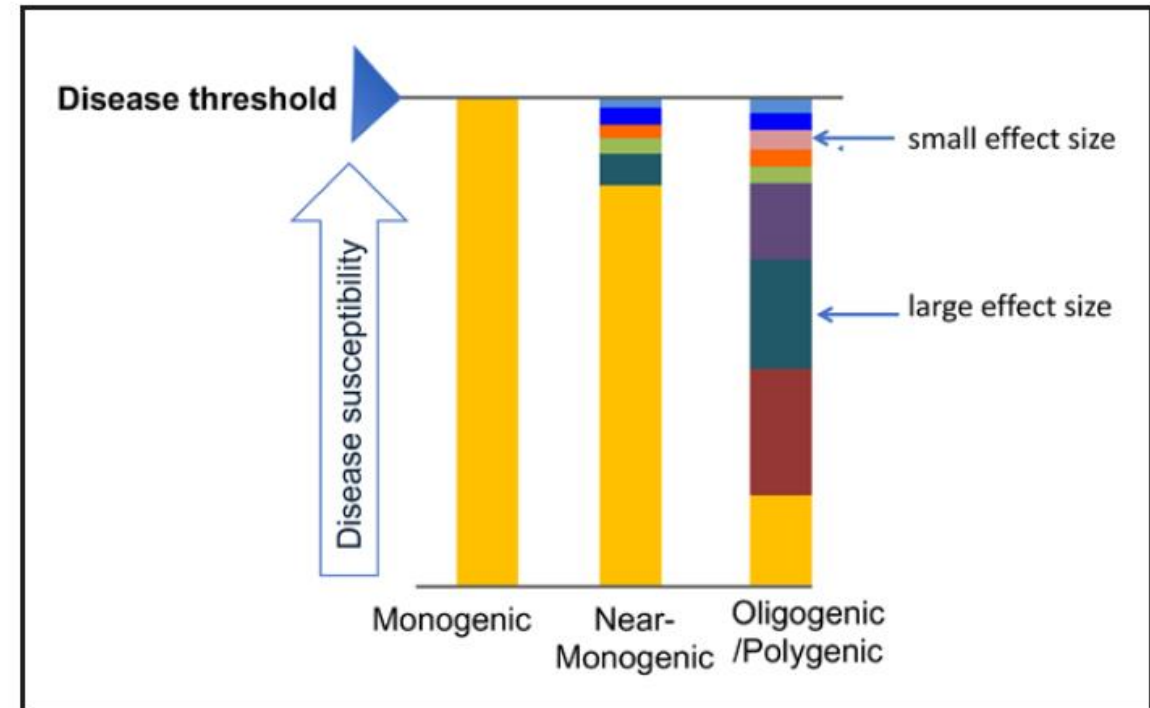
PORTHOS study





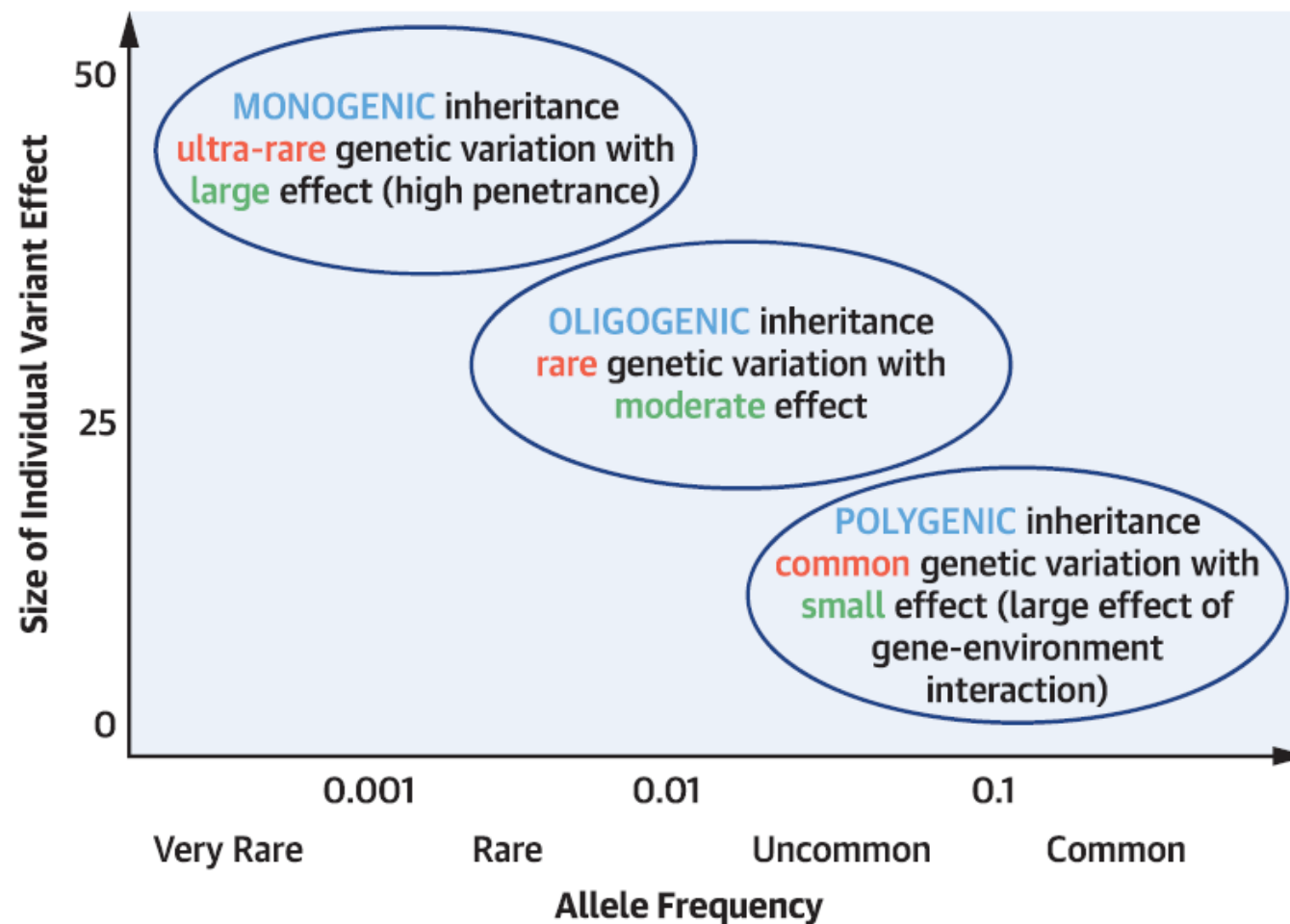
## Genetics in cardiovascular diseases

- **Mendelian genetic** in which **one gene** is associated with the disease, is characterized by **locus and allelic heterogeneity** and highly **variable** intra- and interfamilial **expressivity** with **incomplete/age-related clinical penetrance** (result of modifier genes, epigenetic effects, posttranscriptional and post-translational modifications, and environmental effects)
- **Genetic polymorphisms (SNPs)** modulate the maladaptive pathophysiological response to pathophysiological stressors, disease evolution and the response to therapy, with small effect size.

