

Sudden risk prevention in NICM: a multiparametric approach

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***Centre for Diagnosis and Management of Cardiomyopathies.
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and University of Trieste***

DISCLOSURES

NONE RELATED TO THE PRESENT PRESENTATION

KARDIGAN; BAYER; PFIZER (consultancy)

***GENERAL (Support for attendance to International Meetings;
Fees at meetings and Advisory Boards):***

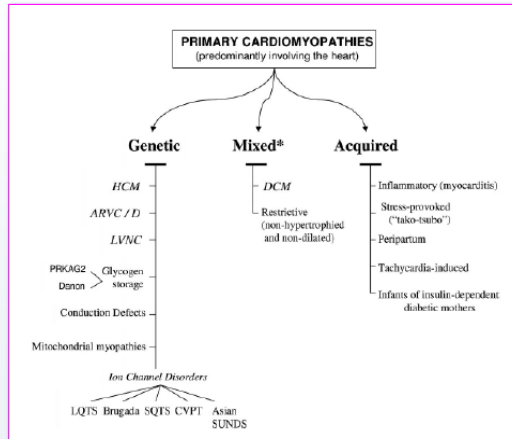
- **ALNYLAM**
- **BAYER**
- **PFIZER**
- **NOVONORDISK**
- **ASTRA ZENECA**



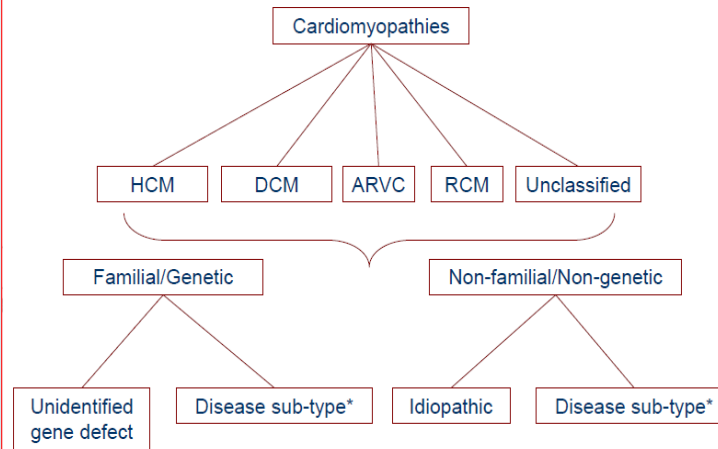
Once upon a time....a long journey

AHA Scientific Statement

Contemporary Definitions and Classification of the Cardiomyopathies



Maron BJ et al. Circulation 2006;113:1807-16



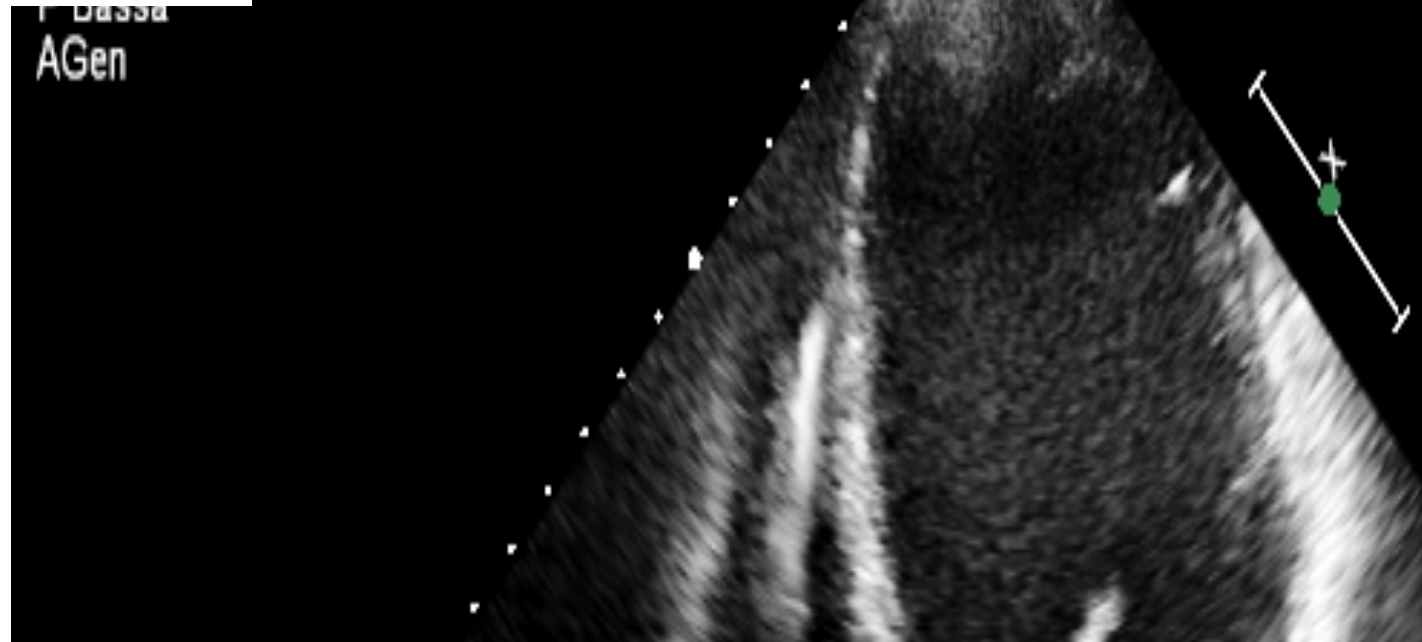
European WG on Myocardial and Pericardial Diseases (Elliott P et al. HJ 2007)

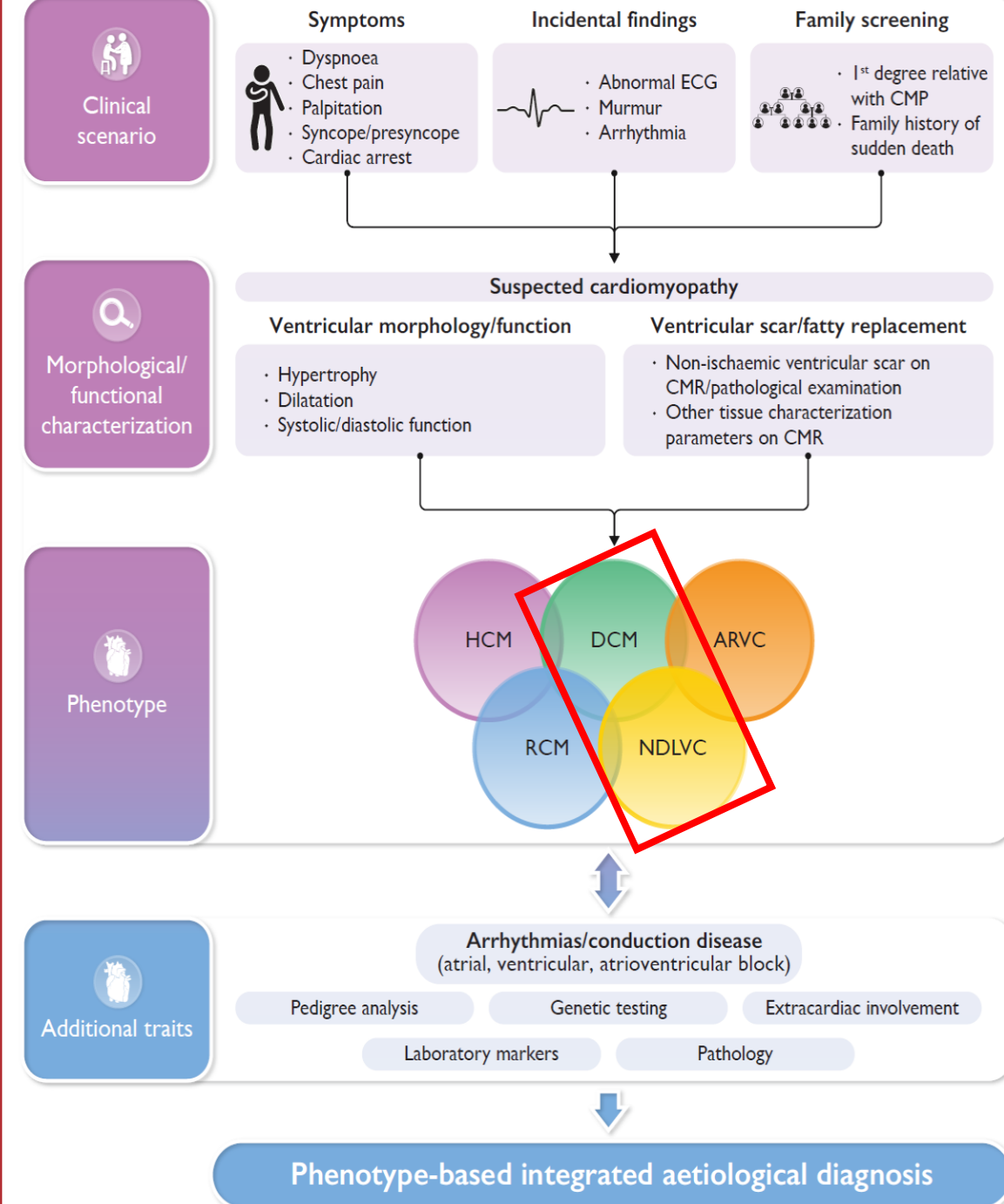
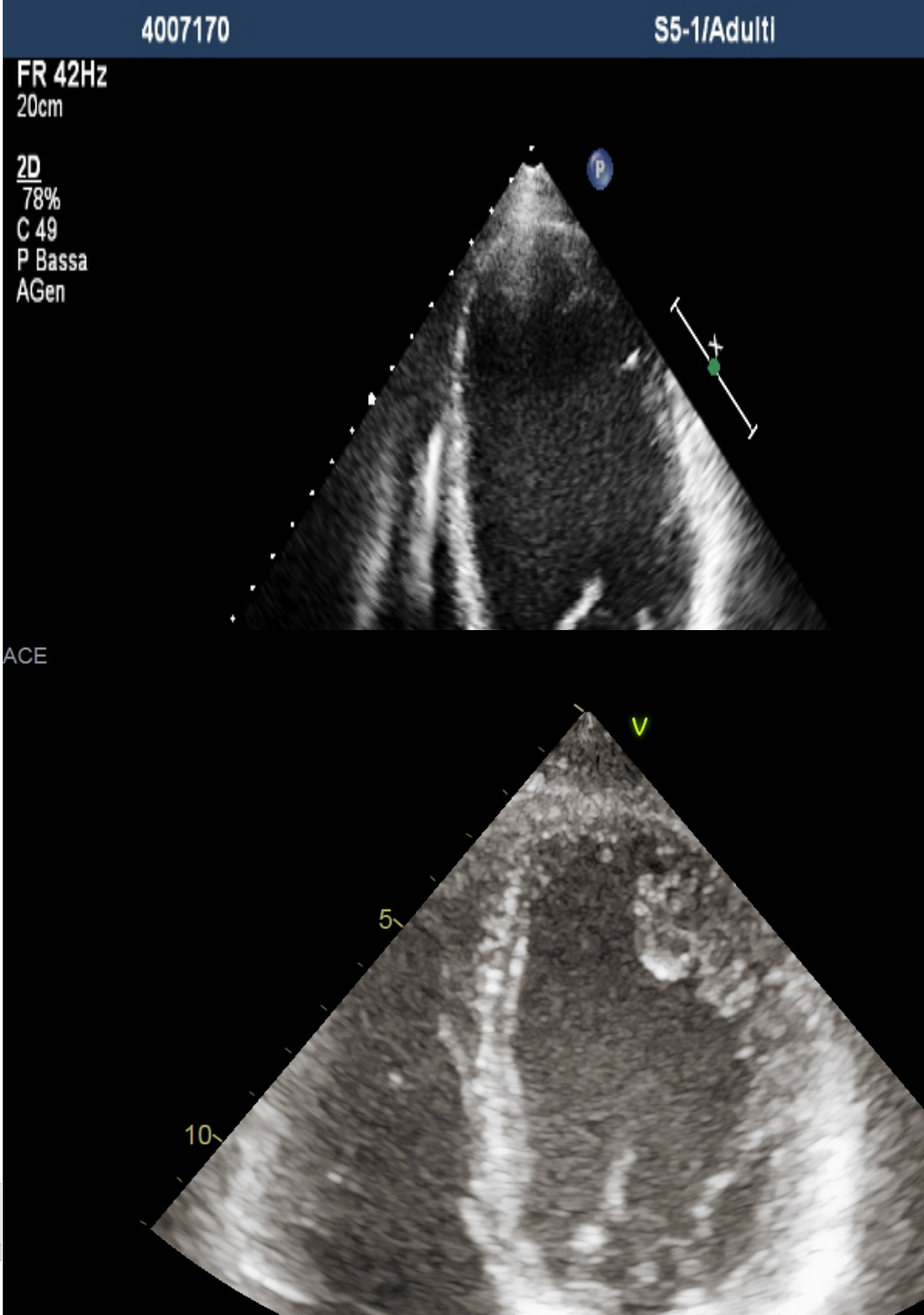
MISTRETTO, SALVATORE

21/10/2014 10:03:10

4007170

S5-1/Adult







GENES RELATED TO CMPs

Gene Category	Gene	HCM	DCM / NDLVC	ARVC	AFD / hATTR
Sarcomeric	<i>MYH7</i>	●●●	●●●	○	—
	<i>MYBPC3</i>	●●●	○	○	—
	<i>TNNT2</i>	●●●	●●●	○	—
	<i>TNNI3</i>	●●●	●●	○	—
	<i>TPM1</i>	●●●	●●	—	—
	<i>ACTC1</i>	●●●	●●	—	—
	<i>TNNC1</i>	●●●	●●●	—	—
	<i>MYL2 / MYL3</i>	●●●	—	—	—
Desmosomal / Cytoskeletal	<i>DSP</i>	○	●●●	●●●	—
	<i>PKP2</i>	—	—	●●●	—
	<i>DSG2 / DSC2</i>	—	—	●●●	—
	<i>JUP</i>	—	—	●●●	—
	<i>TTN</i> (truncating)	○	●●●	○	—
	<i>FLNC</i>	●●● (missense)	●●● (truncating)	●●	—
	<i>NEXN</i>	○	●●	—	—
Ion Channel / Ca ²⁺ Handling/ Splicing factors	<i>DES</i>	●●●	●●●	●●	—
	<i>PLN</i>	●●●	●●●	●●	—
	<i>RBM20</i>	○	●●●	—	—
	<i>SCN5A</i>	—	●●●	○	—
	<i>TMEM43</i>	—	—	●●●	—

