



# ¿A quién pedir y cómo interpretar un estudio genético?

Joel Salazar-Mendiguchía

Health in Code

A Coruña

# Conflicto de intereses





# ESC Core Curriculum for the General Cardiologist (2013)

European Society of Cardiology

Committee for Education

- the major monogenic cardiovascular diseases, such as
  - cardiomyopathies;
  - familial aortopathies;
  - familial arrhythmias;
  - trisomies, in particular trisomy 21;
  - familial dyslipidaemias.

## Skills

The ability to:

- evaluate relevant family history and construct a family pedigree;
- counsel index cases and family members at risk on the probability of being affected by a genetic cardiovascular disorder;
- recognize problems with pedigree interpretation such as incomplete penetrance, variable expressivity, and age-related patterns of expressivity;
- manage the uncertainties associated with genetic testing;
- direct patients and families when appropriate to major centres with a specialized interest in their particular disorder.



# Pasos previos al estudio genético

September 2015

Author

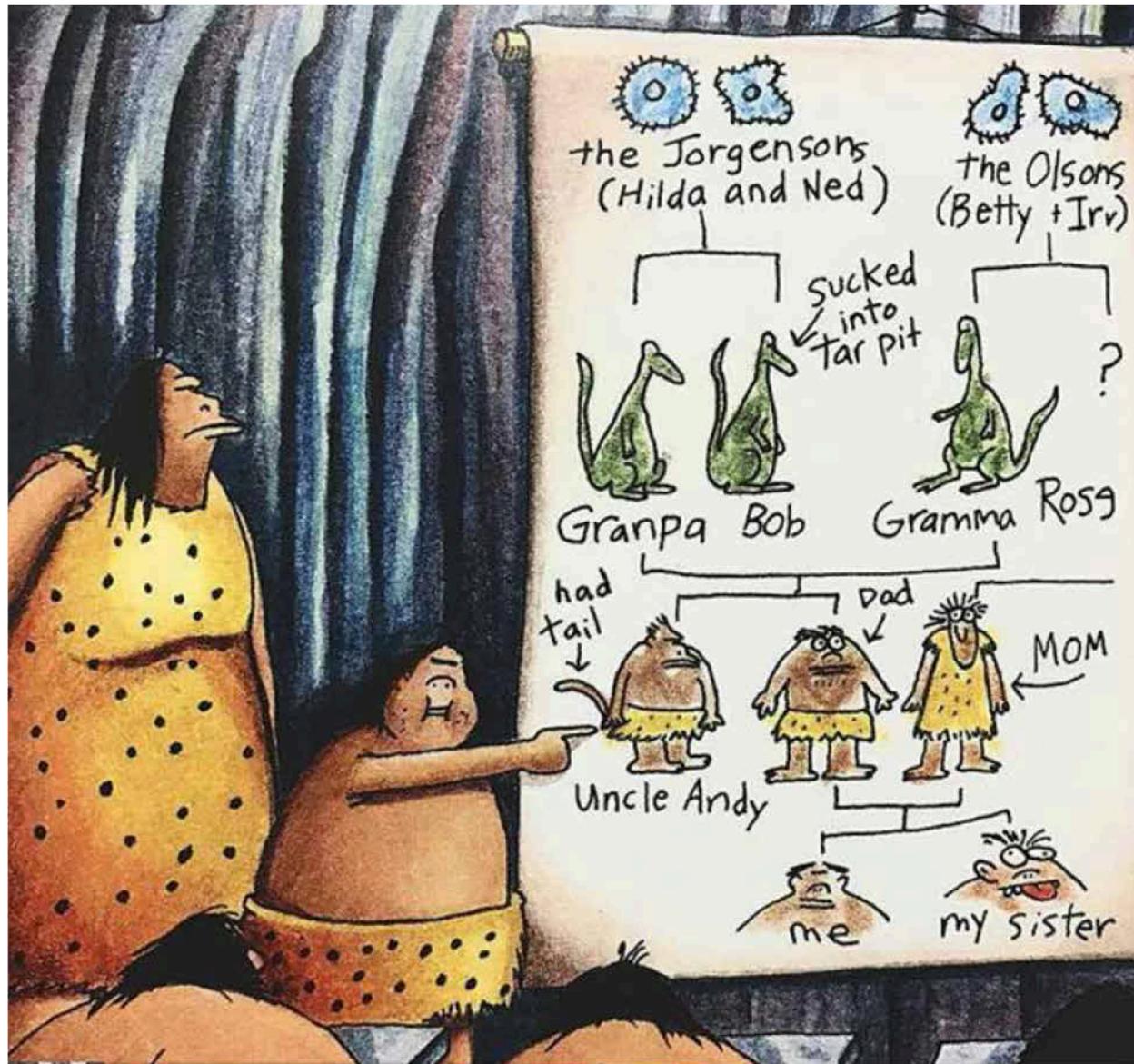
Sobia Raza

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## Phenotyping patients for genomic diagnostics



The realisation of genomic medicine in clinical practice rests on efficient and accurate interpretation of genomic data. Descriptions of a patient's clinical features - their 'phenotypes' - are essential to drive and target the correct analysis of this data. Maximising the benefits of genomic testing and managing the increasing demand for genetic tests depends on significant improvements in capturing and exchanging the appropriate phenotypic information across the NHS.





"Your domestic problems seem to be genetic due to the fact your parents reproduced."