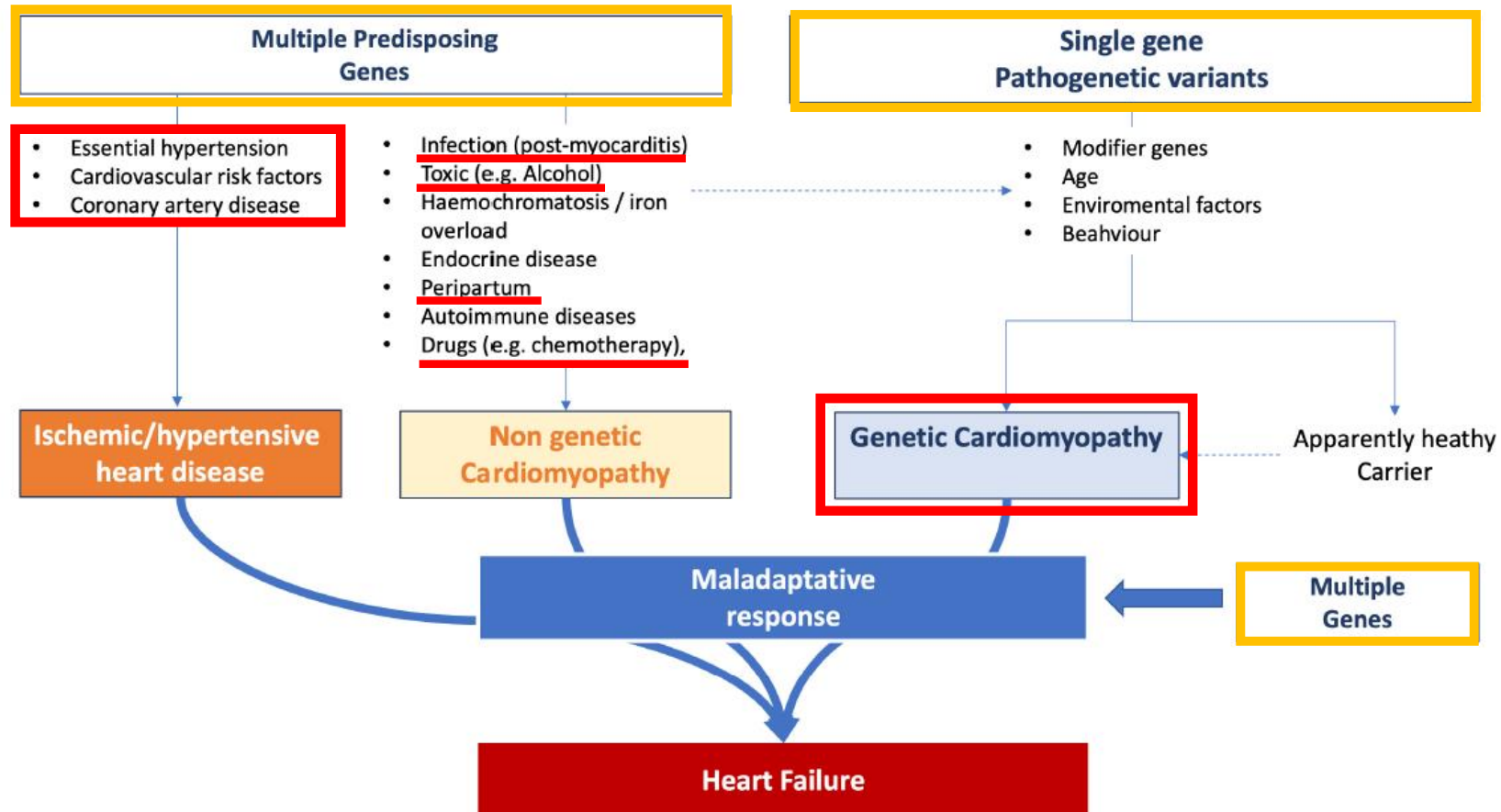


Cerrone M, Circulation 2019

## Genetics in cardiovascular diseases



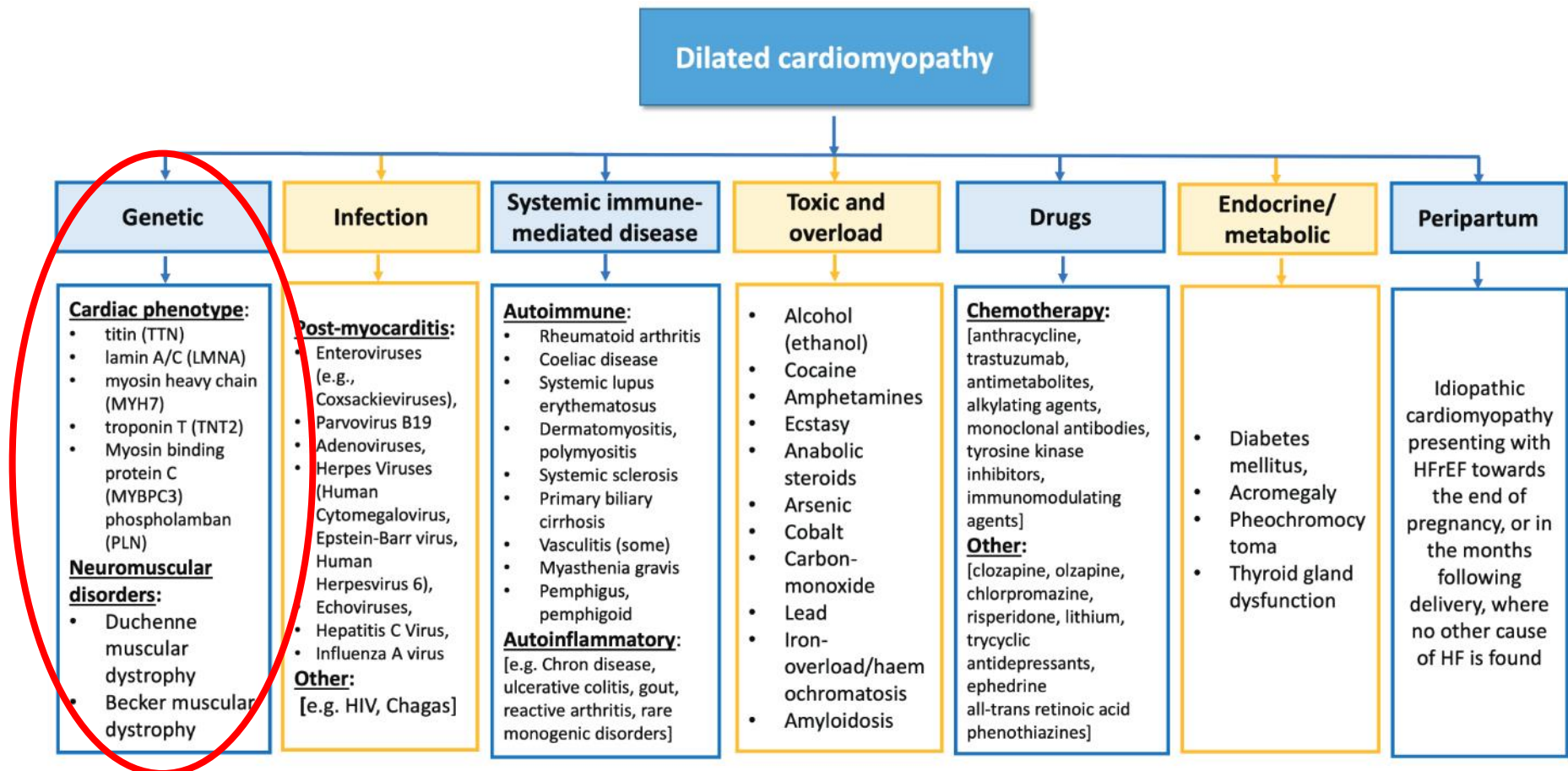
## Influence of genetic background on heart failure onset and progression



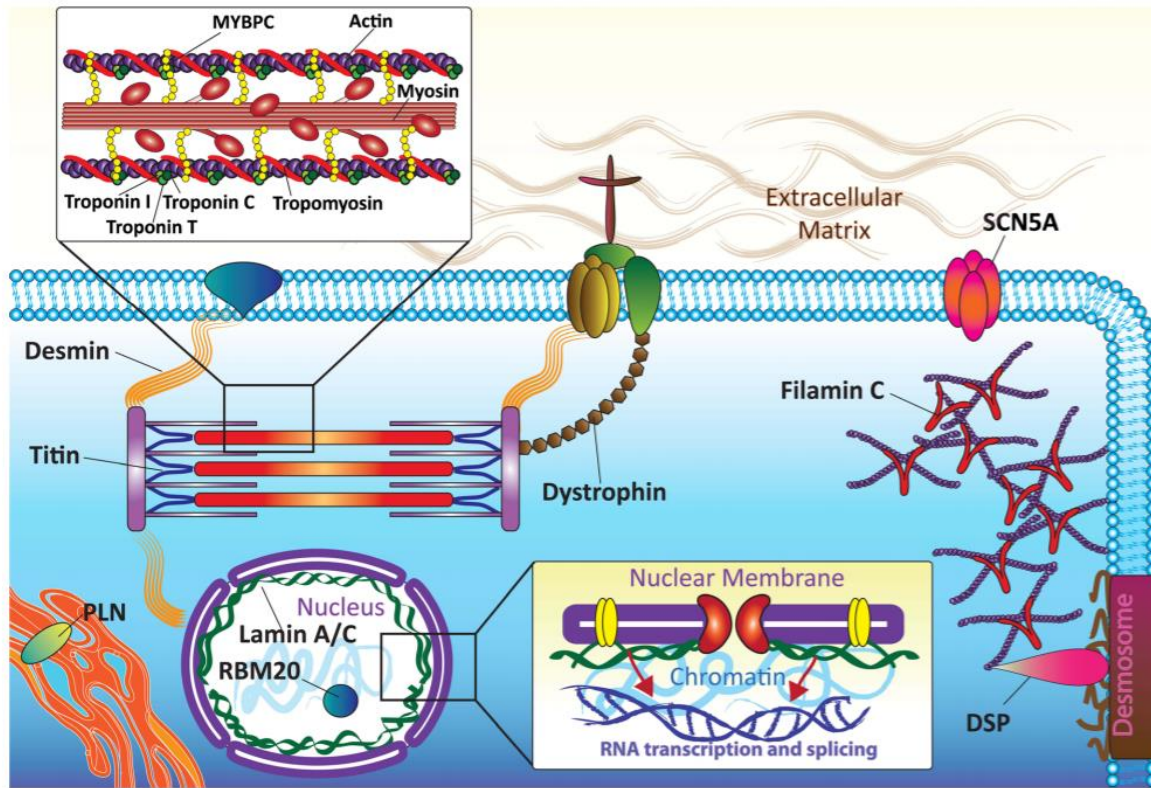


## Cardiomyopathies: Dilated Cardiomyopathy

- DCM has an estimated prevalence of 2:500 and is a leading cause of heart transplant