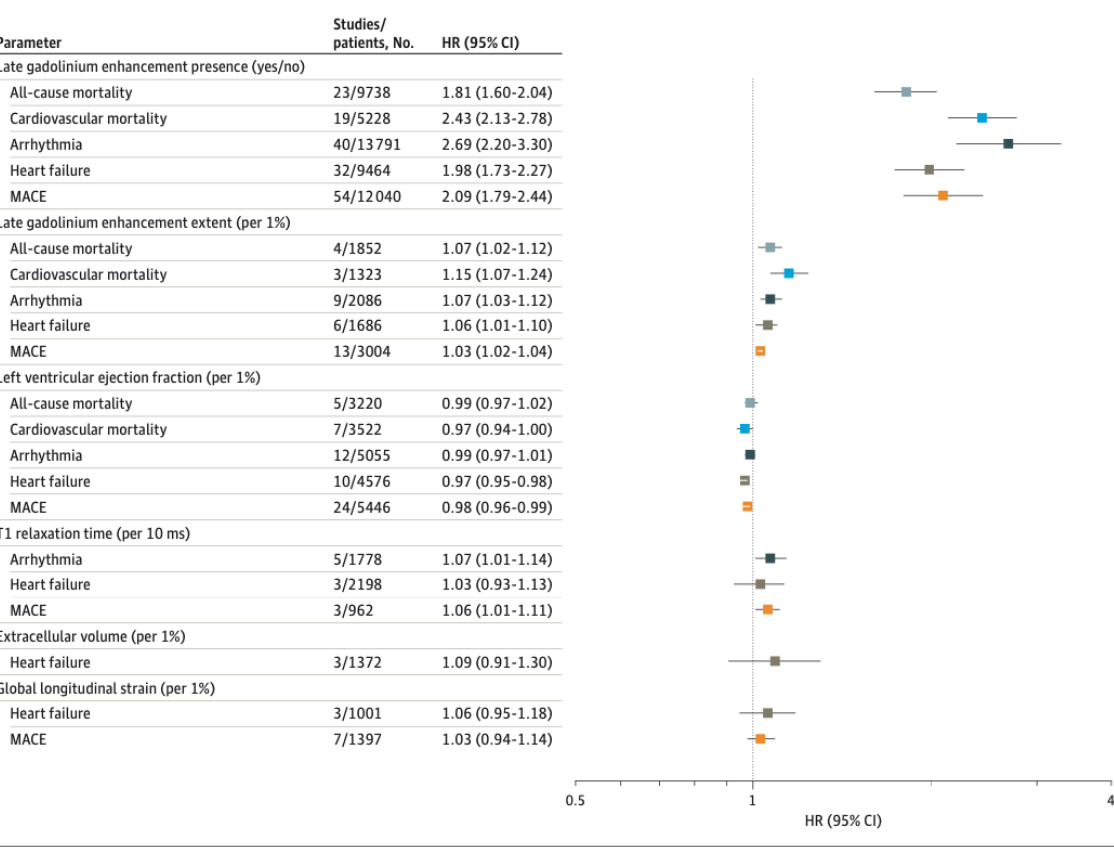
Merlo M et al. Adapted and updated from ESC Guidelines on Cardiomyopathies. unpublished

Cardiac-MRI

JAMA | Original Investigation

Risk Stratification in Nonischemic Dilated Cardiomyopathy Using CMR Imaging A Systematic Review and Meta-Analysis

Figure 1. Cardiac Magnetic Resonance (CMR) Imaging Parameters and Clinical Outcomes

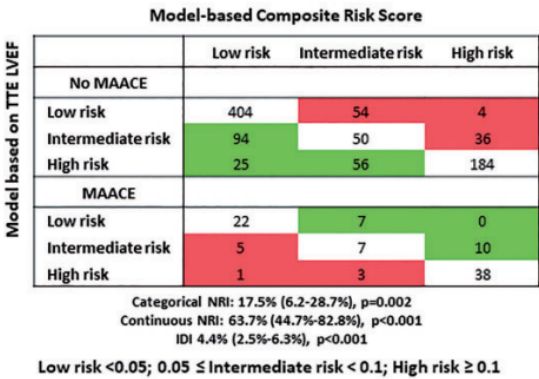


JAMA 2024;332;(18):1535-1550.

CarDiac magnETic Resonance for prophylactic Implantable-cardioVerter defibrillAtor ThErapy in Non-Ischaemic dilated CardioMyopathy: an international Registry

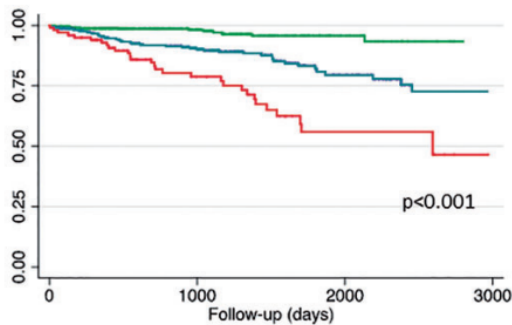
Andrea Igoren Guaricci^{1†}, Pier Giorgio Masci^{2†}, Giuseppe Muscogiuri^{3‡}, Marco Guglielmo^{3‡}, Andrea Baggiano^{3‡}, Laura Fusini³, Valentina Lorenzoni⁴, Chiara Martini^{5‡}, Daniele Andreini^{3‡}, Anna Giulia Pavon⁶, Giovanni D. Aquaro⁷, Andrea Barison⁸, Giancarlo Todiere⁷, Mark G. Rabbat⁸, Emily Tat⁸, Claudia Raineri⁹, Adele Valentini¹⁰, Akos Varga-Szemes¹¹, U. Joseph Schoepf¹¹, Carlo N. De Cecco^{11,12}, Jan Bogaert¹³, Monica Dobrovie¹³, Rolf Symons¹³, Marta Focardi¹⁴, Annalaura Gismondini¹⁴, Jordi Lozano-Torres¹⁵, José F. Rodríguez-Palomares^{15,16}, Chiara Lanzillo¹⁷, Mauro Di Roma¹⁷, Claudio Moro¹⁸, Gabriella Di Giovine¹⁹, Davide Margonato¹⁹, Manuel De Lazzari²⁰, Martina Perazzolo Marra²⁰, Alberto Nese²¹, Grazia Casavecchia²², Matteo Gravina²³, Francesca Marzo²⁴, Samuela Carigi²⁴, Silvia Pica²⁵, Massimo Lombardi²⁵, Stefano Censi²⁶, Angelo Squeri²⁶, Alessandro Palumbo⁵, Nicola Gaibazzi²⁷, Giovanni Camasta²⁸, Stefano Sbarbati²⁹, Patrizia Pedrotti³⁰, Ambra Masi³⁰, Nazario Carrabba³¹, Silvia Pradella³², Mauro Timpani³³, Gloria Cicala³⁴, Cristina Presicci³⁵, Sara Puglisi³⁶, Nicola Sverzellati³⁶, Vincenzo Ezio Santobuono¹, Mauro Pepi³, Juerg Schwitler³, and Gianluca Pontone^{3,4,†,‡}

A



Major Adverse Arrhythmic Cardiac Events

C

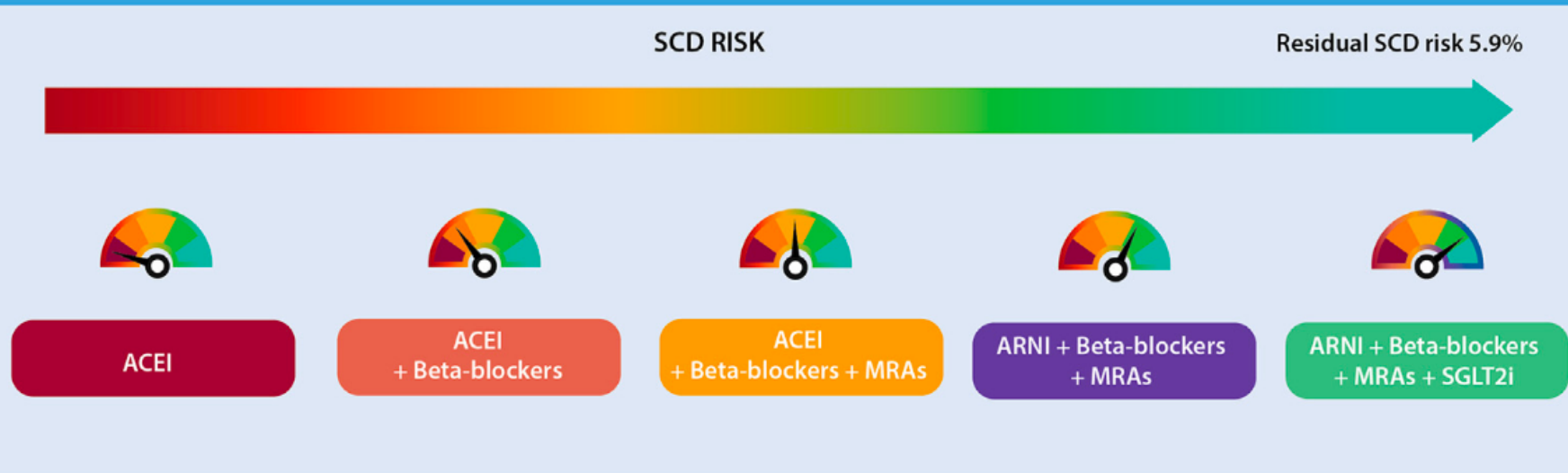


Composite Risk Score ≤2	451	205	50	12
2 < Composite Risk Score ≤5	447	196	53	14
Composite Risk Score >5	102	46	11	0

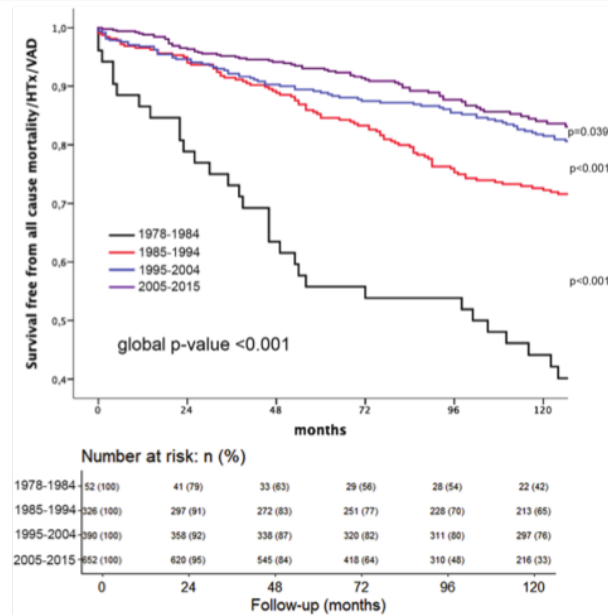
Strongest predictors:

- Male sex
- Higher LV end-diastolic volume index (LVEDVi)
- Presence of extensive midwall fibrosis (>3 segments on LGE)

GDMT Pillars Effect on SCD Risk



Yehya A, et al. JACC Heart Fail. 2025;13(1):1–13.



Merlo M, et al. EJHF 2020

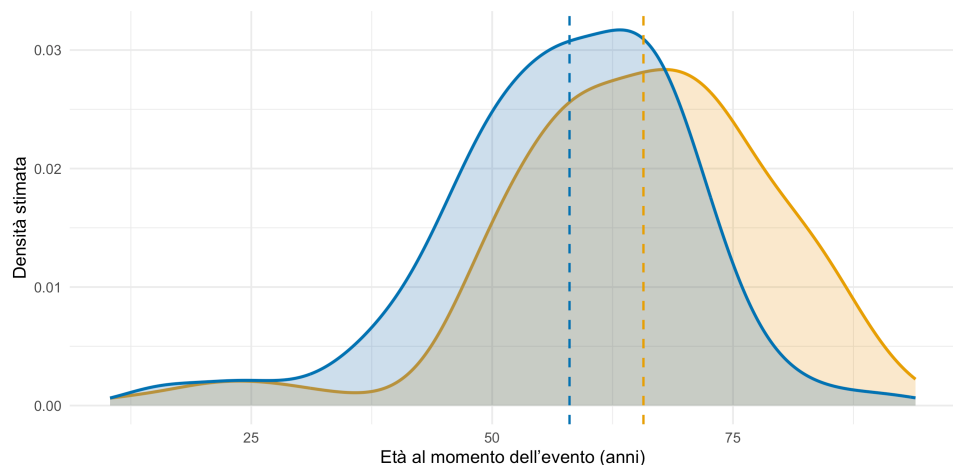


Registro Cardiomiopatie Trieste Aggiornamento 10-2025

Età all'evento — Morte improvvisa vs Altre cause

Distribuzione stimata dell'età al momento dell'evento

Altre cause Morte improvvisa



Unpublished

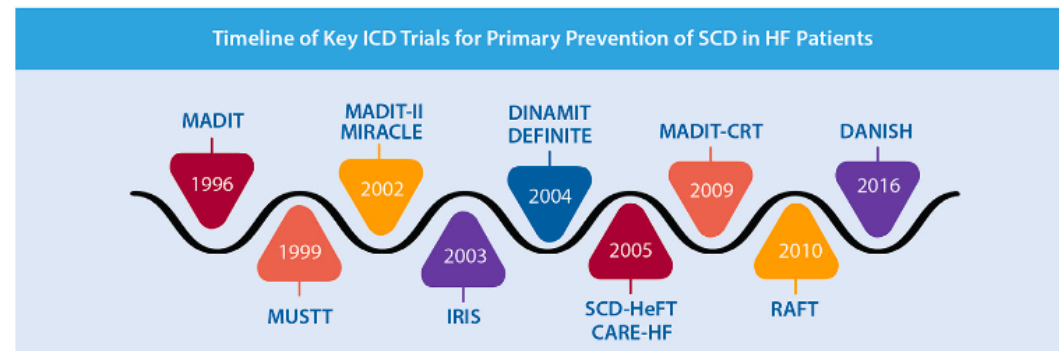
Contemporary survival trends and aetiological characterization in non-ischaemic dilated cardiomyopathy

Marco Merlo^{1*†}, Antonio Cannatà^{1,2†}, Carola Pio Loco¹, Davide Stolfo¹,
Giulia Barbati³, Jessica Artico¹, Rero Gentile¹, Valerio De Paris¹, Federica Ramani¹,
Massimo Zecchin¹, Marta Gigli¹, Bruno Pinamonti¹, Renata Korcova¹,
Andrea Di Lenarda⁴, Mauro Giacca², Luisa Mestroni⁵, Paolo G. Camici⁶,
and Gianfranco Sinagra¹

¹Cardiovascular Department, Centre for Diagnosis and Management of Cardiomyopathies, Azienda Sanitaria Universitaria Integrata di Trieste (ASUITS), University of Trieste, Trieste, Italy; ²Department of Cardiovascular Sciences, Faculty of Life Sciences & Medicine, King's College London, London, UK; ³Biostatistics Unit, University of Trieste, Trieste, Italy; ⁴Cardiovascular Centre, Azienda Sanitaria Universitaria Integrata di Trieste (ASUITS), University of Trieste, Trieste, Italy; ⁵Cardiovascular Institute and Adult Medical Genetics Program, University of Colorado Anschutz Medical Campus, Aurora, CO, USA; and ⁶Vita Salute University and San Raffaele Hospital, Milan, Italy

NDLVC

Sudden Cardiac Death Main Trials



Yehya A, et al. JACC Heart Fail. 2025;13(1):1–13.