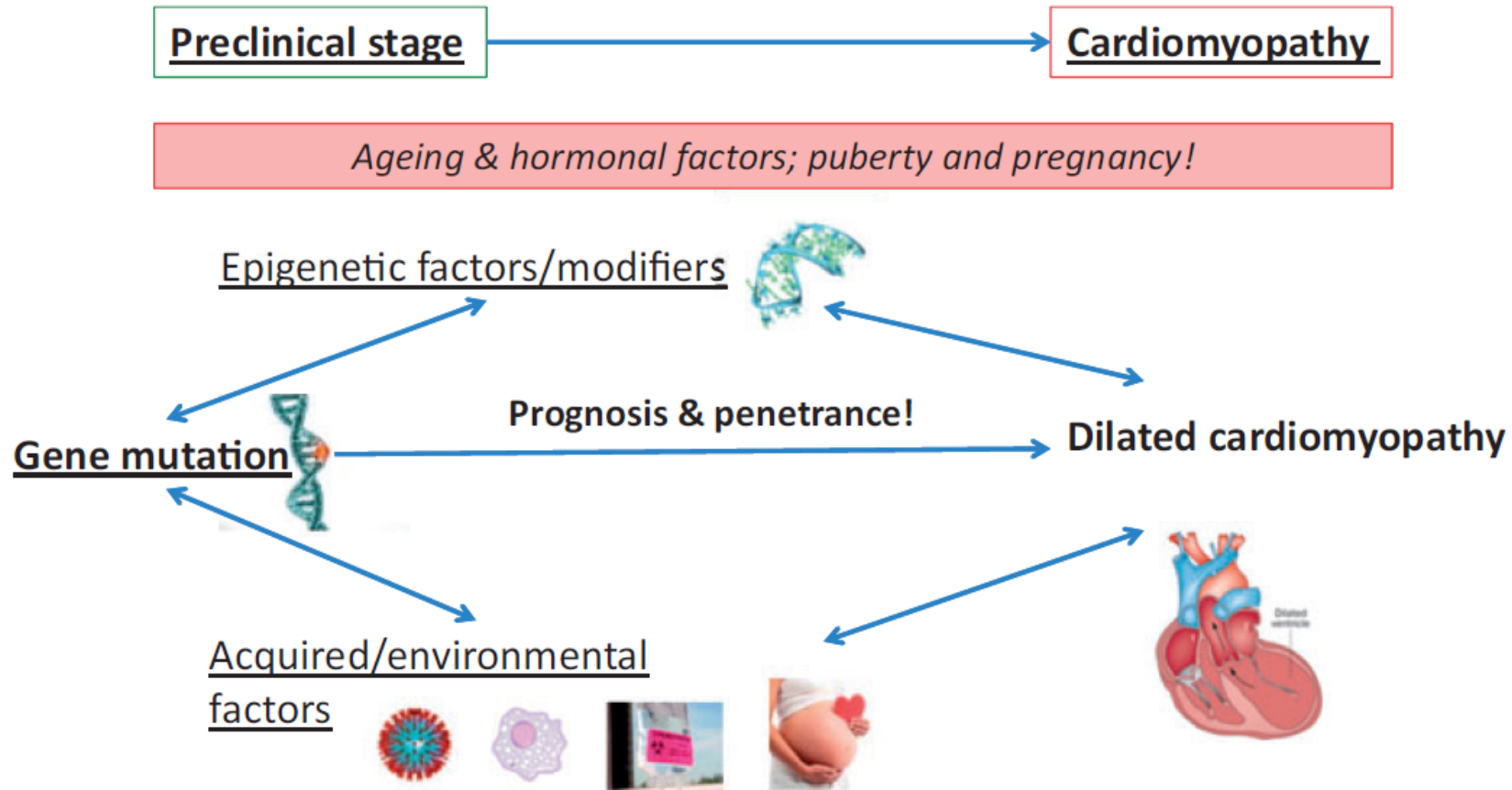
# Genetic Dilated Cardiomyopathy



Sarcomere	ACTC	Actin		
	MYH6	a-myosin heavy chain		
	<b>MYH7*</b>	<b>b-myosin heavy chain</b>	<b>Autosomal Dominant</b>	<b>4% Familial DCM</b>
	<b>MYPN</b>	<b>Myopalladin</b>	<b>Autosomal Dominant</b>	<b>2% Familial DCM</b>
	<b>MYBPC3</b>	<b>Myosin-binding protein C</b>	<b>Autosomal Dominant</b>	<b>2% Familial DCM</b>
	<b>TNNT2*</b>	<b>Troponin T</b>	<b>Autosomal Dominant</b>	<b>2% Familial DCM</b>
	TNNC1	Troponin C		
	TNNI3*	Troponin I		
	TPM1	a-tropomyosin		
	Cytoskeleton	ACTN2	a-actinin 2	
SGC		sarcoglycan		
CAV3		Caveolin		
LDB3		Cypher/ZASP		
SYNM		Desmulin		
DMD		Dystrophin	X-linked	
FKTN		Fukutin		
ILK		Integrin-linked kinase		
VCL		Metavinculin		
NEXN		Nexilin		
Sarcomeric Reticulum	<b>TTN</b>	<b>Titin</b>	<b>Autosomal Dominant</b>	<b>20-25% Familial DCM</b>
	<b>PLN</b>	<b>Phospholamban</b>	<b>Autosomal Dominant</b>	<b>1% Familial DCM</b>
Ion Channel	<b>SCN5A</b>	<b>Sodium channel type V</b>	<b>Autosomal Dominant</b>	<b>2% Familial DCM</b>
	ABCC9	Sulfonylurea receptor 2A		
Mitochondria	CPT2	Carnitine palmitoyltransferase 2	Mitochondrial	
	mtDNA	Mitochondrial respiratory chain	Mitochondrial	
Heat Shock Protein	TAZ/G4.5	Tafazin		
	<b>BAG3</b>	<b>BaCL2-associated athanogene 3</b>		
Nuclear Membrane	<b>LMNA</b>	<b>Lamin A/C</b>	<b>Autosomal Dominant</b>	<b>6% Familial DCM</b>
	TMPO	Thymopoietin		
Cell Nucleus	EMD	Emerin		
	ANKRD1	Cardiac ankyrin repeat protein		
	EYA4	Eyes absent 4		
	NFKB1	NF-kappa B1		
	PRDM16	PR domain-containing 16		
	ZBTB17	Zinc finger and BTB domain-containing protein 17		
	<b>RBM20</b>	<b>RNA-binding protein 20</b>	<b>Autosomal Dominant</b>	<b>2% Familial DCM</b>
	DES	Desmin		
Desmosome	DSC2	Desmocollin 2		
	DSG2	Desmoglein 2		
	DSP	Desmoplakin		
	PKP2	Plakophilin 2		
	DSP	Desmoplakin		
Extracellular matrix	LAMA2	Laminin-a-2		
	LAMA4	Laminin-a-4		



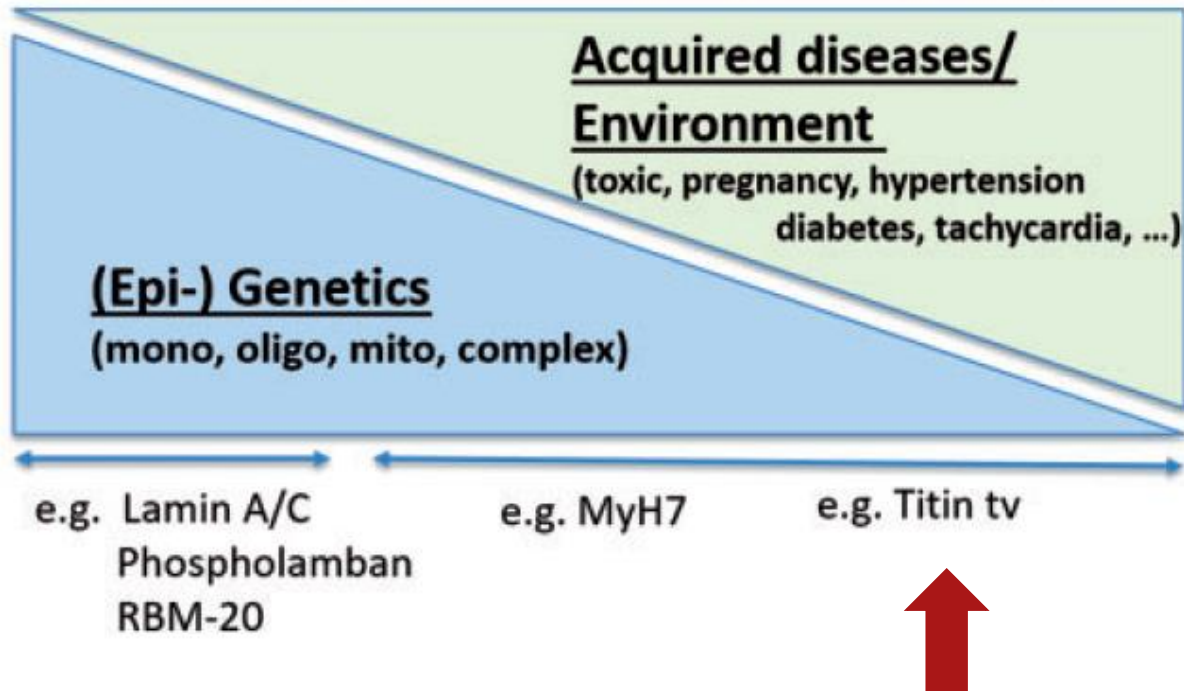
## Dilated Cardiomyopathy





## Dilated Cardiomyopathy

DCM phenotype: gene-environmental interaction



## Shared Genetic Predisposition in Peripartum and Dilated Cardiomyopathies

Ware JS et al. NEJM 2016; 374:233-41

## Genetic Etiology for Alcohol-Induced Cardiac Toxicity

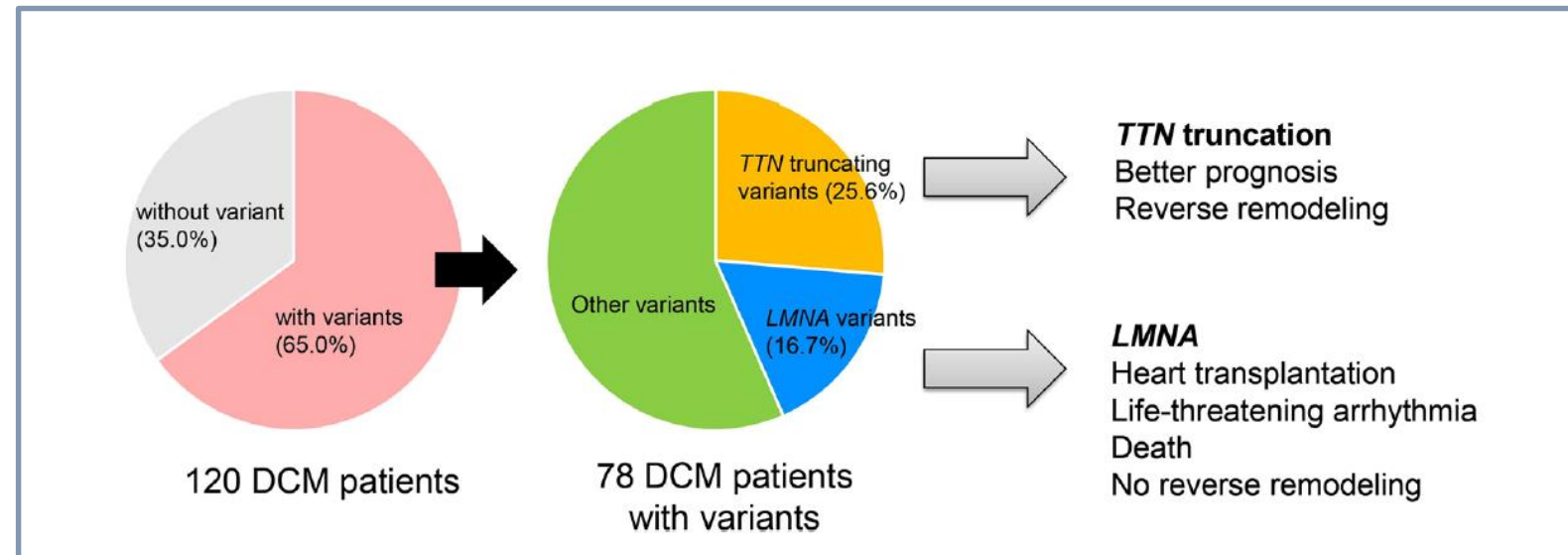
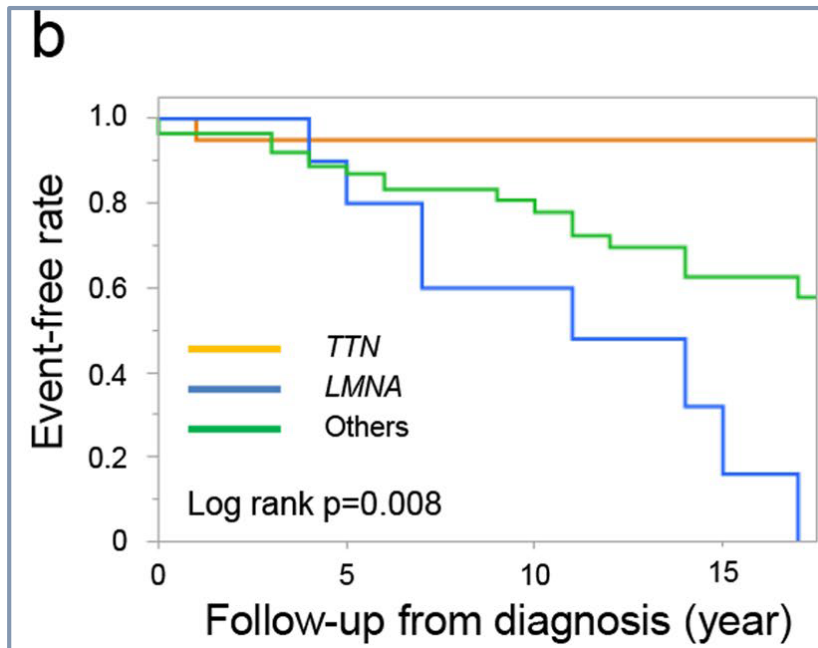
Ware JS et al. JACC 2018; 71:2293-302

## Genetic Variants Associated With Cancer Therapy-Induced Cardiomyopathy

Garcia-Pavia P et al. Circulation 2019; 140:31-41

## Dilated Cardiomyopathy – prognosis and left ventricular reverse remodeling

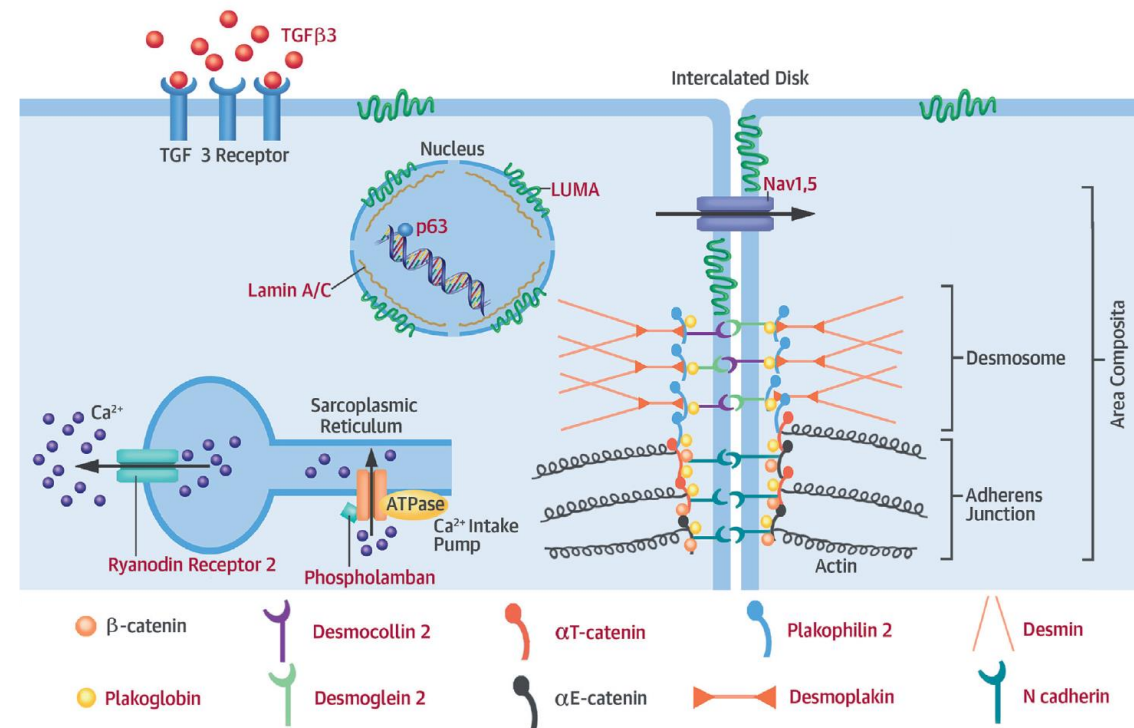
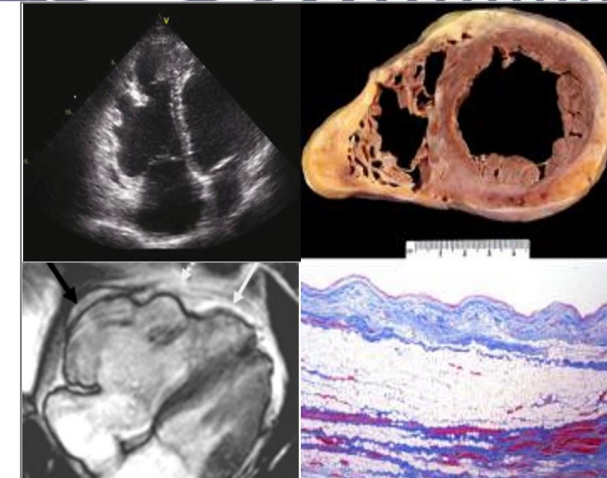
- *TTN*tv carriers have better prognosis and more reverse remodeling than *LMNA* variants carriers



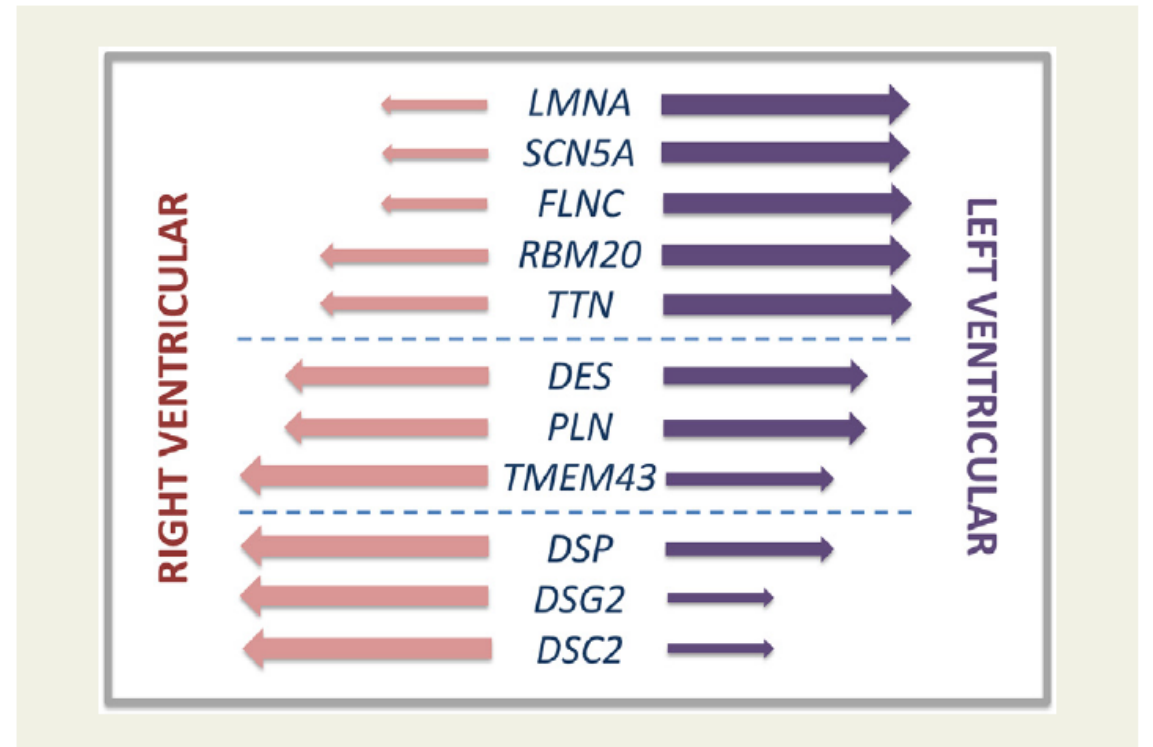
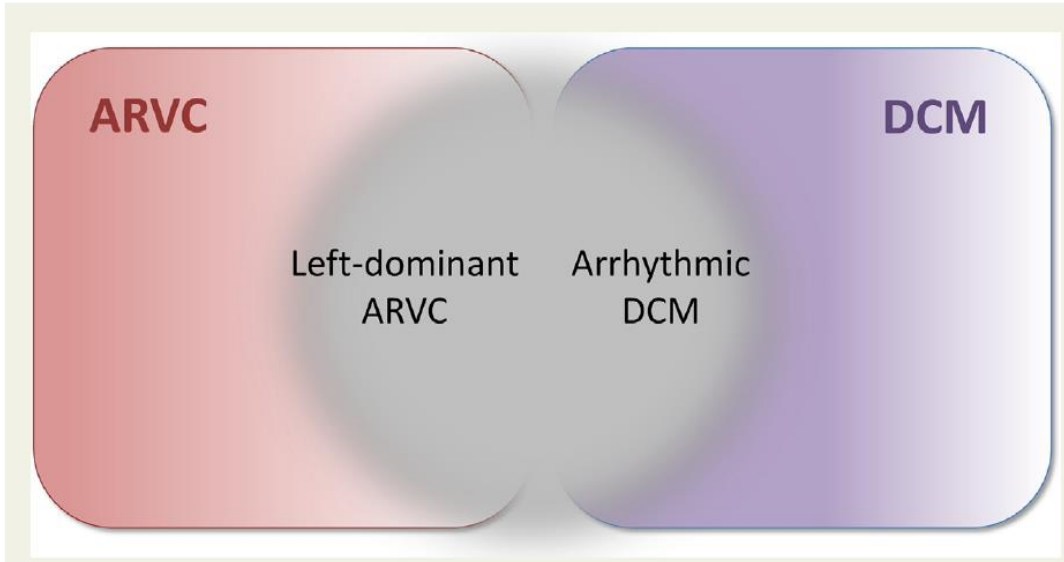


## Arrhythmogenic (right ventricular) cardiomyopathy

- Prevalence 1/2000-5000; Males>Females (3:1)
- Progressive fibrofatty replacement of ventricular myocardium, apoptosis and inflammation
- Frequent sustained ventricular arrhythmias and high risk of sudden cardiac death (10% per year); progressive ventricular dysfunction and heart failure (later in the course of the disease)

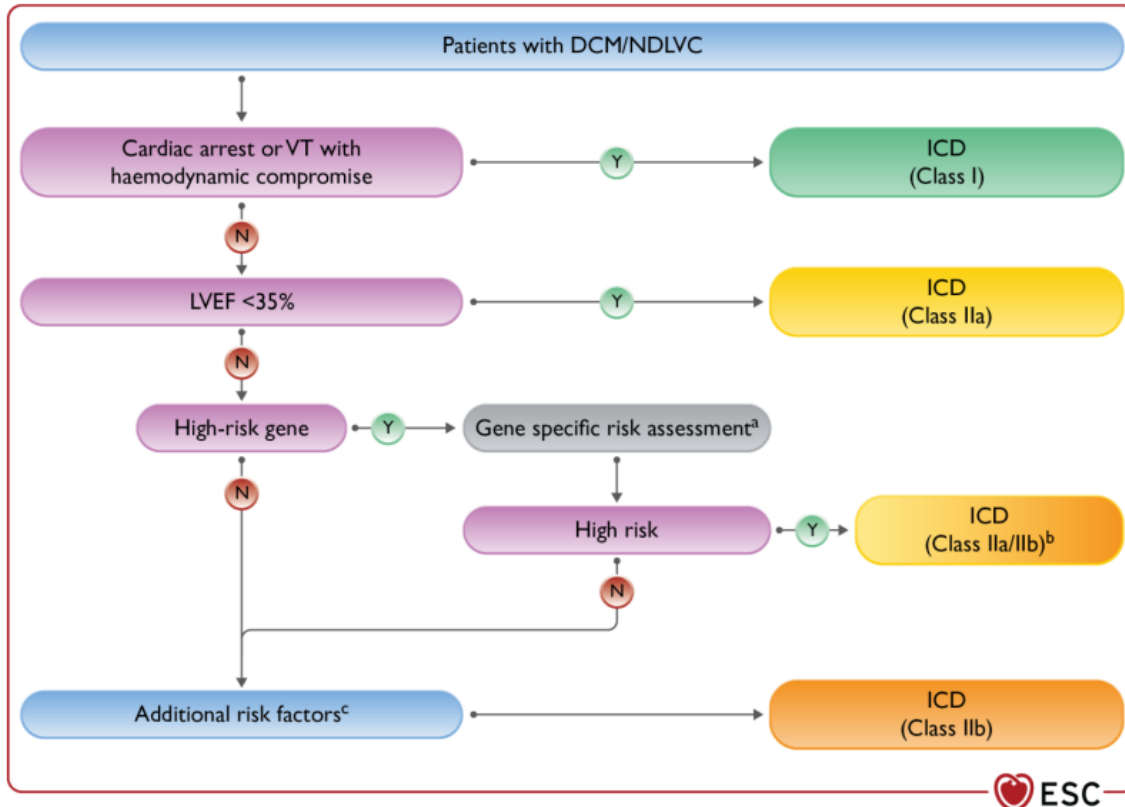


## Arrhythmogenic cardiomyopathies





## Prevention of sudden cardiac death



**Additional risk factors:** include syncope, LGE presence on CMR

### Primary prevention

An ICD should be considered to reduce the risk of sudden death and all-cause mortality in patients with DCM, symptomatic heart failure, and LVEF  $\leq 35\%$  despite  $>3$  months of OMT.

IIa	A
-----	---

The patient's genotype should be considered in the estimation of SCD risk in DCM.

IIa	B
-----	---

An ICD should be considered in patients with DCM with a genotype associated with high SCD risk and LVEF  $>35\%$  in the presence of additional risk factors.