DANISH-Trial-Age analysis (2017)

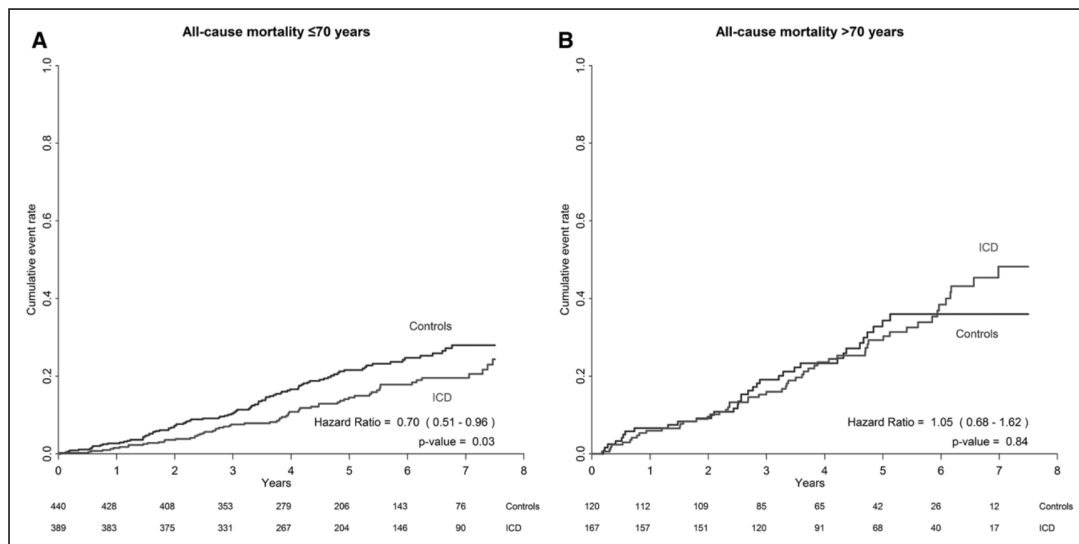


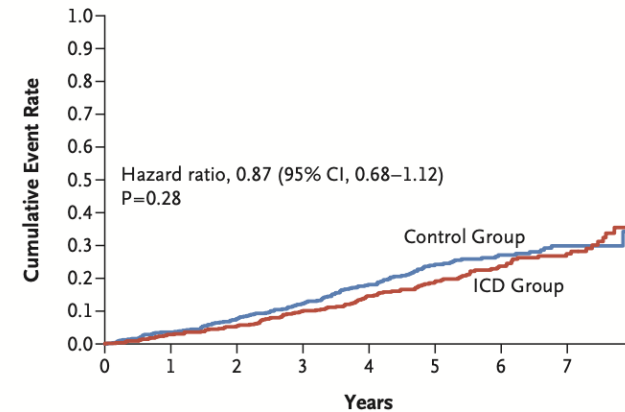
Figure 4. All-cause mortality for the entire population in (A) patients ≤70 years old and (B) patients >70 years old. Black lines represent patients in the control group; gray lines, patients randomized to implantable cardioverter-defibrillator (ICD) treatment.

Circulation. 2017;136:1772–1780.

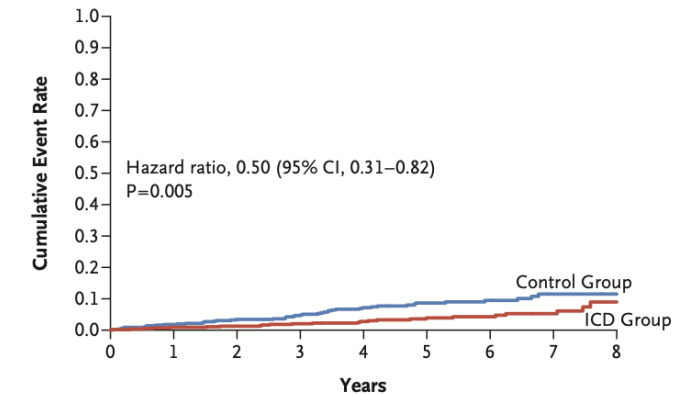
DANISH-Trial (2016)

-Inclusion criteria: EF<35% non-ischemic.
-Follow up: 67 months.

A Death from Any Cause

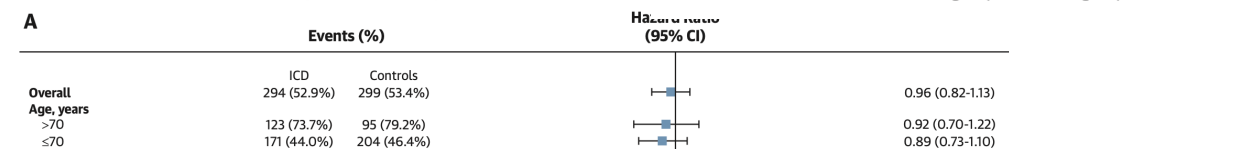
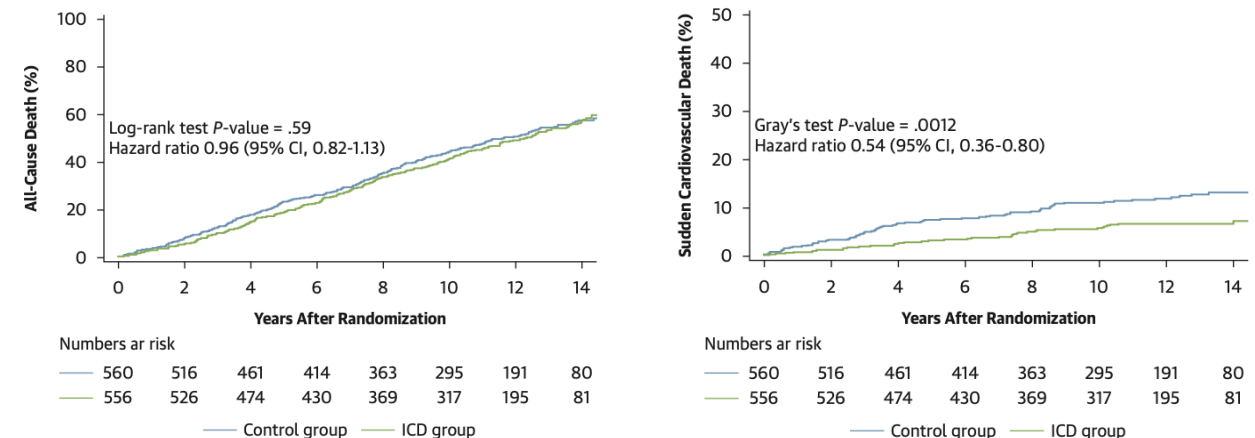


C Sudden Cardiac Death



2016 N Engl J Med 2016;375:1221-1230

Extended Follow-Up Analysis of DANISH (2025)



Extended Follow-Up Analysis of DANISH-JACC 2025 JACC; 2025

Why EF isn't enough?

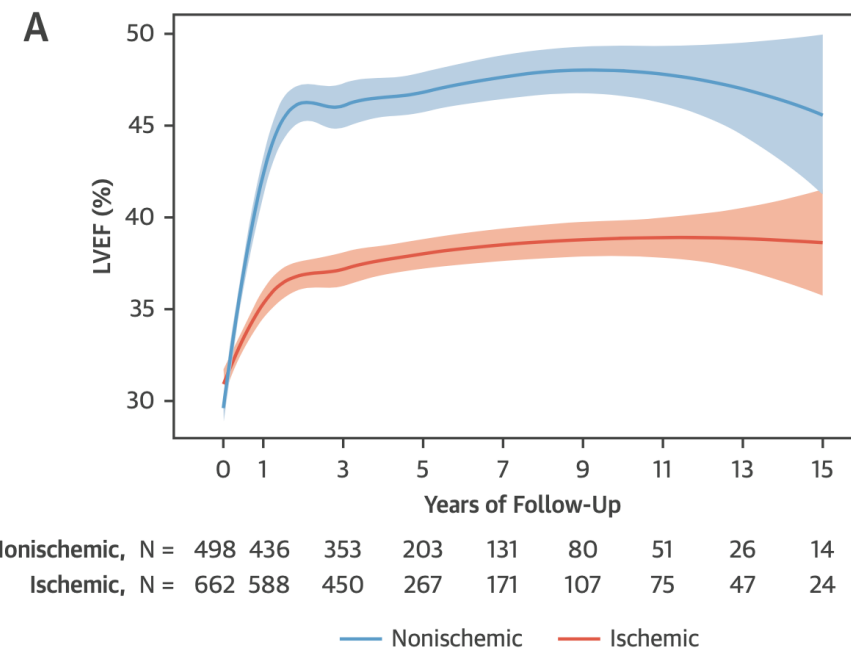
- **SINGLE.** Older age, frailty, CKD, diabetes, or recurrent HF hospitalization increase non-arrhythmic mortality — reducing the proportion of deaths that an ICD can prevent.
- **IMPRECISE:** arrhythmic risk depends on the **substrate**, not just pump function. Genetics, fibrosis on CMR drive arrhythmic vulnerability independently of EF.

ORIGINAL INVESTIGATIONS

Dynamic Trajectories of Left Ventricular Ejection Fraction in Heart Failure

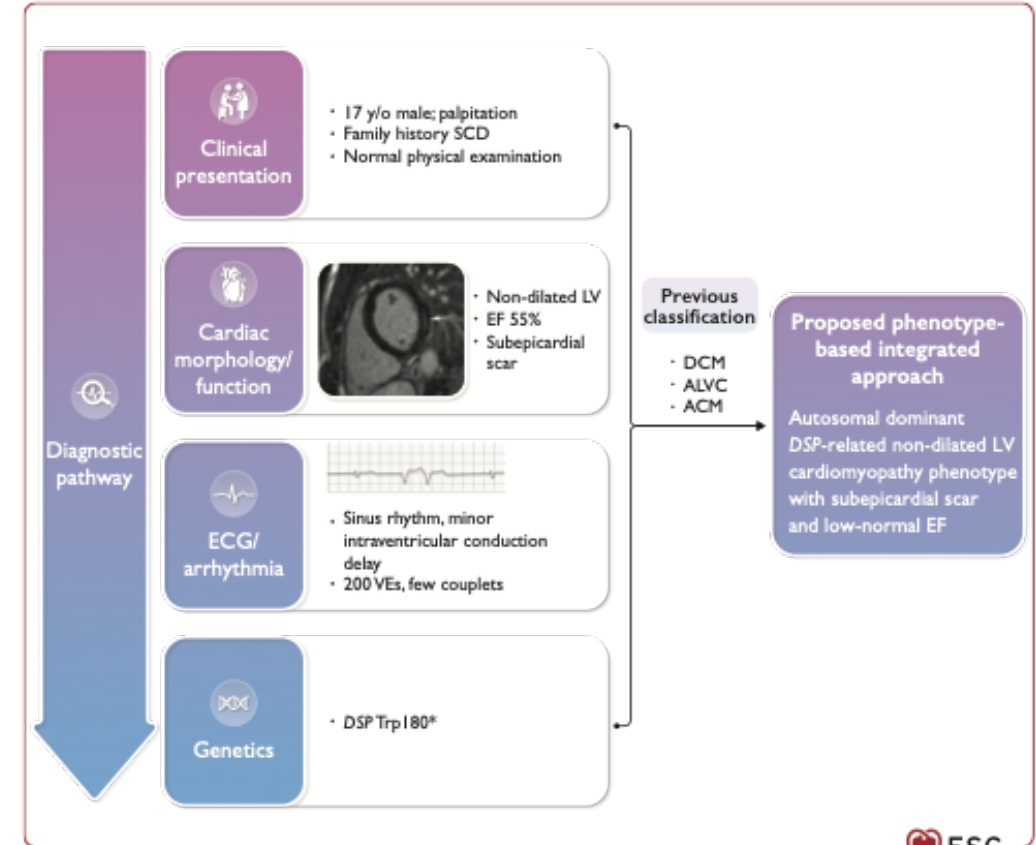
Josep Lupón, MD, PhD,^{a,b,c,d} Giovana Gavidia-Bovadilla, MSc,^{e,f} Elena Ferrer, MD,^b Marta de Antonio, MD, PhD,^{a,b} Alexandre Perera-Lluna, PhD,^{f,g,h} Jorge López-Ayerbe, MD,^b Mar Domingo, MD, PhD,^a Julio Núñez, MD, PhD,^{d,i,j} Elisabet Zamora, MD, PhD,^{a,b,c,d} Pedro Moliner, MD,^{a,b} Patricia Díaz-Ruata, MSc,^{f,g} Javier Santesmases, MD,^a Antoni Bayés-Genís, MD, PhD^{a,b,c,d}

JACC vol 72, no 6, 2018:591-601



TIME DEPENDENT EVALUATION

CARDYOPATHY MINDSET



THE ERA OF THE SCORES!