IIa	C
-----	---

An ICD may be considered in selected patients with DCM with a genotype associated with high SCD risk and LVEF  $>35\%$  without additional risk factors.

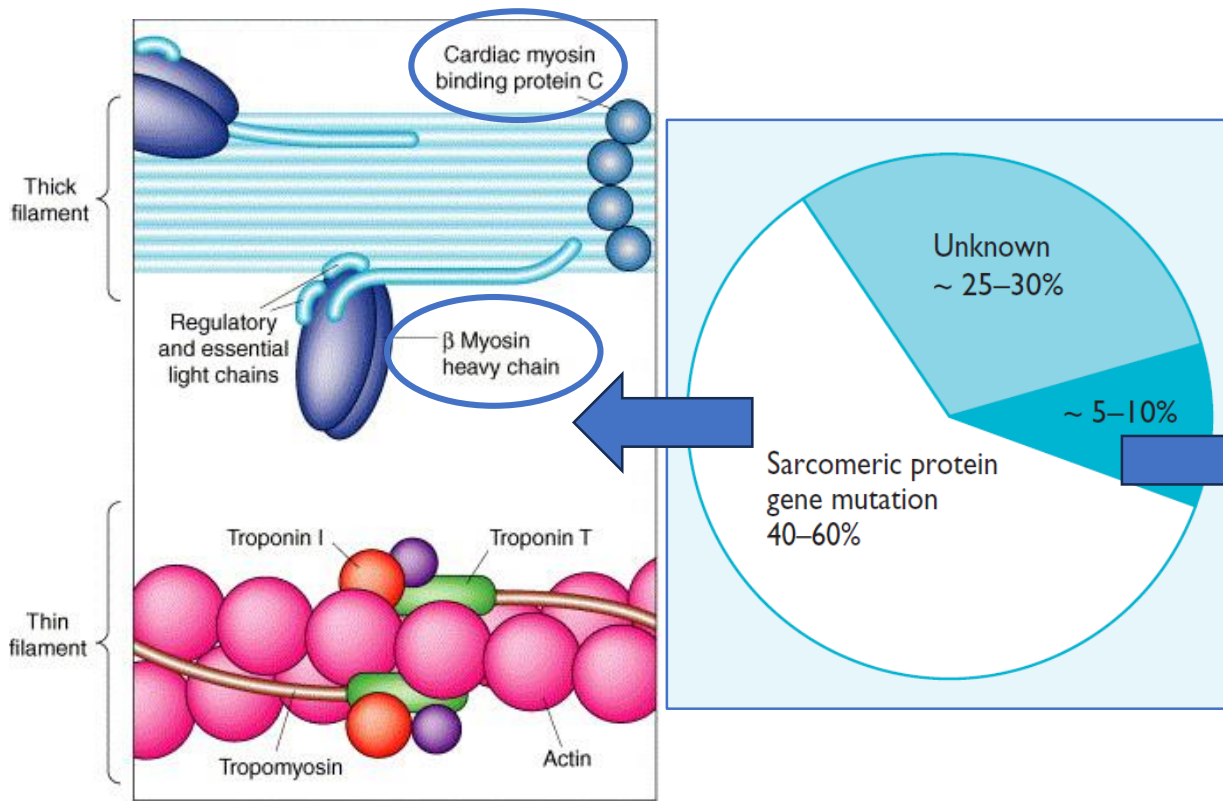
IIb	C
-----	---

An ICD may be considered in patients with DCM without a genotype associated with high SCD risk and LVEF  $>35\%$  in the presence of additional risk factors.

IIb	C
-----	---

Gene	Annual SCD rate	Predictors of SCD
<b>LMNA</b>	5–10%	Estimated 5-year risk of life-threatening arrhythmia using LMNA risk score <a href="https://lmna-risk-vta.fr">https://lmna-risk-vta.fr</a>
<b>FLNC-truncating variants</b>	5–10%	LGE on CMR LVEF $<45\%$
<b>TMEM43</b>	5–10%	Male Female and any of the following: LVEF $<45\%$ , NSVT, LGE on CMR, $>200$ VE on 24h Holter ECG
<b>PLN</b>	3–5%	Estimated 5-year risk of life-threatening arrhythmia using PLN risk score <a href="https://plnriskcalculator.shinyapps.io/final_shiny">https://plnriskcalculator.shinyapps.io/final_shiny</a> LVEF $<45\%$ LGE on CMR NSVT
<b>DSP</b>	3–5%	LGE on CMR LVEF $<45\%$
<b>RBM20</b>	3–5%	LGE on CMR LVEF $<45\%$

# Hypertrophic cardiomyopathy



## • Inborn errors of metabolism

- Glycogen storage diseases:
  - Pompe
  - Danon
- AMP-Kinase (PRKAG2)
- Carnitine disorders
- Lysosomal storage diseases
  - Anderson-Fabry

## • Neuromuscular diseases

- Friedreich's ataxia
- FHLI

## • Mitochondrial diseases

- MELAS
- MERFF

## • Malformation Syndromes

- Noonan
- LEOPARD
- Costello
- CFC

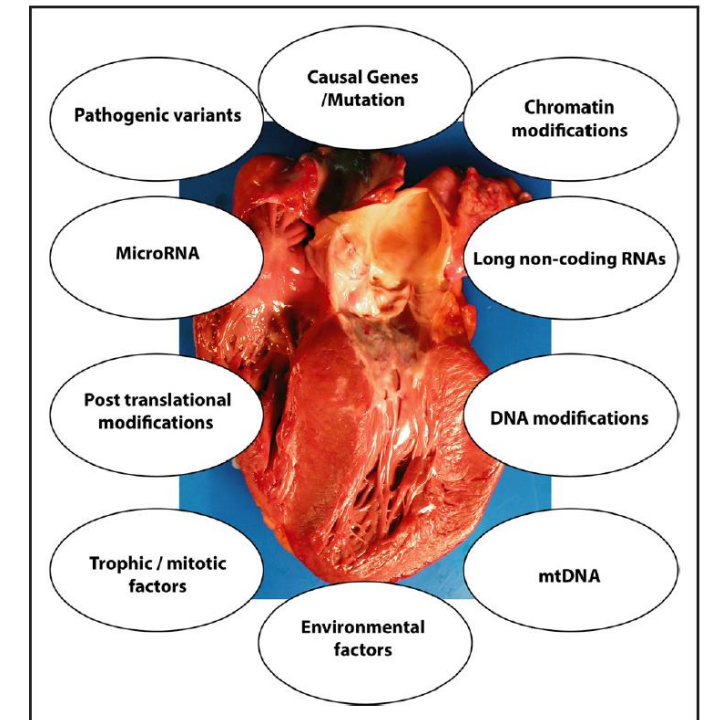
## • Amyloidosis

- Familial ATTR
- Wild type TTR (senile)
- AL amyloidosis

## • Newborn of diabetic mother

## • Drug-induced

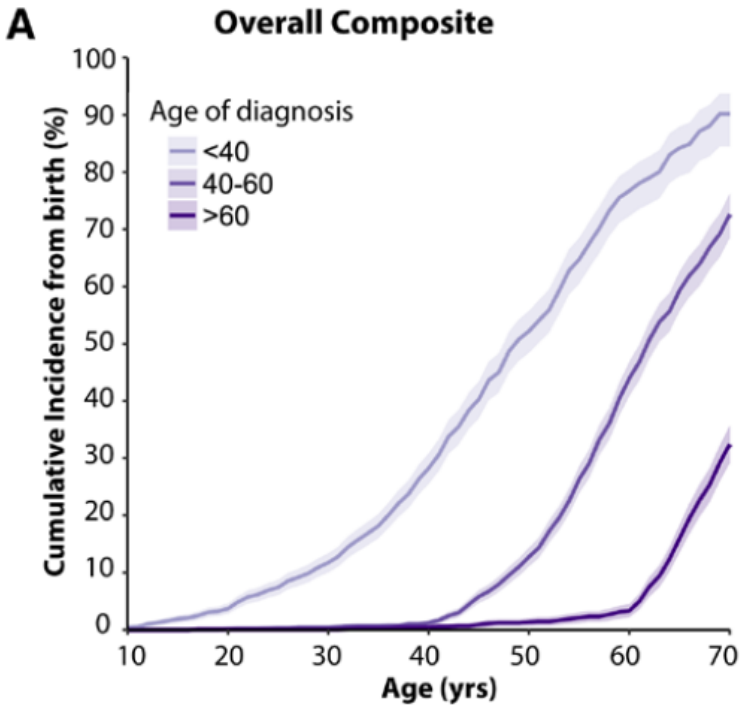
- Tacrolimus
- Hydroxychloroquine
- Steroids





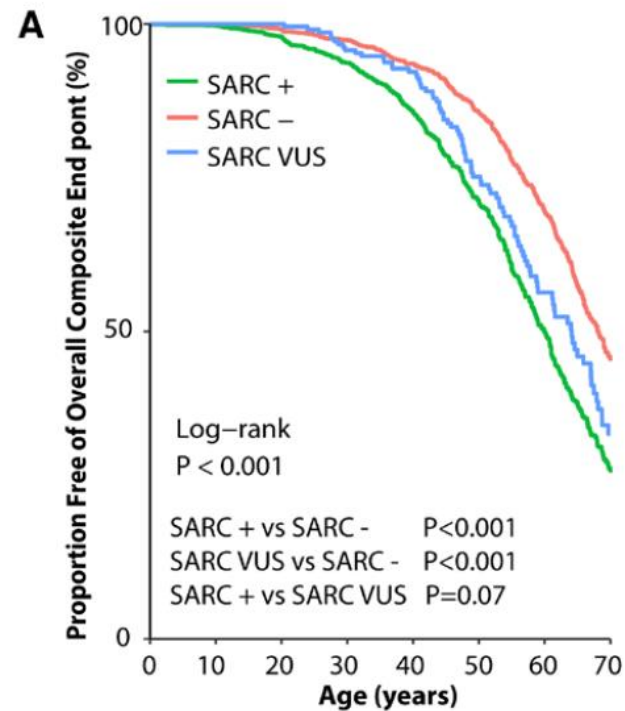
# Genotype and Lifetime Burden of Disease in Hypertrophic Cardiomyopathy

Insights From the Sarcomeric Human Cardiomyopathy Registry (SHaRe)



<40	1614	1424	1068	573	238	55	9
40-60	1659	1658	1653	1643	1191	411	85
>60	909	908	908	905	897	879	452

Patients at risk



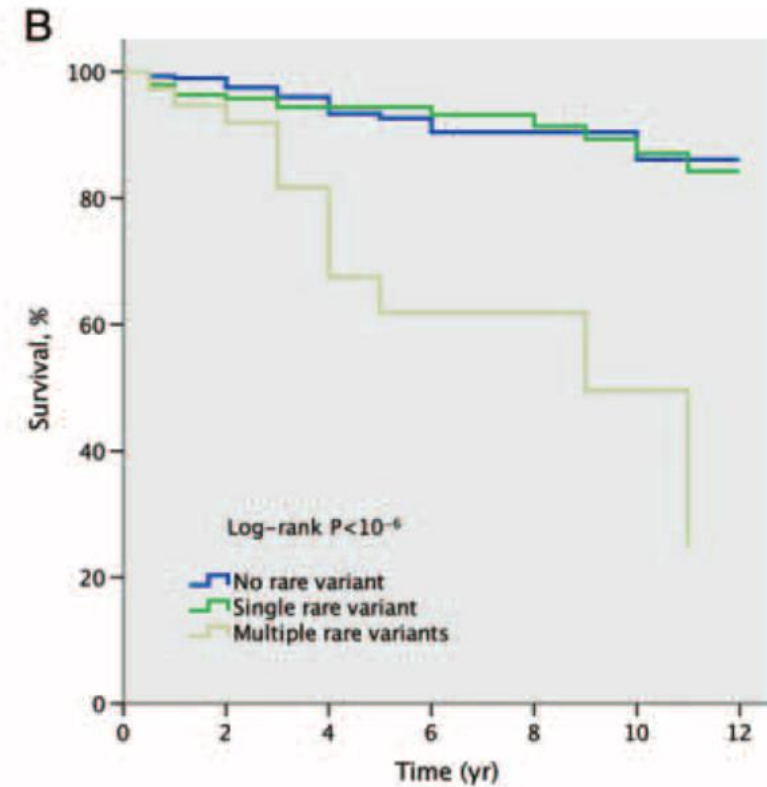
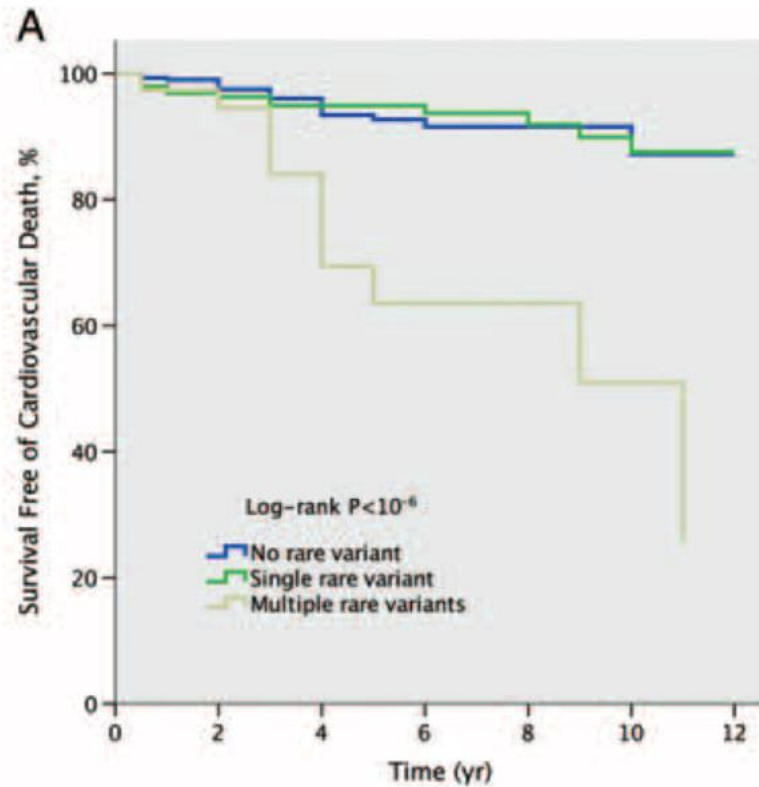
SARC +	1254	1244	1164	1016	800	522	248	78
SARC -	1199	1196	1159	1085	972	786	480	206
SARC VUS	241	237	225	197	176	115	60	23

Patients at risk

- Cumulative incidence of adverse end-points is higher in patients with earlier diagnosis
- Patients without sarcomeric variants have better prognosis than patients with VUS or pathogenic variants in sarcomeric genes.

## Malignant effects of multiple rare variants in sarcomere genes on the prognosis of patients with hypertrophic cardiomyopathy

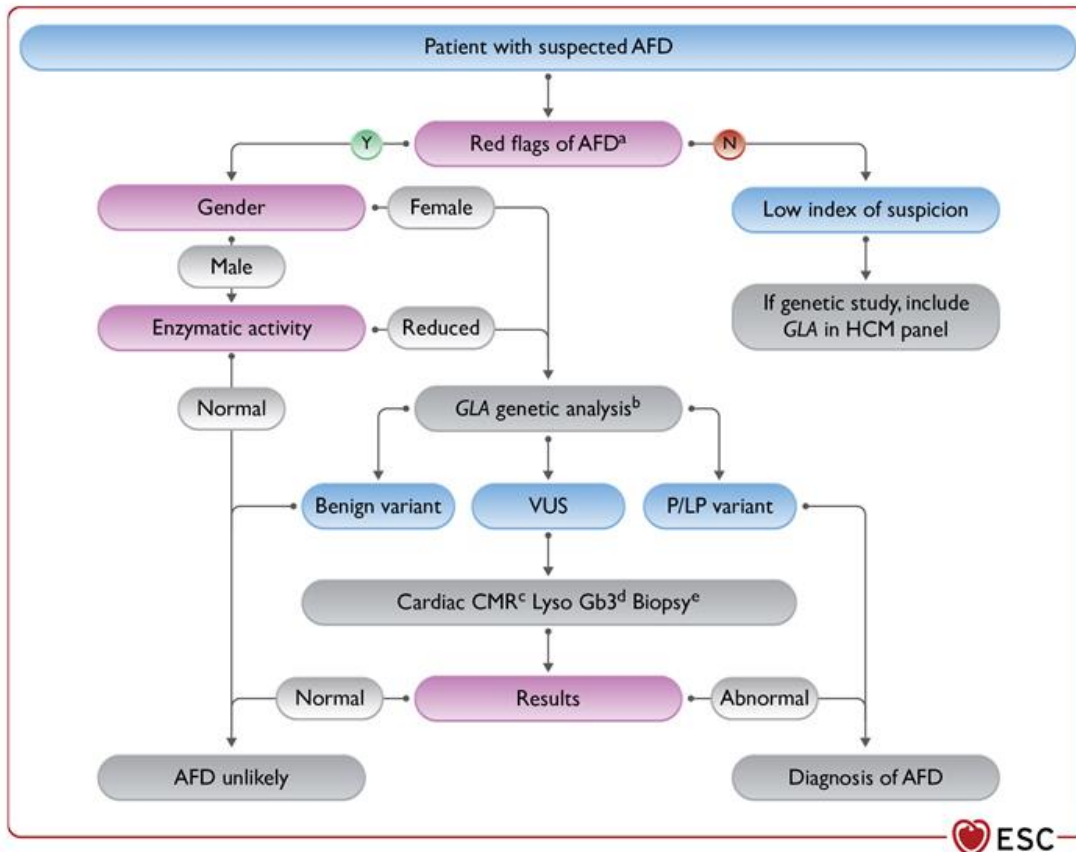
- Up to 5% of HCM patients present with multiple genetic variants