Suspected cardiomyopathy

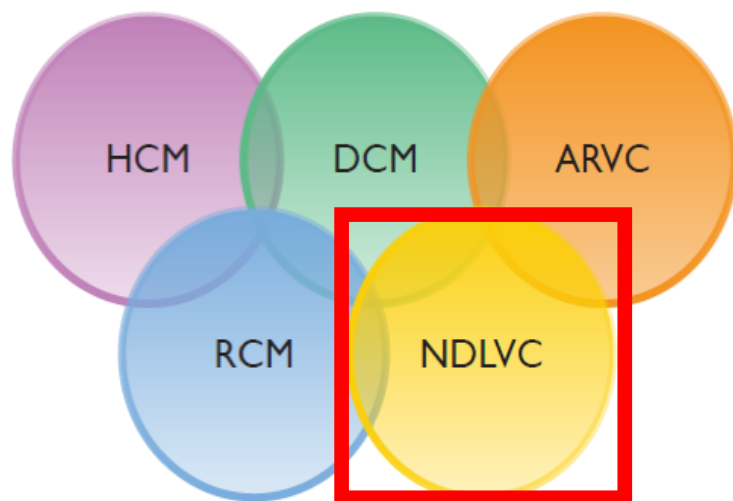
Normal morphology/function

Ventricular scar/fatty replacement

Normal

Normal systolic function

- Non-ischaemic ventricular scar on CMR/pathological examination
- Other tissue characterization parameters on CMR



Arrhythmias/conduction disease
(atrial, ventricular, atrioventricular block)

Genetic analysis

Genetic testing

Extracardiac involvement

NDLVC

Key Question

What predicts the occurrence of the first major arrhythmic event (MAE) in non-dilated left ventricular cardiomyopathy (NDLVC)?

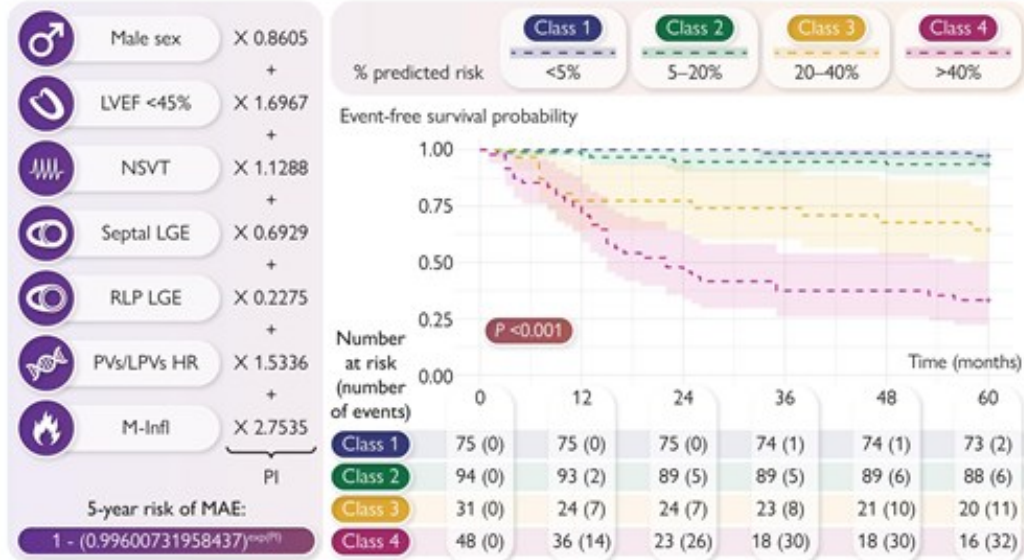
Key Finding

In NDLVC, male sex, non-sustained ventricular tachycardia, left ventricular ejection fraction <45%, septal and ring-like late gadolinium enhancement, high-risk genotypes, and myocardial inflammation predicted the first episode of MAE by 60 months. A new risk score (NDLVC-5y) was subsequently derived.

Take Home Message

A multi-parametric approach improves the arrhythmic risk stratification of NDLVC.

NDLVC-5y risk score for the prediction of 5-year MAE risk



Peretto G, Merlo M et al. Eur Heart J 2025

DOI: [10.1093/eurheartj/ehaf477](https://doi.org/10.1093/eurheartj/ehaf477)

GENES IN RISK SCORES

5 y risk of major arrhythmic event according to genotype

NDLVC Score: 15,65%

Male sex: Yes ☐

LVEF <45%: No ☐

Nonsustained ventricular tachycardia: Yes ☐

Septal LGE: No ☐

Ring-like pattern LGE: Yes ☐

Pathogenic/likely pathogenic variants in "high-risk" genes: Yes ☐

Myocardial inflammation: No ☐

LMNA score: 25%

Genetic Sex:
Female ☐ Male ☒

History of NSVT:
yes ☒ No ☐

Non-Missense Mutation:
yes ☒ No ☐

1st Degree AV Block:
yes ☐ No ☒

2nd or 3rd Degree AV Block:
yes ☐ No ☒

Left Ventricular Ejection Fraction:
48

DSP score: 10%

Genetic Sex:
Female ☐ Male ☒

History of NSVT:
yes ☒ No ☐

Left Ventricular Dysfunction (EF < 50%):
yes ☒ No ☐

Right Ventricular Dysfunction (Moderate to Severe):
yes ☐ No ☒

24 hour PVC Burden on Ambulatory Monitoring:
170

FLNC score: 39,2%

Age (years):
1 41 93
1 11 21 31 41 51 61 71 81 93

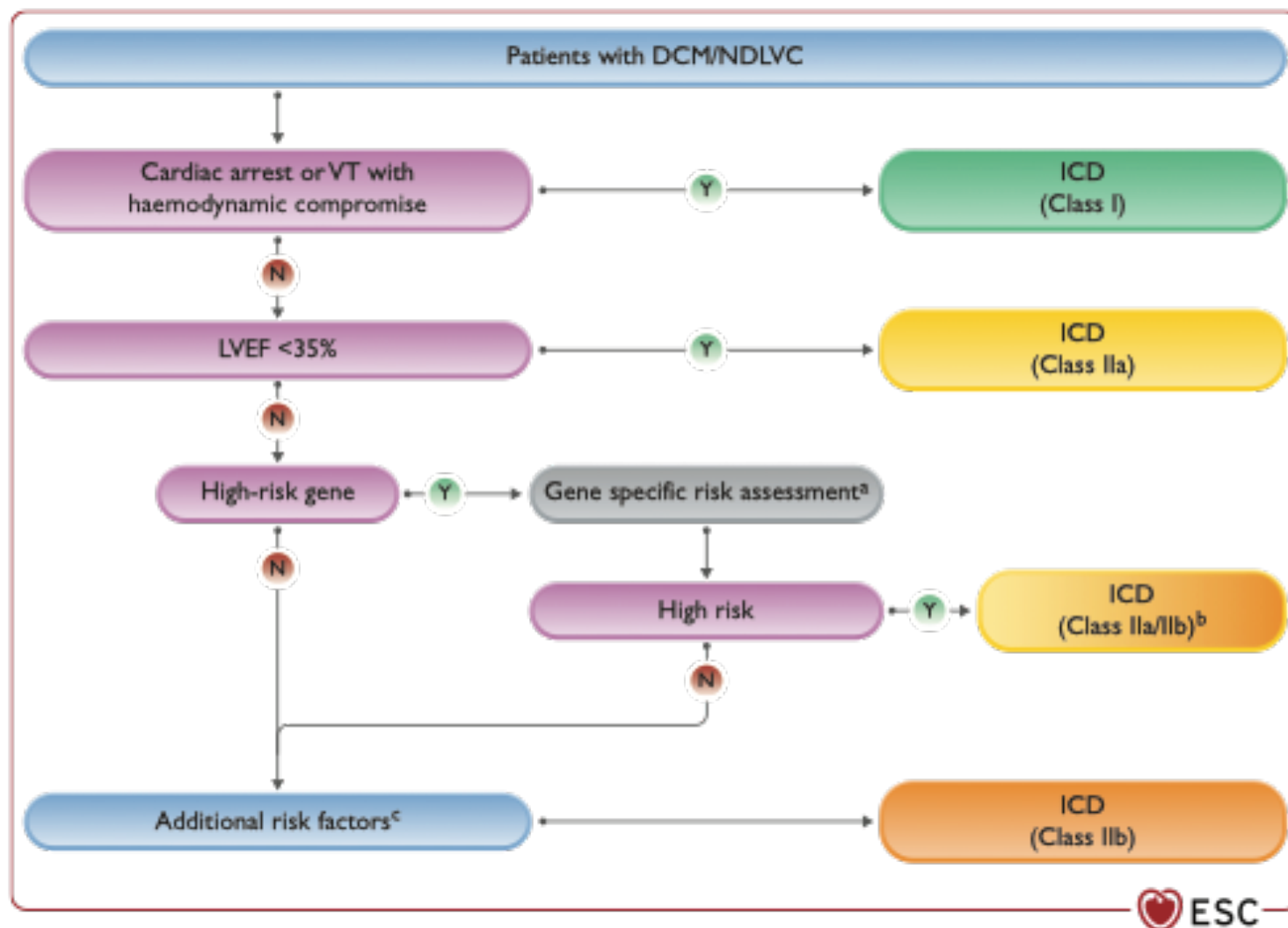
Sex:
Male ☐

Non-sustained ventricular tachycardia (NSVT):
Yes ☐

History of syncope:
No ☐

LVEF (%):
10 48 75
10 17 24 31 38 45 52 59 66 73 75

DCM/NDLVC: 2023 ESC guidelines



Gene	Annual SCD rate	Predictors of SCD
<i>LMNA</i> ^{185,186,438,541,865,879,879}	5–10%	Estimated 5-year risk of life-threatening arrhythmia using <i>LMNA</i> risk score (https://lmna-risk-vta.fr)
<i>FLNC</i> -truncating variants ^{866,867,880}	5–10%	LGE on CMR LVEF < 45%
<i>TMEM43</i> ^{868,881}	5–10%	Male Female and any of the following: LVEF < 45%, NSVT, LGE on CMR, >200 VE on 24h Holter ECG
<i>PLN</i> ^{542,882,883}	3–5%	Estimated 5-year risk of life-threatening arrhythmia using <i>PLN</i> risk score (https://plnriskcalculator.shinyapps.io/final_shiny/) LVEF < 45% LGE on CMR NSVT
<i>DSP</i> ^{185,186}	3–5%	LGE on CMR LVEF < 45%
<i>RBM20</i> ⁸⁶⁹	3–5%	LGE on CMR LVEF < 45%

The role of genetics

nature reviews cardiology

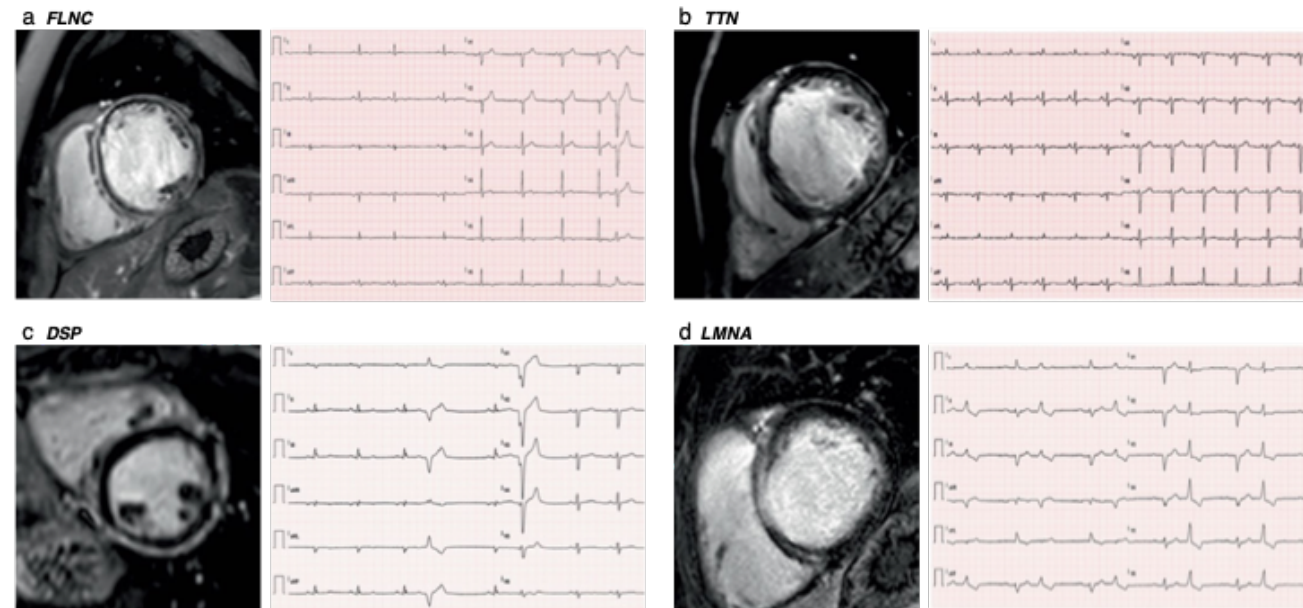
<https://doi.org/10.1038/s41569-024-01074-2>