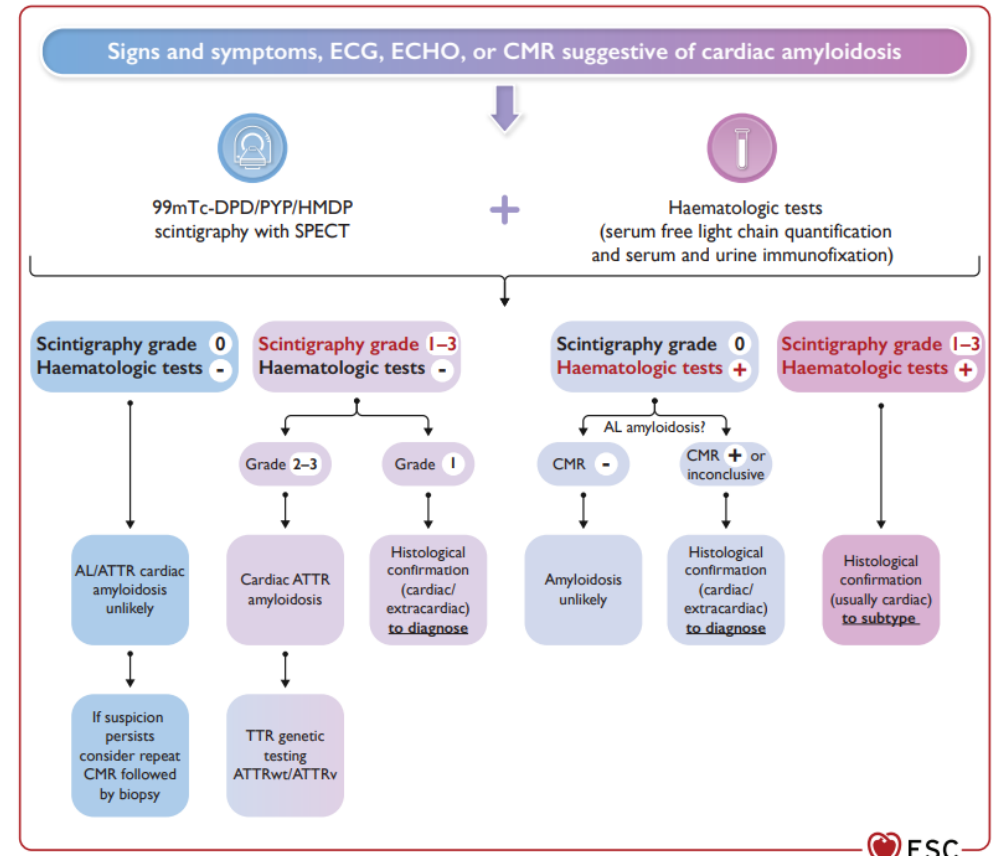


# Hypertrophic cardiomyopathy: phenocopies with specific treatment

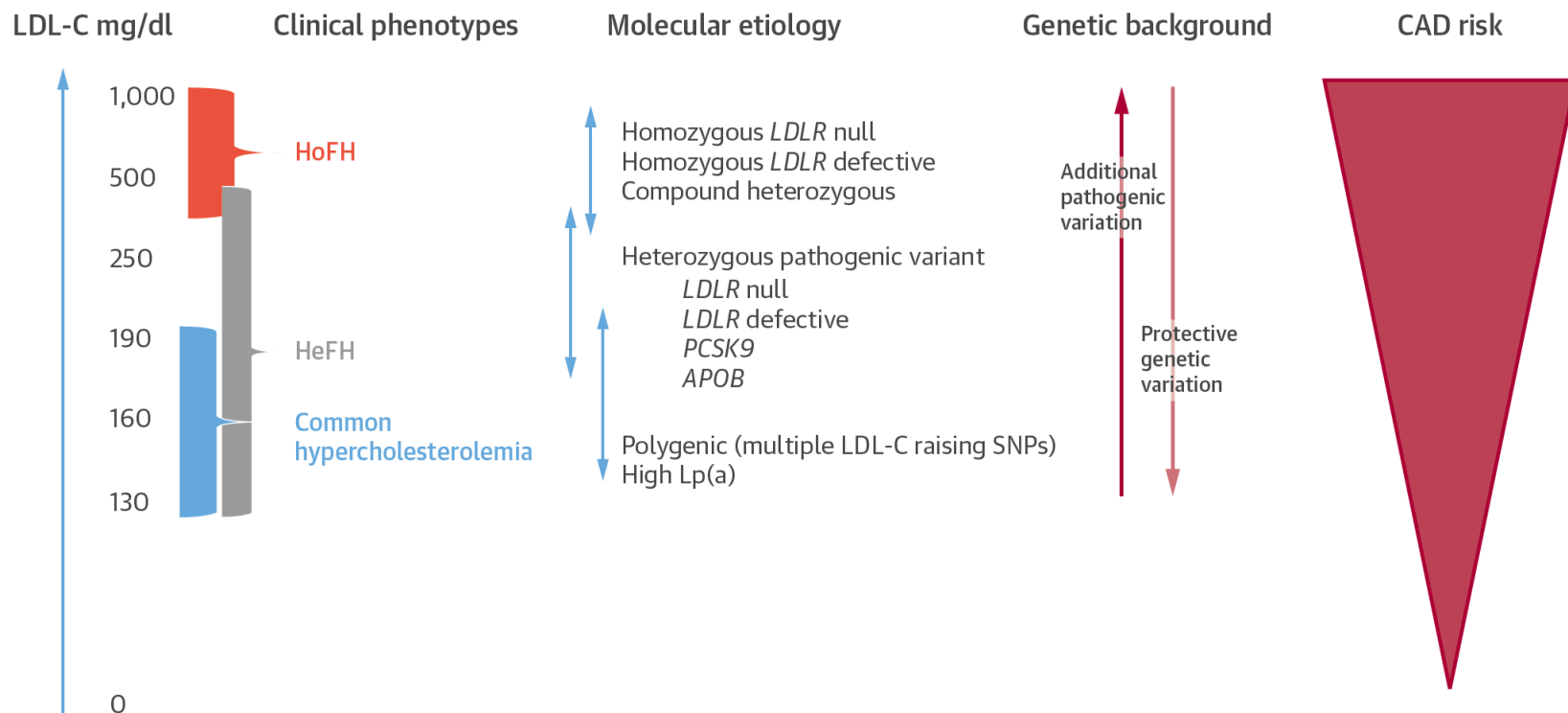
## Anderson – Fabry Disease



## Cardiac amyloidosis (TTR)



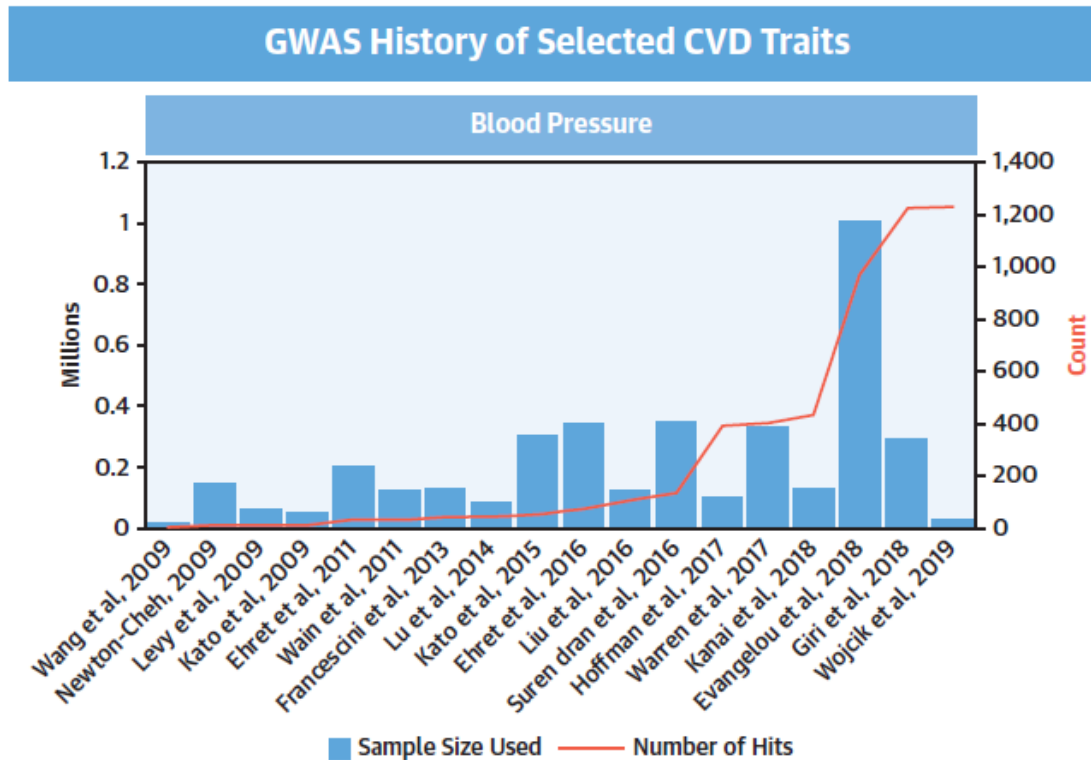
## Cardiovascular risk factors and coronary disease: Familial Hypercholesterolemia



- Prevalence 1:220
- Potentially fatal, treatable and underdiagnosed
- Genetic testing:
  - Definite diagnosis
  - Proper treatment, earlier and increased adherence
  - Familial screening
  - Better risk stratification



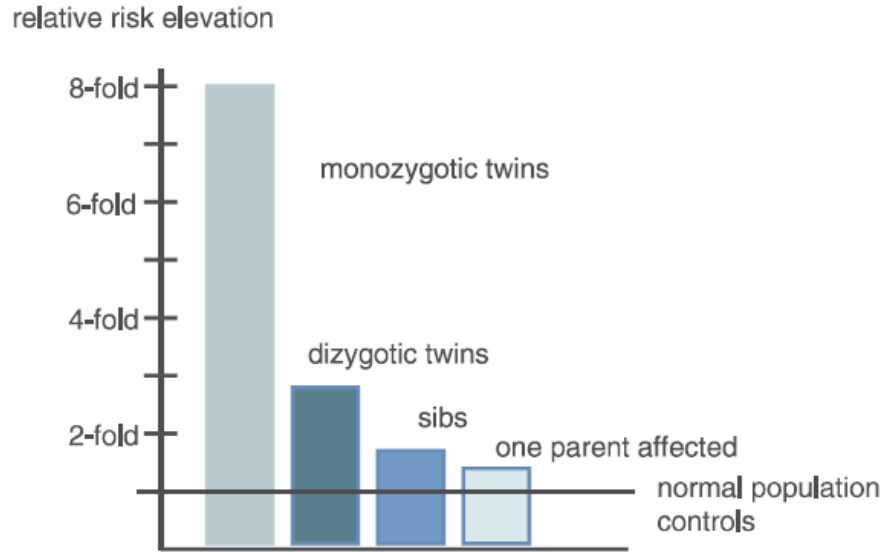
## Cardiovascular risk factors and coronary disease: Arterial hypertension



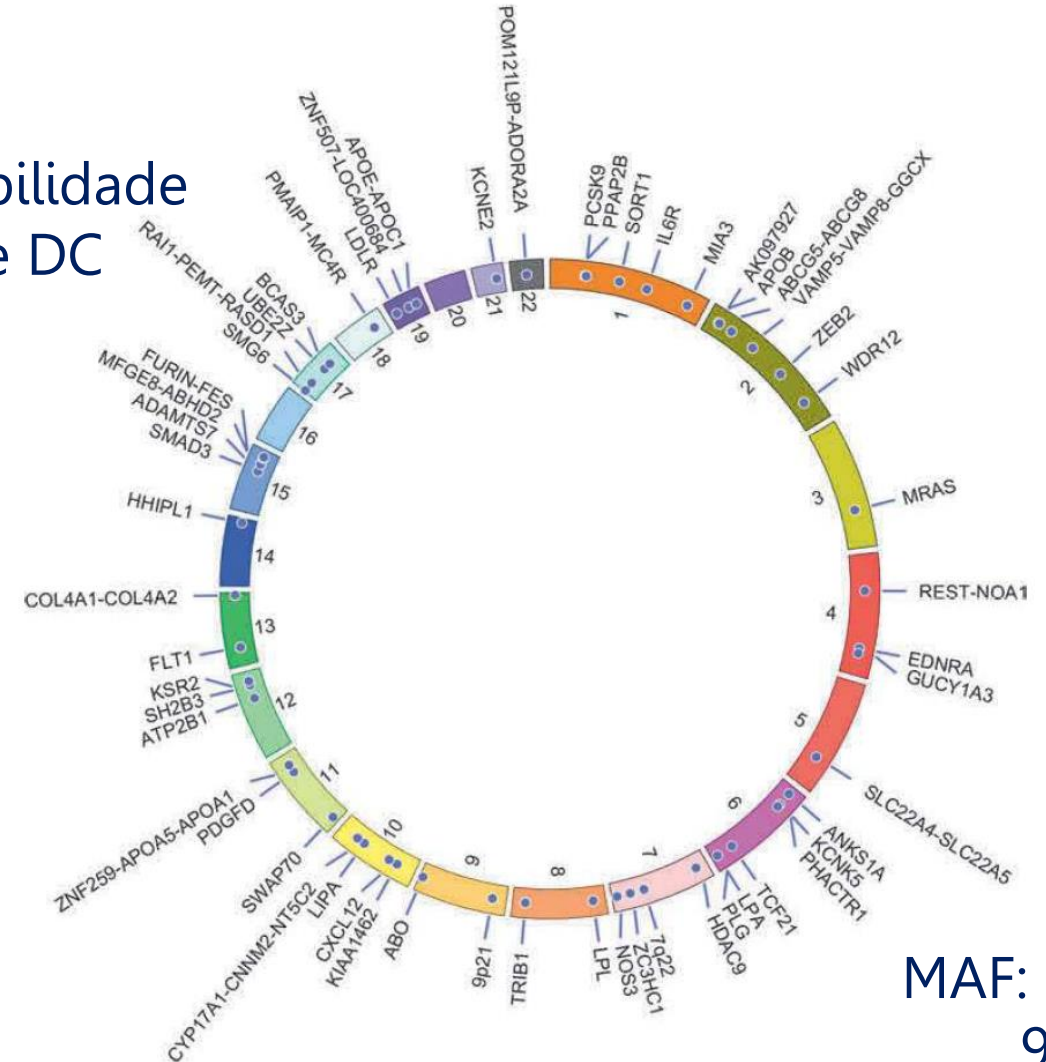
- Blood pressure is highly heritable, with heritable factors accounting for 30% to 50% of a given individual's blood pressure.
- There are more than 505 independent loci associate with one or more blood pressure traits.