Review article

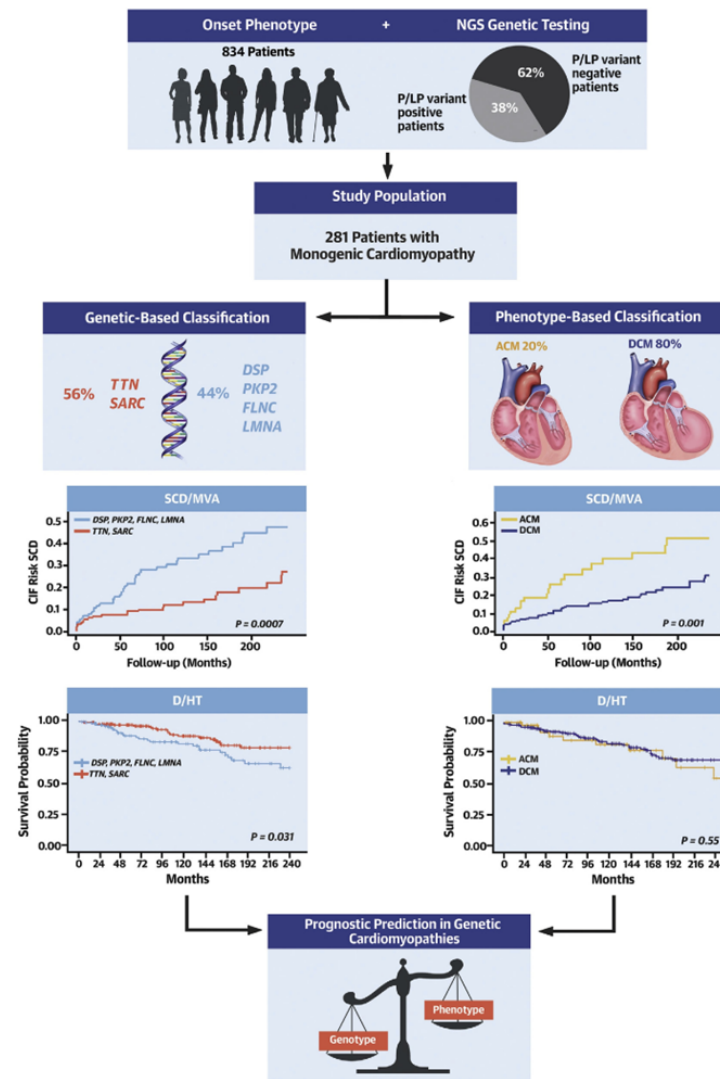
Check for updates

Pathophysiology of dilated cardiomyopathy: from mechanisms to precision medicine

Marta Gigli¹, Davide Stolfo^{1,2}, Marco Merlo¹, Gianfranco Sinagra¹, Matthew R. G. Taylor³ & Luisa Mestroni¹✉



CENTRAL ILLUSTRATION: Toward Genotype-Based Classification of Nonhypertrophic Cardiomyopathies for Precise Risk Prediction



Paldino A, et al. J Am Coll Cardiol. 2022;80(21):1981-1994.

GENES → DROWBACKS

INTERPRETABILITY → VUS!!

INTER-DISCIPLINARY TEAMS

ANXIETY AND PSYCHOLOGICAL

**ISSUES
RE-CLASSIFICATION**



DROWBACKS – referral centers

GENERAL POPULATION

«*genotype-first*»

Titin-truncating variants affect heart function in disease cohorts and the general population



nature
genetics

Prevalence of Titin Truncating Variants in General Population

Oyediran Akinrinade¹, Juha W. Koskenvuo^{2,3}, Tero-Pekka Alastalo^{1,2*}

Prevalence of DCM-associated TTNtv:

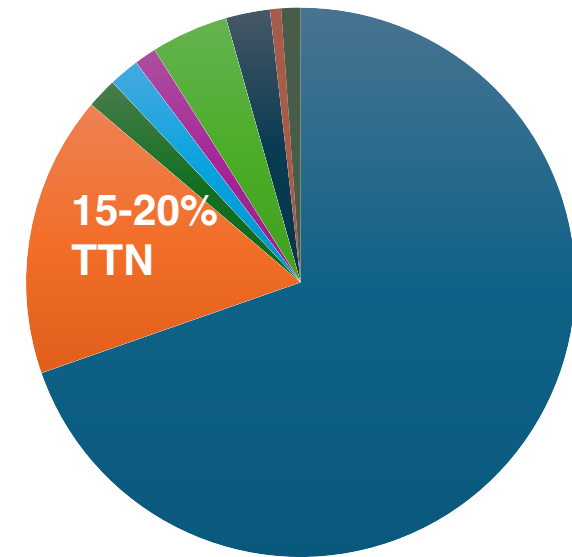
0.36% to 0.5%

≤37.5 million people may carry a DCM-associated TTNtv and potentially at an increased risk of developing heart failure and cardiac arrhythmia

Schafer et al., *Nat Gen*, 2017
Akinrinade et al., *Plos One*, 2015

REGISTRIES

«*phenotype-first*»



DROWBACKS – referral centers

GENERAL POPULATION

PENETRANCE

TI

REGISTRIES

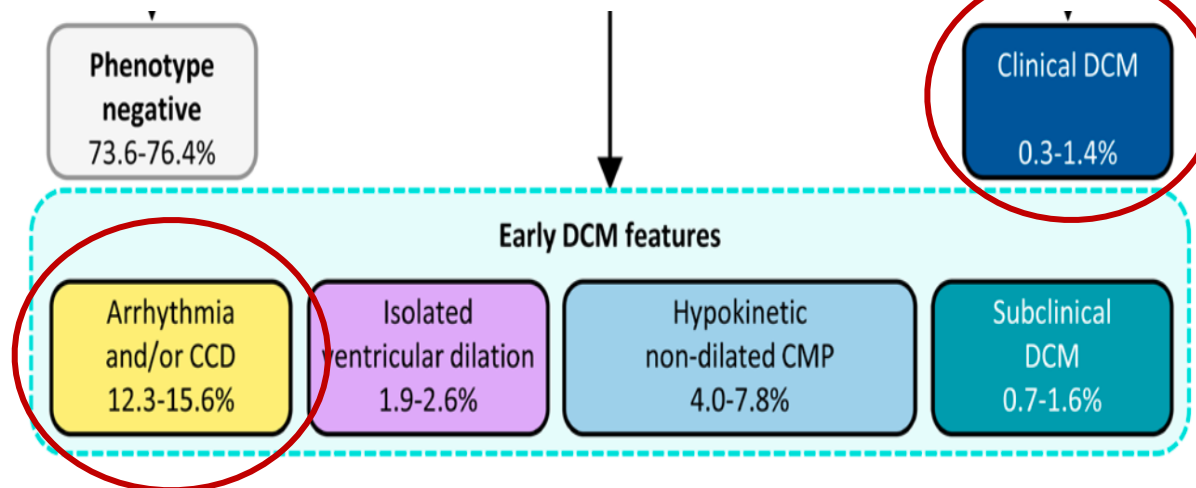
Y

Genetic background

← VARIABLE EXPRESSIVITY →

Overt phenotype

Main Variant Annotation Strategy					Ultra Strict ClinVar ≥2-Star P/LP Only				
			HR	CI 95%				HR	CI 95%
	Mortality					Mortality			
	Cardiomyopathy					Cardiomyopathy			
	Composite Outcomes					Composite Outcomes			
CMP					CMP				
			1.13	1.01-1.25				1.37	1.09-1.71
			5.75	4.58-7.23				9.25	6.25-13.65
			1.29	1.20-1.39				1.65	1.42-1.91
	Mortality					Mortality			
	Cardiomyopathy					Cardiomyopathy			
	Composite Outcomes					Composite Outcomes			
DCM					DCM				
			1.13	1.01-1.27				1.50	1.01-1.27
			6.46	5.05-8.27				10.73	6.72-17.15
			1.33	1.26-1.44				1.68	1.38-2.03
	Mortality					Mortality			
	Cardiomyopathy					Cardiomyopathy			
	Composite Outcomes					Composite Outcomes			
HCM					HCM				
			1.07	0.90-1.27				1.7	1.26-2.29
			4.50	3.04-6.67				11.38	6.70-19.32
			1.14	1.01-1.28				1.64	1.32-2.05
	Mortality					Mortality			
	Cardiomyopathy					Cardiomyopathy			
	Composite Outcomes					Composite Outcomes			
ARVC					ARVC				
			1.19	0.92-1.55				1.14	0.69-1.86
			4.16	2.15-8.04				4.38	1.41-13.61
			1.24	1.03-1.50				1.58	1.15-2.17



Asatryan et al, *JACC HF*, 2023
Shah et al., *Circulation*, 2022

Diagnostic yield in the current era of whole genetic testing

HCM



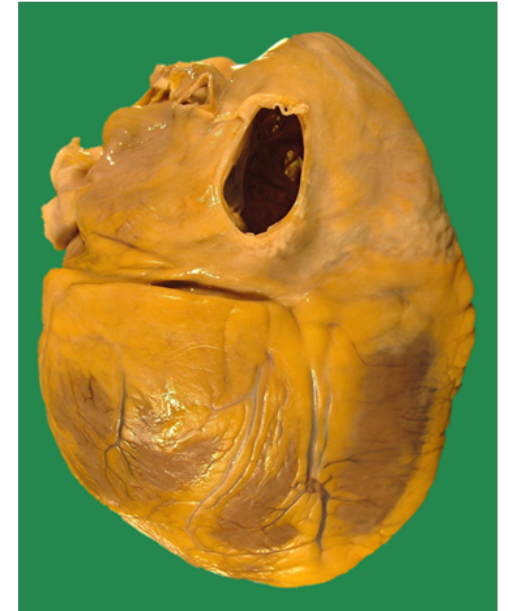
up to 50%

ARVC



60-70%

DCM



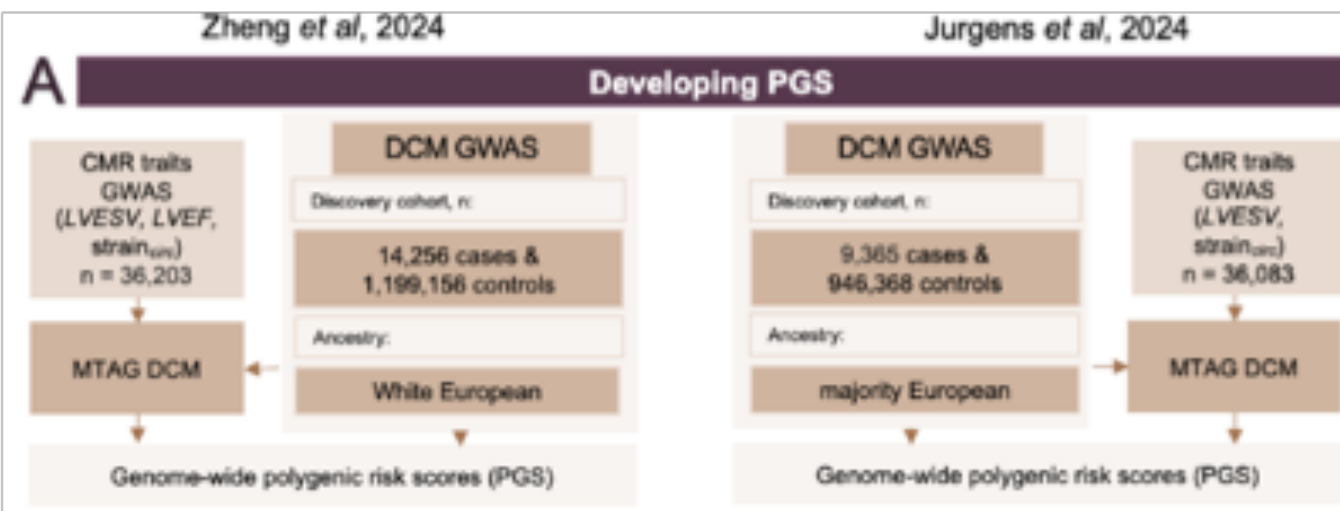
30-40%

THE MAJORITY OF CARCIOMYOPATHY PTs IN CLINICAL PRACTICE ARE GENE ELUSIVE!!

POLYGENIC RISK SCORES

Polygenic Risk Scores in Dilated Cardiomyopathy: Towards the Future

Daria R. Kramarenko^{1,4} · Sean J. Jurgens^{1,2,3} · Yigal M. Pinto^{1,4,5} · Connie R. Bezzina^{1,4} · Ahmad S. Amin^{1,4,5}



B **Testing PGS**

PGS from MTAG (~700K SNPs)

DCM/NI-DCM risk (UKB)

Cohort	OR per SD	[95%CI]	AUC
UKB	1.76	[1.64-1.76]	0.71

Comparing risk of individuals from different centiles

	OR	[95%CI]
Top 1% vs middle 20%	3.83	[2.52-5.79]
Top 1% vs bottom 1%	7.04	[2.42-20.5]

Cumulative hazards for lifetime DCM diagnosis

	HR	[95%CI]
Top 1% vs bottom 20%	6.10	[3.90-9.40]

PGS in genotype positive cohort (UKB)

Cumulative hazards for lifetime DCM diagnosis

	HR	[95%CI]
Top 20% vs median 20%	2.30	[1.20-4.30]
Top 20% vs bottom 20%	4.40	[2.10-9.40]

Association with CMR traits (UKB)

Outcome	Per PGS SD	[95%CI]
LVEF, %	-0.66	[-0.73 to -0.59]
LVEDV, ml	2.12	[1.83 to 2.41]
LVESV, ml	1.89	[1.71 to 2.07]

PGS from MTAG (~1.1M SNPs)

DCM/NI-DCM risk

Cohort	OR per SD	[95%CI]	AUC
AoU	1.64	[1.54-1.75]	0.73
AUMC	1.93	[1.79-2.07]	0.73

Different ancestries (AoU)

Cohort	OR per SD	[95%CI]	AUC
European	1.73	[1.59-1.88]	0.75
African	1.61	[1.39-1.87]	0.67
Adm. American	1.34	[1.11-1.62]	0.74

Genetic sex (AUMC)

Cohort	OR per SD	[95%CI]	AUC
Females	2.00	[1.79-2.24]	0.73
Males	1.87	[1.70-2.06]	0.71

PGS in genotype positive vs negative cohort (AUMC)