## (Premature) Coronary Disease

GWAS  
~15%  
hereditabilidade  
de EAM e DC



**Fig. 22.1** The relative increase in the risk of myocardial infarction (MI)/coronary artery disease (CAD) is shown in relation to different familial backgrounds. The risk for monozygotic (MZ) and dizygotic (DZ) twins is based on the hypothesis that the partner twin died of MI at the age of 55 years



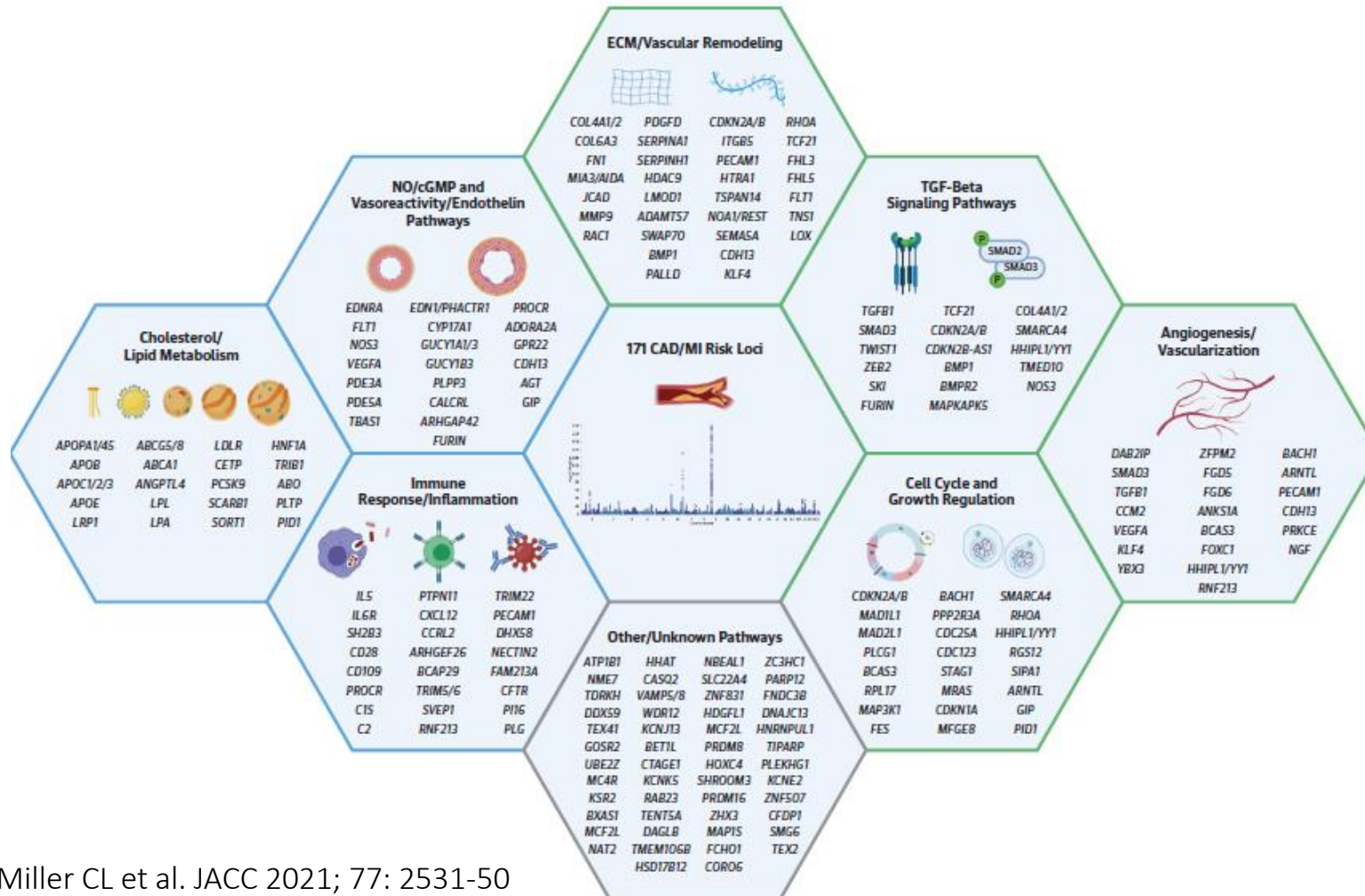
MAF: 10-90%

OR: 1.05-1.30



## (Premature) Coronary Disease

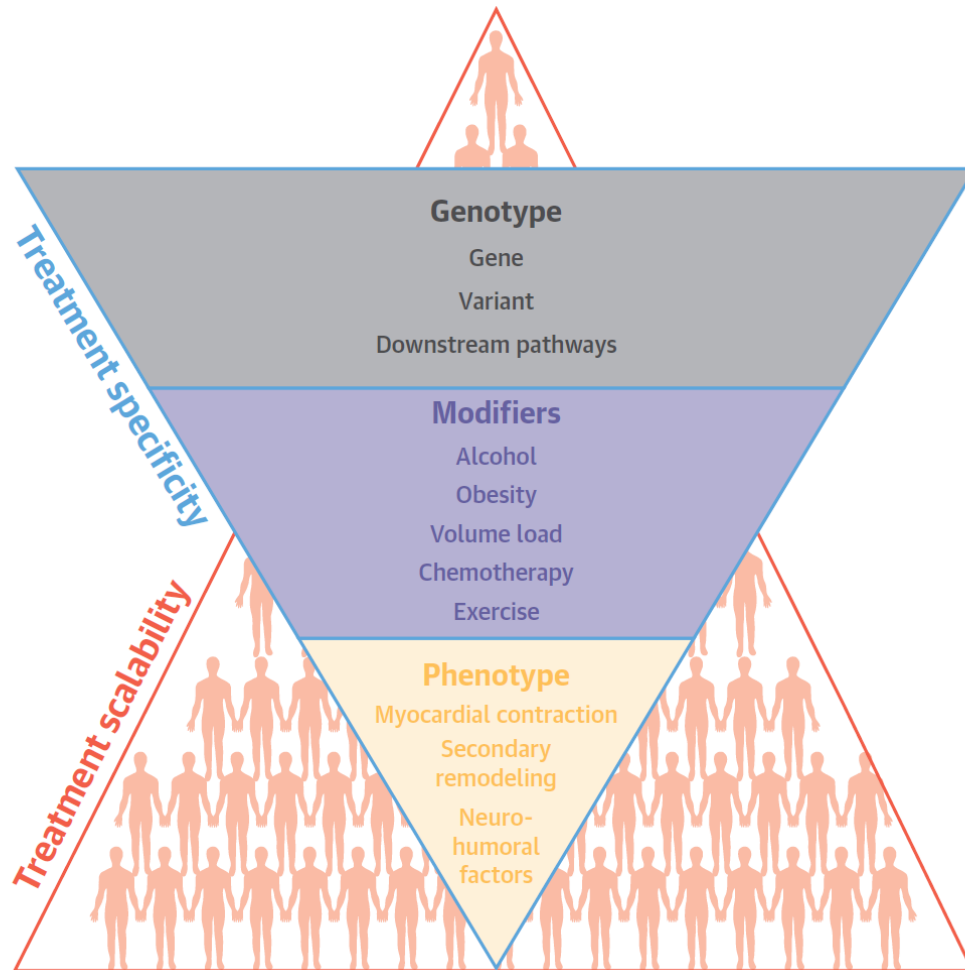
### - Annotated Genes and Pathways Associated With CAD and/or MI



- There are at least 168 reported genome-wide significant loci and >400 suggestive loci associated with CAD causality
- Polygenic risk scores

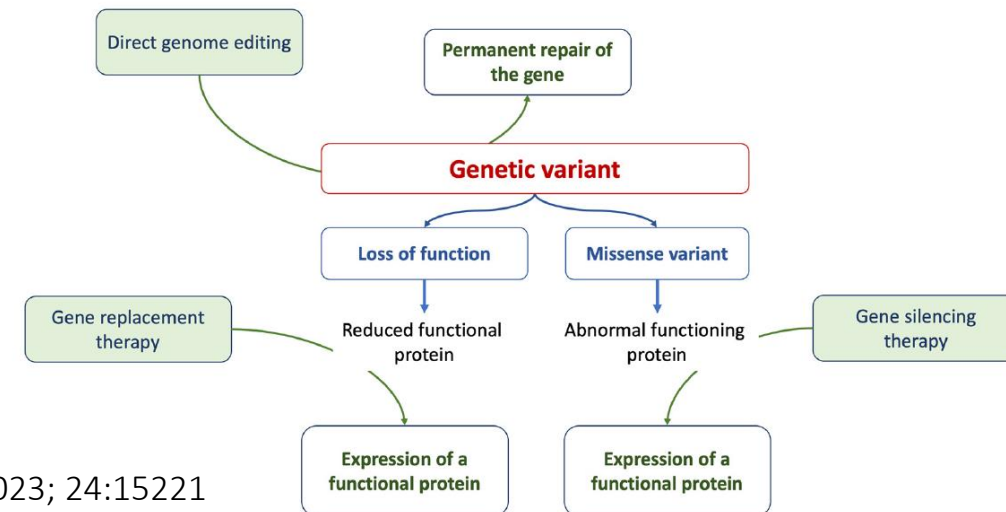


## Genotype-based therapy – Precision Medicine



- Improvement of clinical consequences: improved sudden death risk stratification
- Target the molecular consequences of a specific gene mutation (ex. replacement therapies)
- Early implementation of preventive measures
- Address the genetic alteration

Fatkin D et al. JACC 2019; 74:2921-38

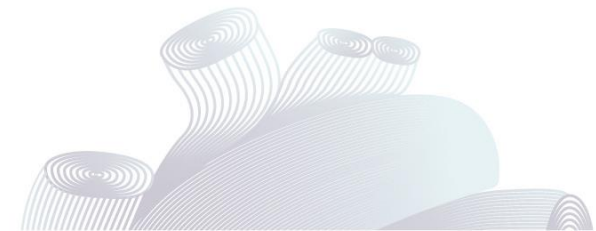
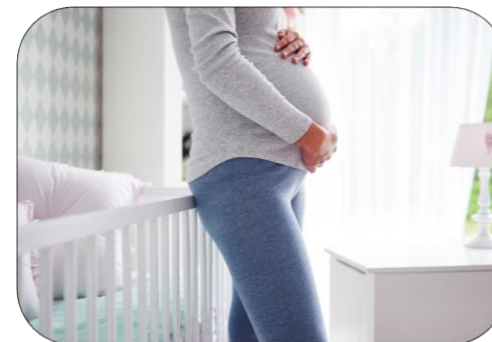


Palmieri J et al. Int J Mol Sci 2023; 24:15221

## Personalized and early approach

### FOR THE PATIENT

- More refined diagnosis
- Individual risk assessment
- Preventive measures and lifestyle modifications (exercise and reproductive issues)
- Specific therapies

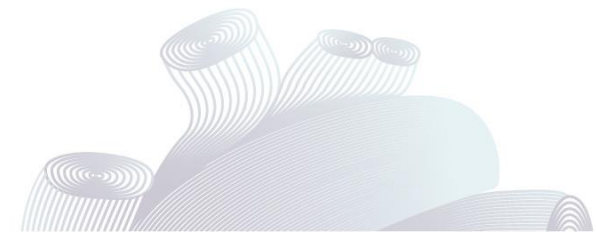




## Personalized and early approach

### FOR THE FAMILY

- Early diagnosis of the disease in asymptomatic
- Identifying at-risk family members
  - Genotype positive-phenotype negative family member need regular screening (individualized plans)
    - Early detection of the disease and management of incipient disease
    - Sports
    - Reproductive issues
- Genetic counseling and psychological support



## TAKE-HOME MESSAGES

- Heart failure is a major health burden
- Up 30-40% might be attributable to genetic factors
- Knowledge of genetic background and gene-to-gene, epigenetics and ambiental interactions allows:
  - Early diagnosis
  - Improved individual risk assessment
  - Possibility of targeted preventive measures (increased health monitoring, early therapeutic interventions, lifestyle modifications) and specialized diagnostic procedures and therapeutics
  - Improved family management



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