	OR per SD	[95%CI]	AUC
Gen + vs controls	1.54	[1.33-1.79]	0.69
Gen - vs controls	2.05	[1.81-2.32]	0.73

PGS in gen + is significantly lower compared to gen - (p=0.0015)

Association with systolic HF (AoU)

Outcome	OR per SD	[95%CI]
Syst. HF (excl. DCM/HCM)	1.24	[1.20-1.28]

C **Comparison by Jurgens et al.**

DCM/NIDCM risk

Cohort	OR per SD	[95%CI]	AUC (univ)	[95%CI]	R ²
AoU EUR	1.70	[1.45-1.99]	0.64	[0.62-0.67]	0.07
UKB EUR	1.83	[1.65-2.05]	0.66	[0.64-0.67]	0.08
AUMC EUR	1.87	[1.55-2.26]	0.66	[0.64-0.68]	0.1

DCM/NIDCM risk

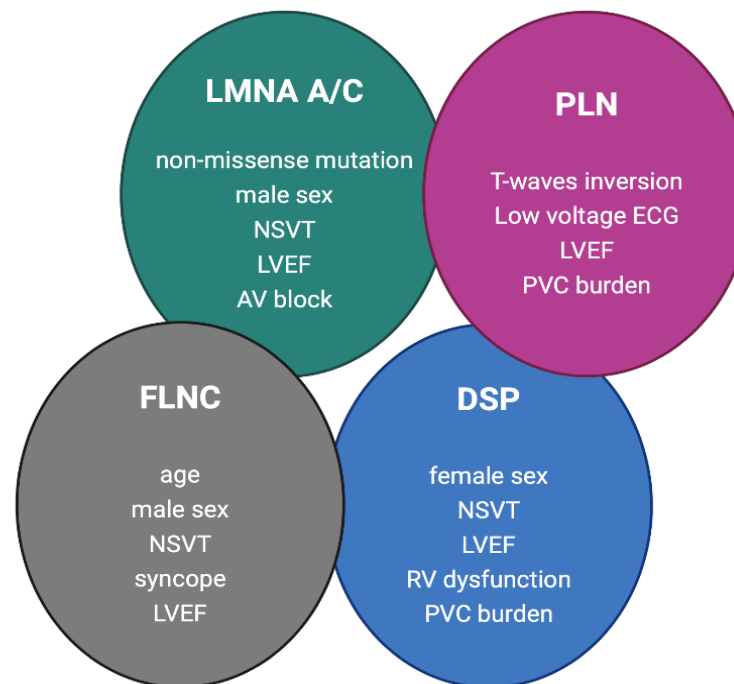
Cohort	OR per SD	[95%CI]	AUC (univ)	[95%CI]	R ²
AoU EUR	1.73	[1.46-2.04]	0.66	[0.63-0.68]	0.08
UKB EUR	1.91	[1.69-2.15]	0.68	[0.66-0.69]	0.1
AUMC EUR	1.93	[1.58-2.35]	0.67	[0.65-0.69]	0.11

DCM/NDLVC: MULTIPARAMETRIC APPROACH deep phenotype the gene!

Future development of arrhythmogenic risk scores in patients with heart failure and inherited dilated cardiomyopathy. A scientific statement of the Heart Failure Association of the ESC

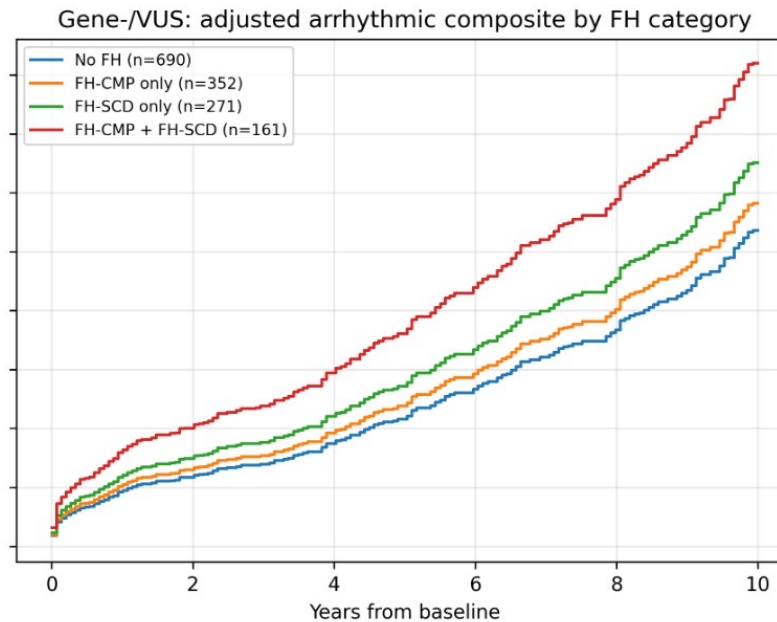
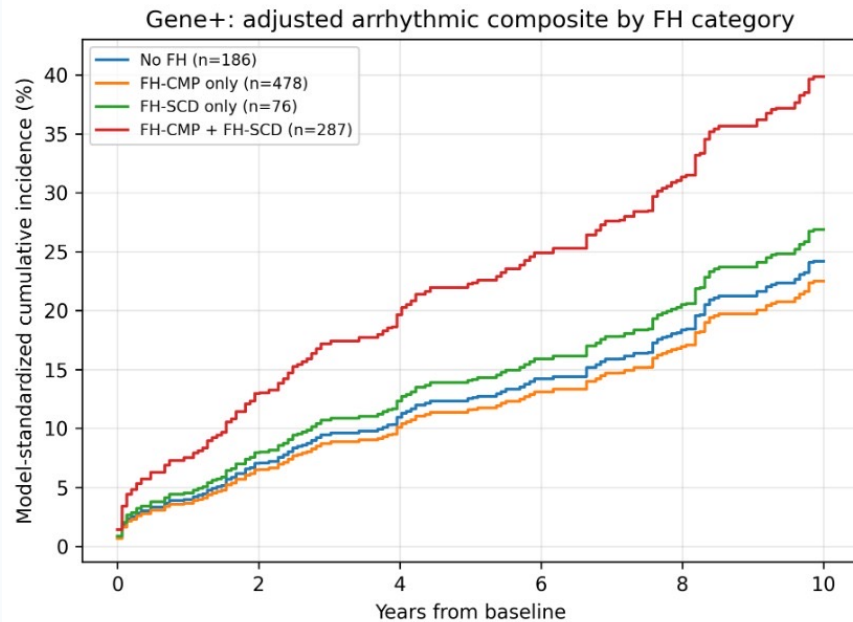
Marta Gigli^{1†}, Job A.J. Verdonchot^{2,3†}, Pablo Garcia-Pavia^{4,5†}, Davide Stolfo^{1,6}, Lorenzo Monserrat⁷, Sanjay Prasad^{8,9}, Andrea Mazzanti^{10,11}, Folkert W Asselbergs^{12,13,14†}, Barbara Bauce^{15†}, Philippe Charron^{16†}, Dana Dawson¹⁷, Brian P Halliday^{8,9}, Luisa Mestroni¹⁸, Petar Seferovic^{19,20,21}, Upasana Tayal^{8,9}, Maria Teresa Tome Esteban²², Peter Van Tintelen^{23†}, Stephane Heymans^{3†}, Antonis Pantazis²⁴, Marco Metra²⁵, and Gianfranco Sinagra^{1*†}

Gene-specific personalized risk estimation



FAMILY HISTORY

SHARE REGISTRY – 2545 PATIENTS



Detailed categories

No FH

FH-CMP only

FH-SCD only

FH-CMP + FH-SCD

Highest risk:
combined FH-CMP + FH-SCD

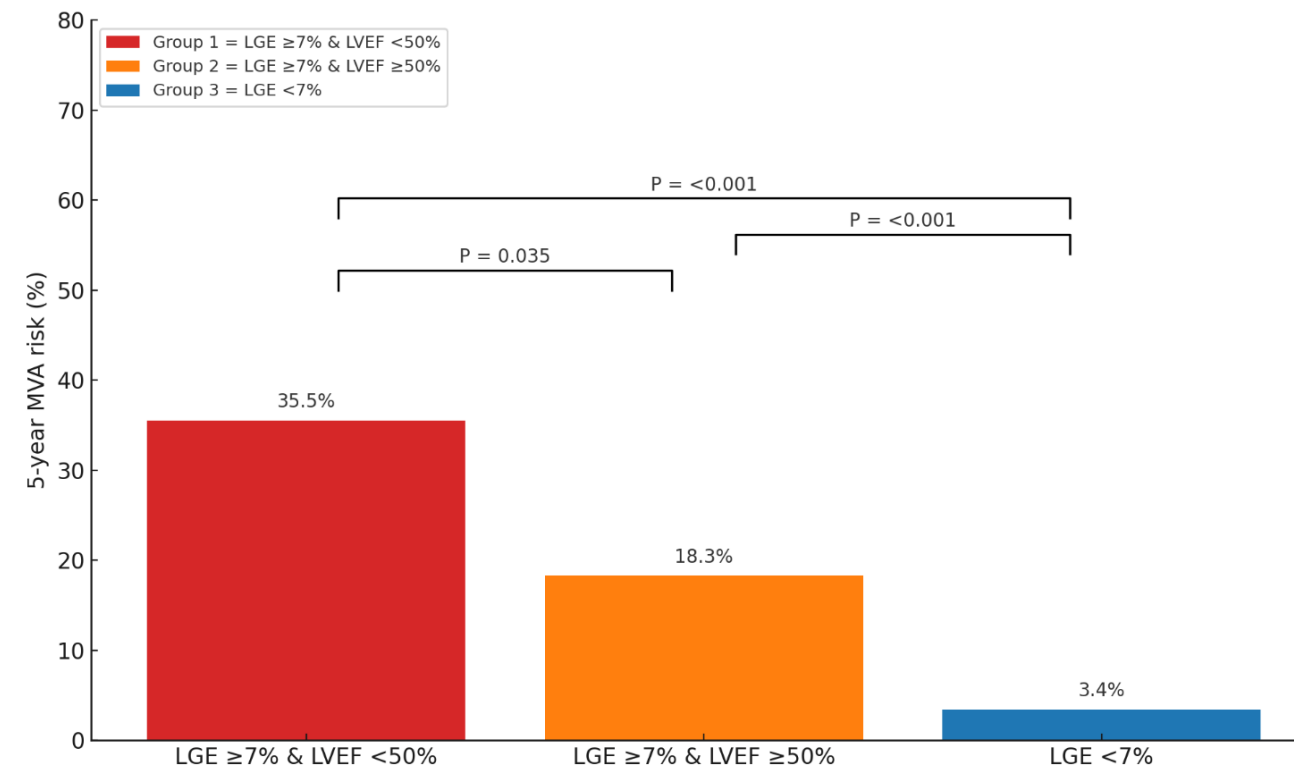
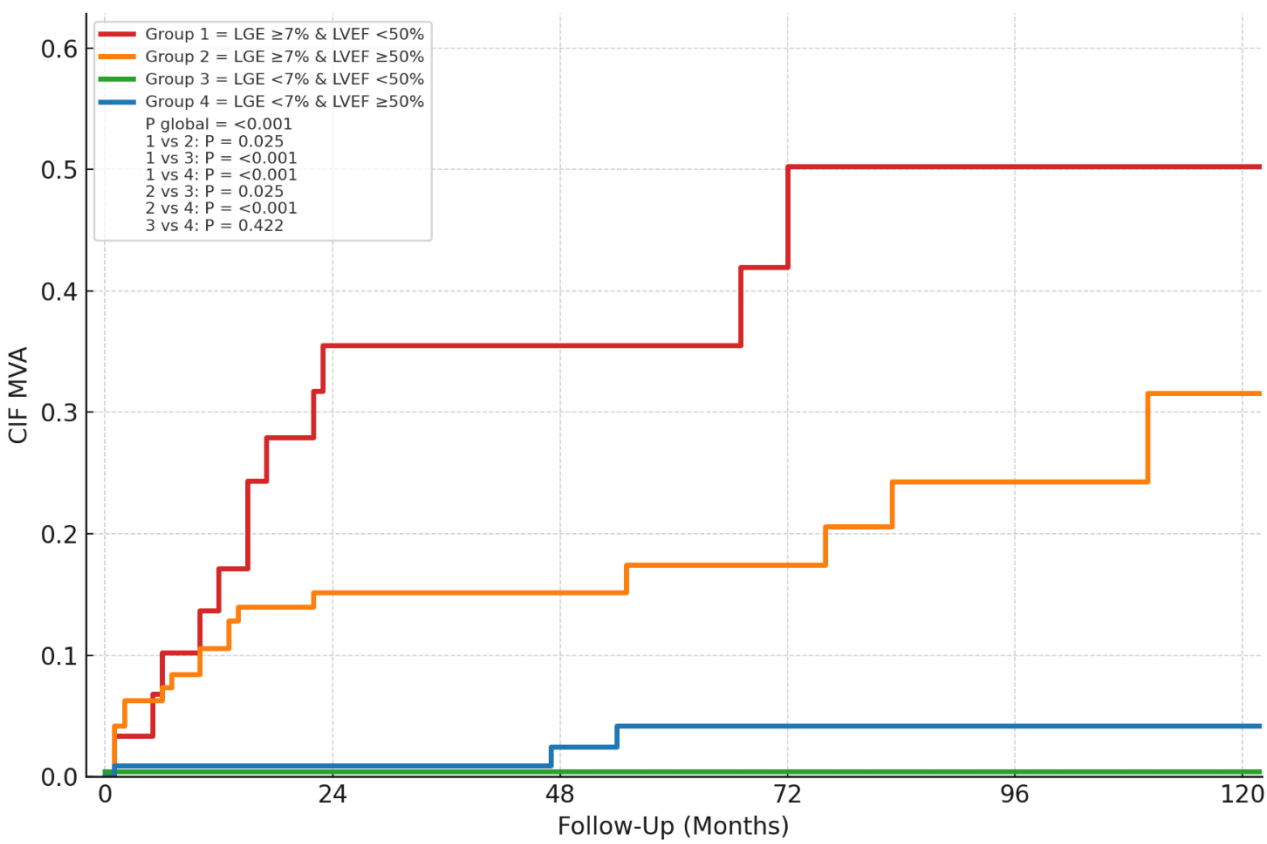
This supports a graded familial burden: the highest risk appears when cardiomyopathy and sudden death coexist in the pedigree.

Unpublished

NDLVC

Radesich C,Merlo M, SUBMITTED

NDLVC



Burelli M,Merlo M, SUBMITTED

GENES IN NATURAL HISTORY: LVRR

Association between mutation status and left ventricular reverse remodelling in dilated cardiomyopathy

Matteo Dal Ferro,¹ Davide Stolfo,¹ Alessandro Altinier,¹ Marta Gigli,¹ Martina Perrieri,¹ Federica Ramani,¹ Giulia Barbatì,¹ Alberto Pivetta,¹ Francesca Brun,¹ Lorenzo Monserrat,² Mauro Giacca,³ Luisa Mestroni,⁴ Marco Merlo,¹ Gianfranco Sinagra¹

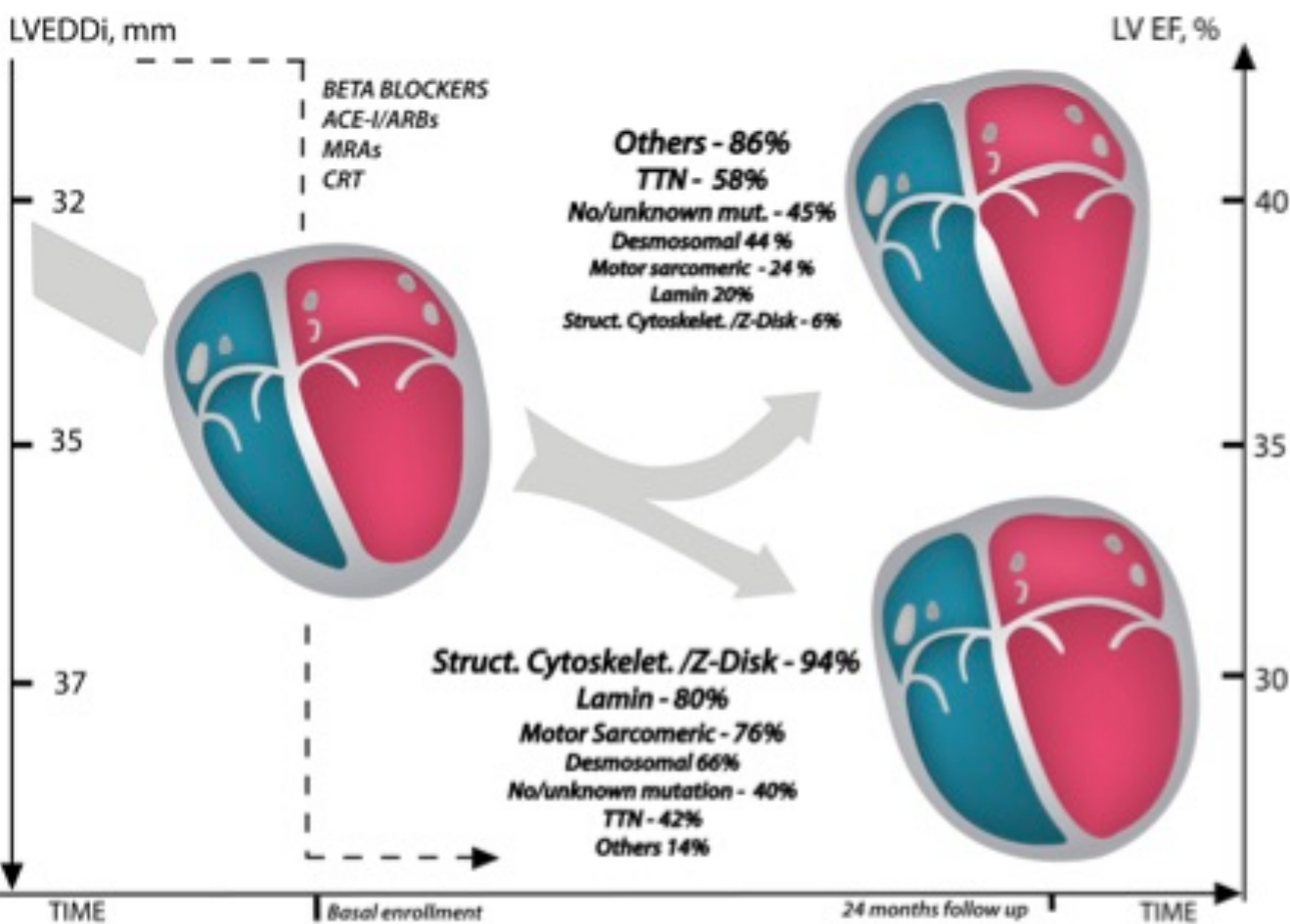


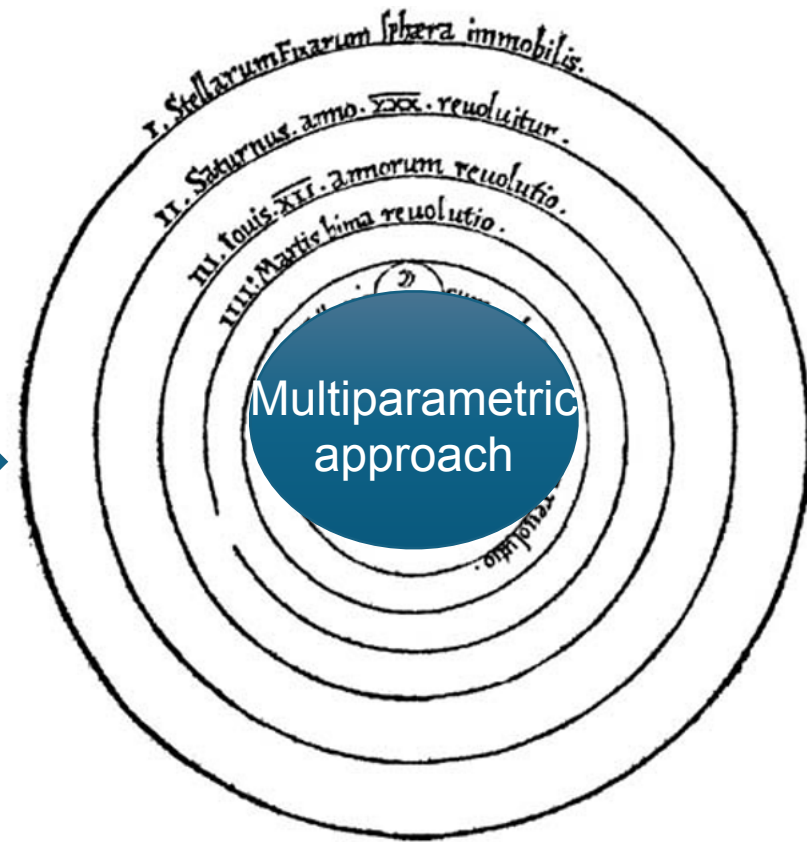
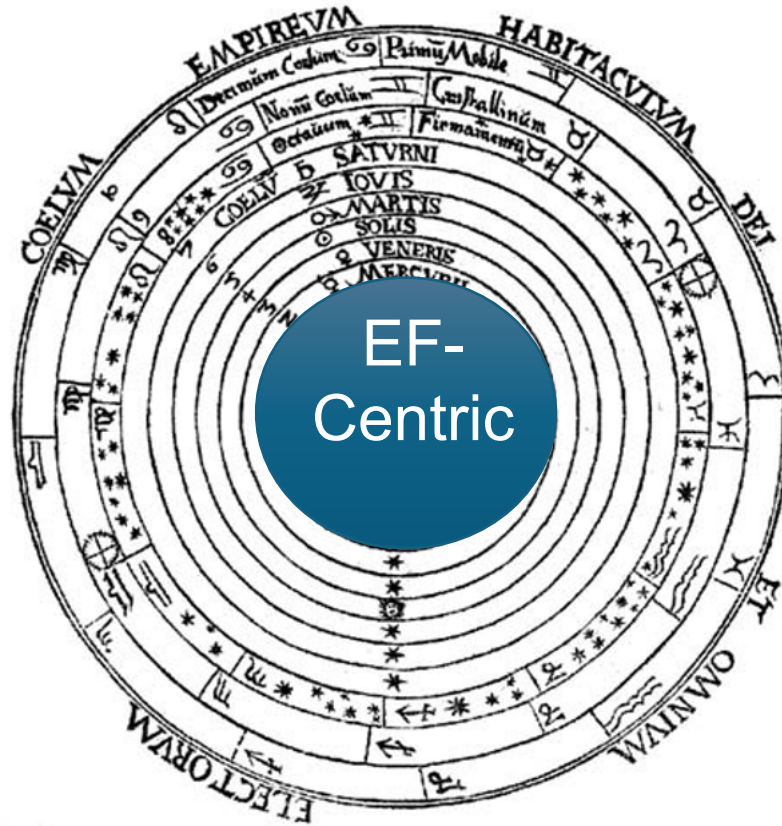
Table 5 Association between structural cytoskeleton Z-disk gene mutations and absence of left ventricular reverse remodelling at multivariable logistic regression analysis.

(5a) Only pathogenic and likely pathogenic variant carriers included			
	OR	95% CI	p
Structural cytoskeleton Z-disk genes	0.065	0.008 to 0.535	0.011
LBBB	0.385	0.160 to 0.926	0.033
LVEF*	0.955	0.920 to 0.992	0.016
SBP*	1.017	0.994 to 1.039	0.145

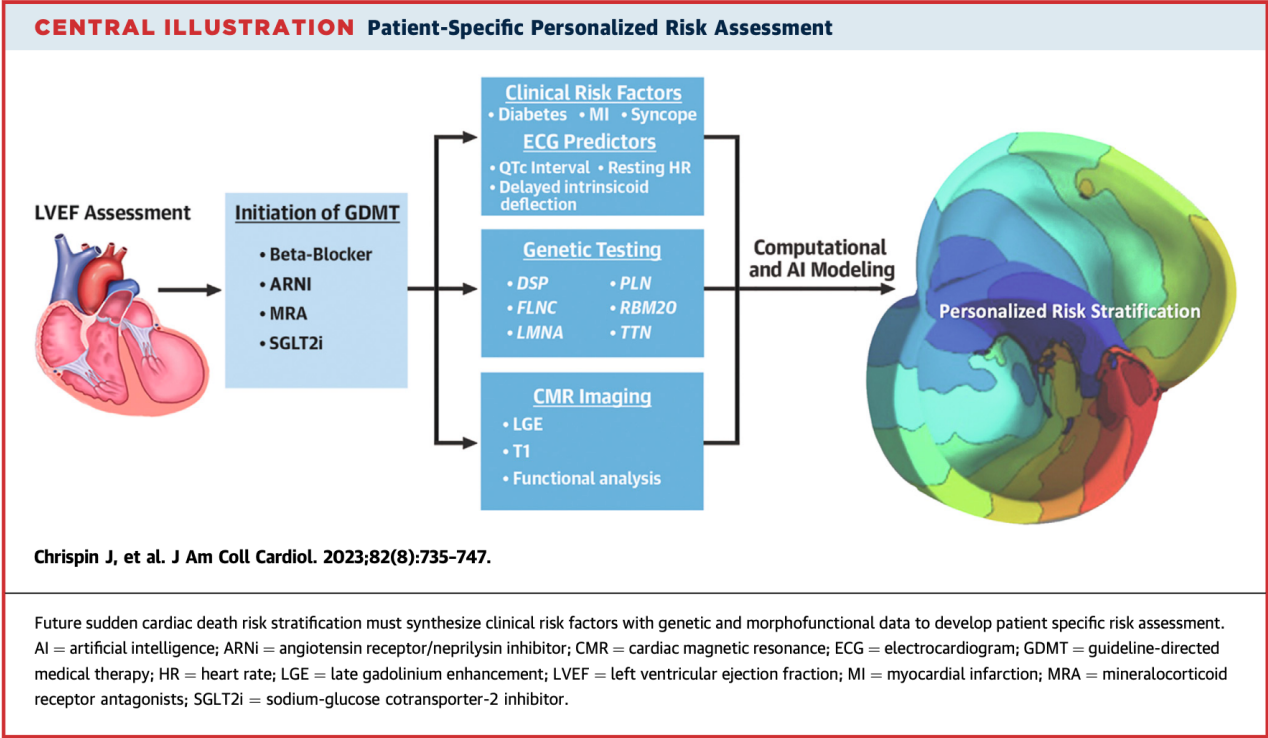
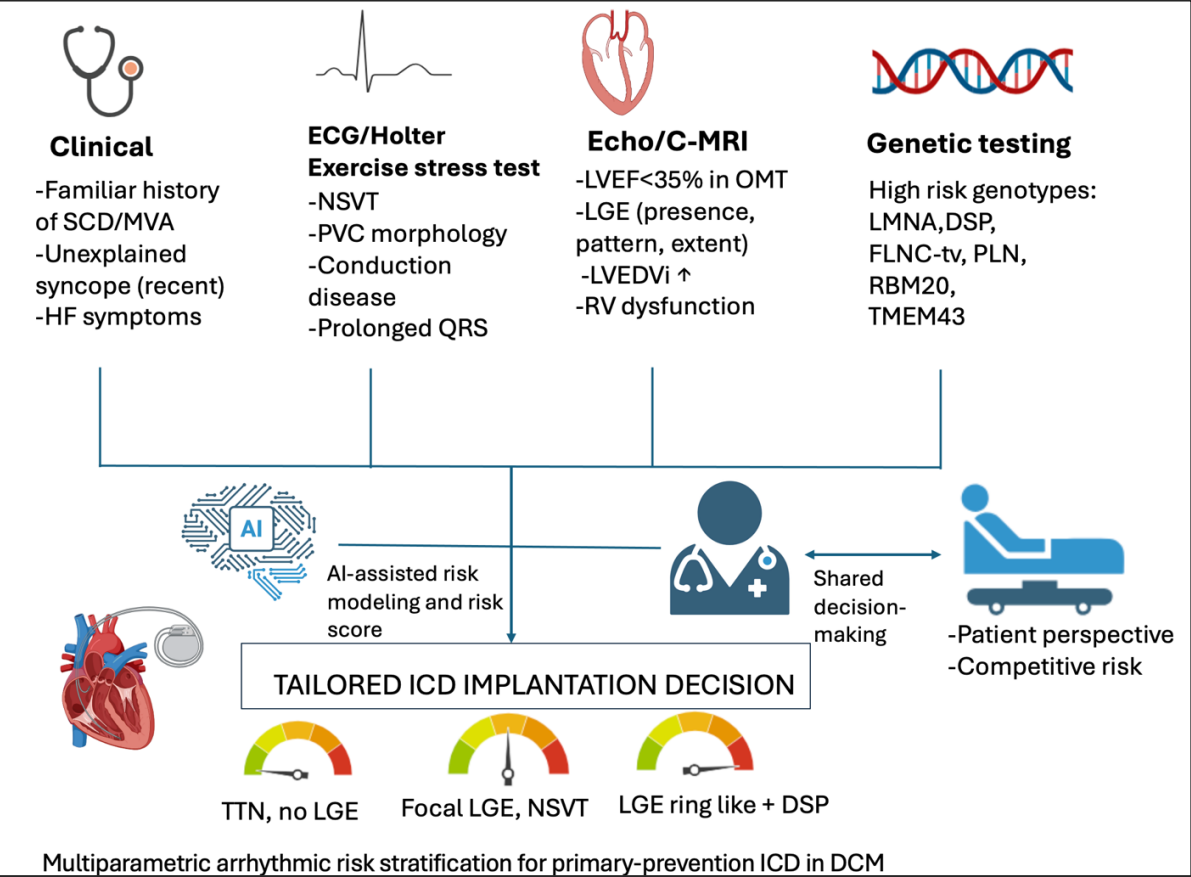
(5b) Pathogenic, likely pathogenic and possibly pathogenic rare variants (PPrV) carriers included			
	OR	95% CI	p
Structural cytoskeleton Z-disk genes	0.131	0.035 to 0.490	0.003
LBBB	0.365	0.150 to 0.886	0.026
LVEF*	0.995	0.920 to 0.992	0.016
SBP*	1.017	0.994 to 1.039	0.147

OR estimation is referred to every unit increase or decrease for continuous variables. Previously established clinical predictors of LVRR were entered into the multivariable model.⁸
LBBB, left bundle branch block; LVEF, left ventricular ejection fraction; SBP, systolic blood pressure.

The Copernican revolution



We need a multiparametric approach!



Garoia F. ..Merlo M., Sinagra G. et al, 2025 (Springer Book- Cardiomyopathies in Practice-From Deep Phenotyping to Precision Medicine-Submitted)

Future directions

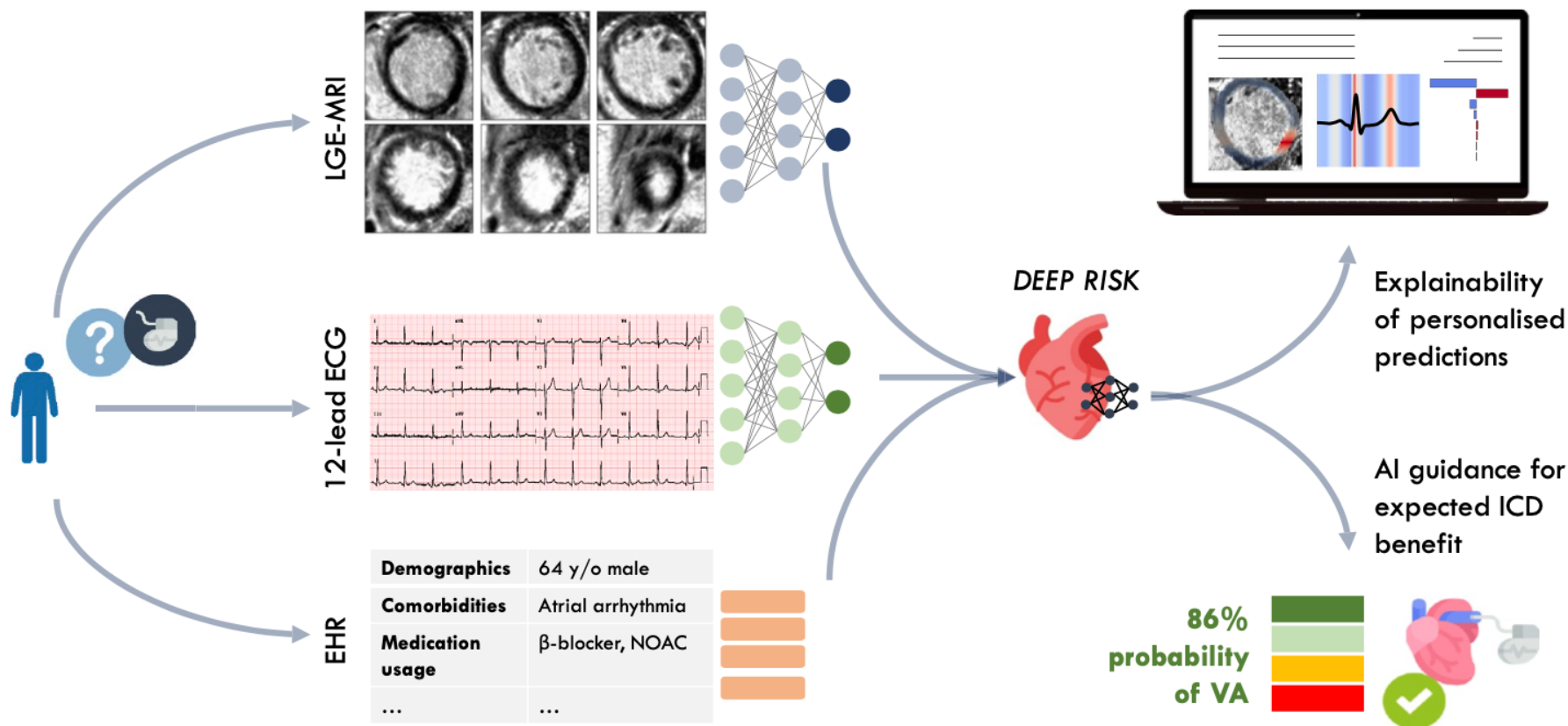
scientific reports

OPEN

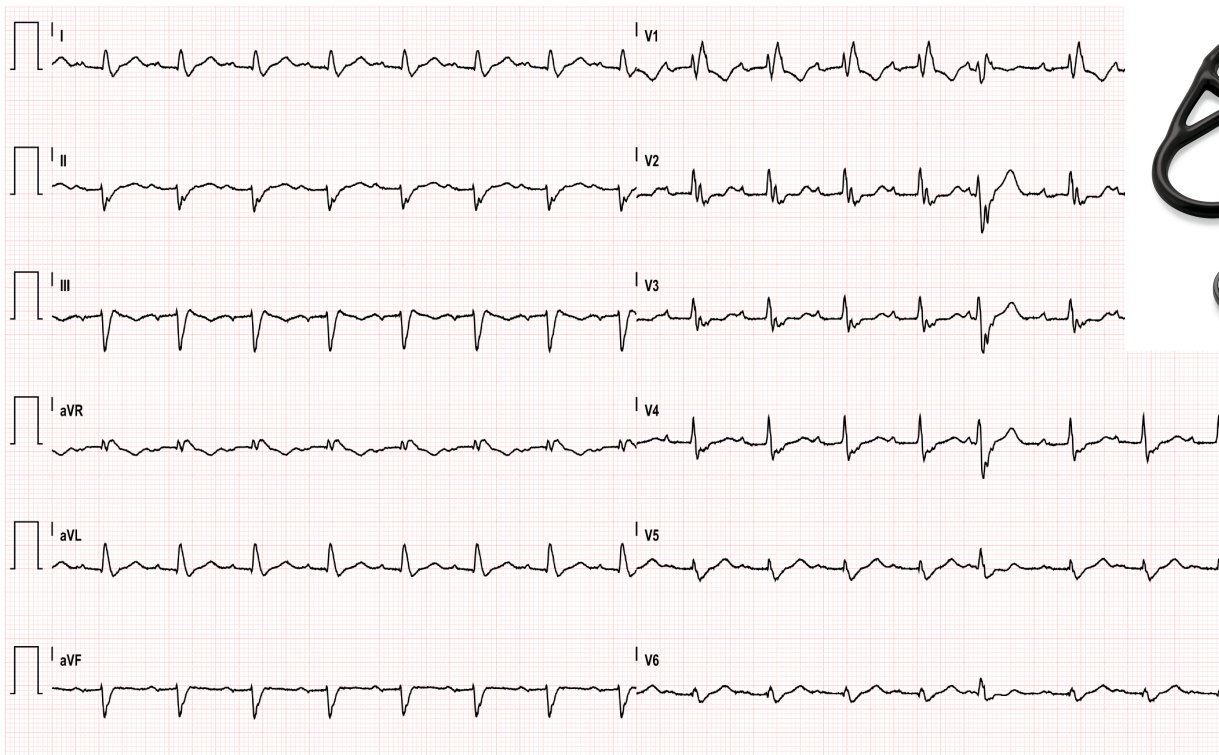
Multimodal explainable artificial intelligence identifies patients with non-ischaemic cardiomyopathy at risk of lethal ventricular arrhythmias

Maarten Z. H. Kolk^{1,2}, Samuel Ruipérez-Campillo^{3,4}, Cornelis P. Allaart⁵, Arthur A. M. Wilde^{1,2}, Reinoud E. Knops^{1,2}, Sanjiv M. Narayan¹, Fleur V. Y. Tjong^{1,2,3,6} & DEEP RISK investigators*

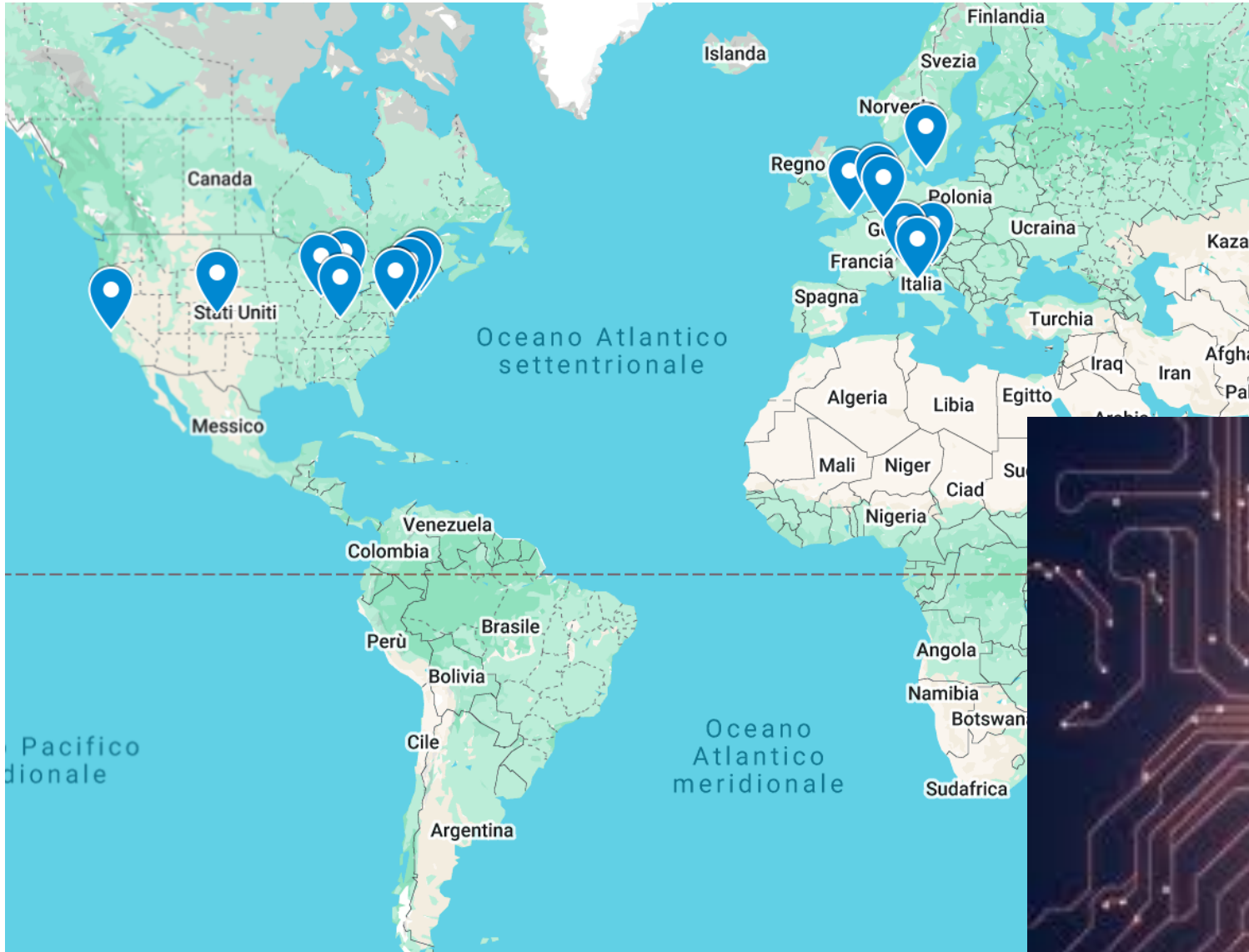
A DEEP RISK pipeline: personalised risk prediction



Nature, 2024. Kolk at



Share center



GRAZIE



INCONTRI *in* CARDIOLOGIA 2026



UPDATE SU SCOMPENSO CARDIACO E CARDIOMIOPATIE

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ERN GUARD-HEART Rete malattie Cardiache Rare

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DIPARTIMENTO CARDIORACOVASCOLARE
SC CARDIOLOGIA


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for rare or low prevalence
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SCUOLA DI SPECIALIZZAZIONE
IN MALATTIE DELL'APPARATO CARDIOVASCOLARE