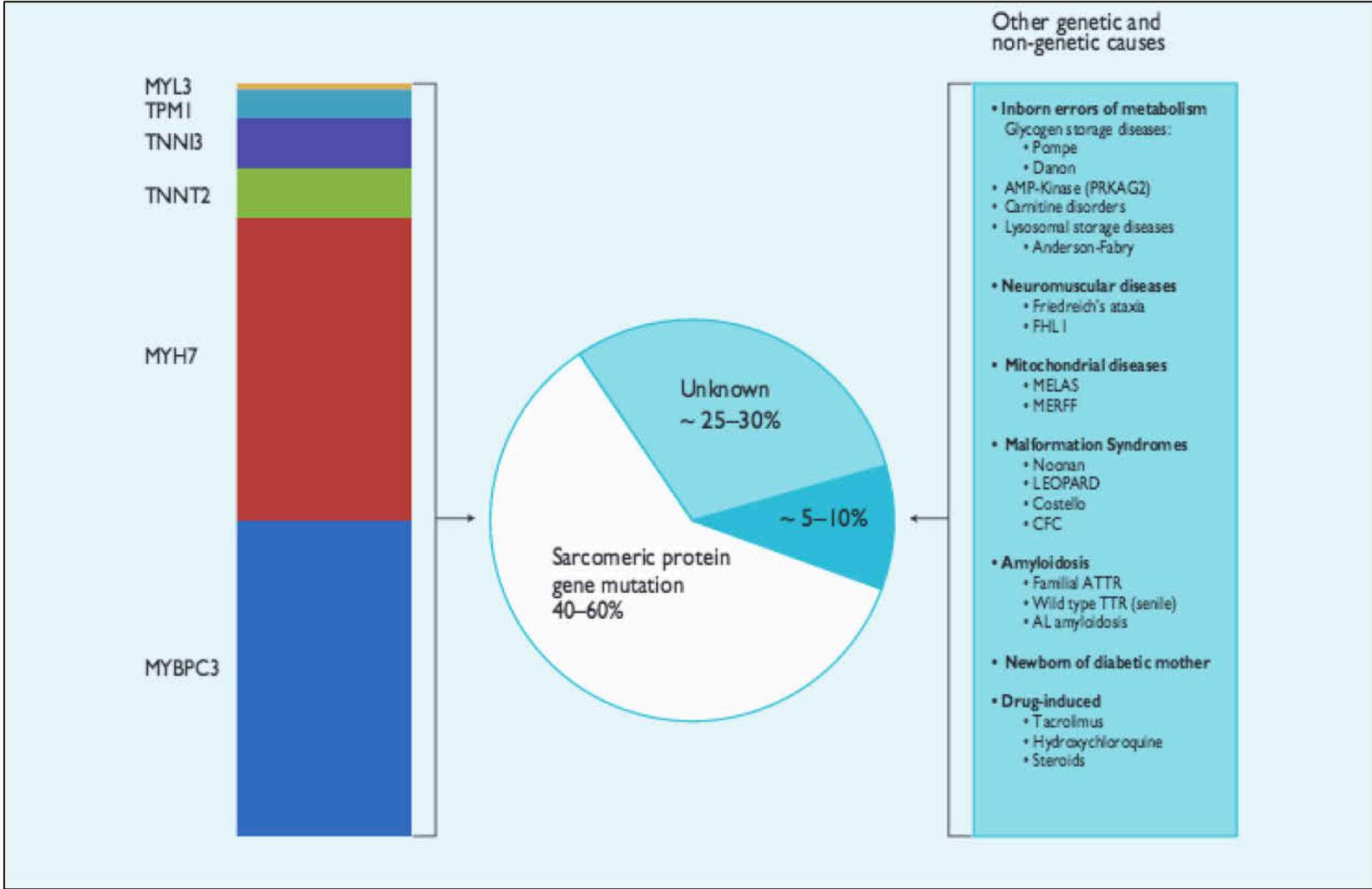
# HRS/EHRA Expert Consensus Statement on the State of Genetic Testing for the Channelopathies and Cardiomyopathies

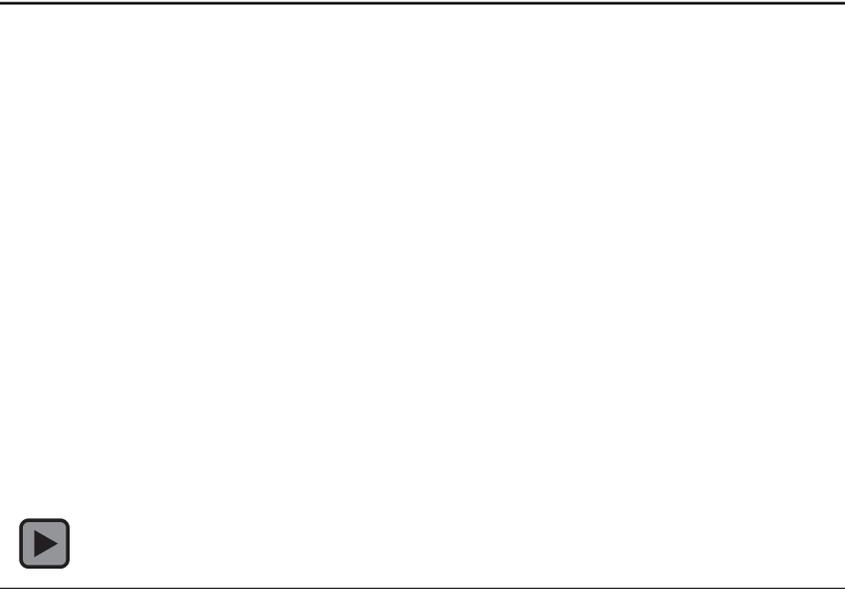
Section # – Disease	Diagnostic	Prognostic
Section VII – HCM	+++	++
Section VIII – ACM/ARVC	+	+/-
Section IX – DCM	+/-	-
Section IX – DCM + CCD	++	++
Section X – LVNC	+	-
Section XI – RCM	+	+



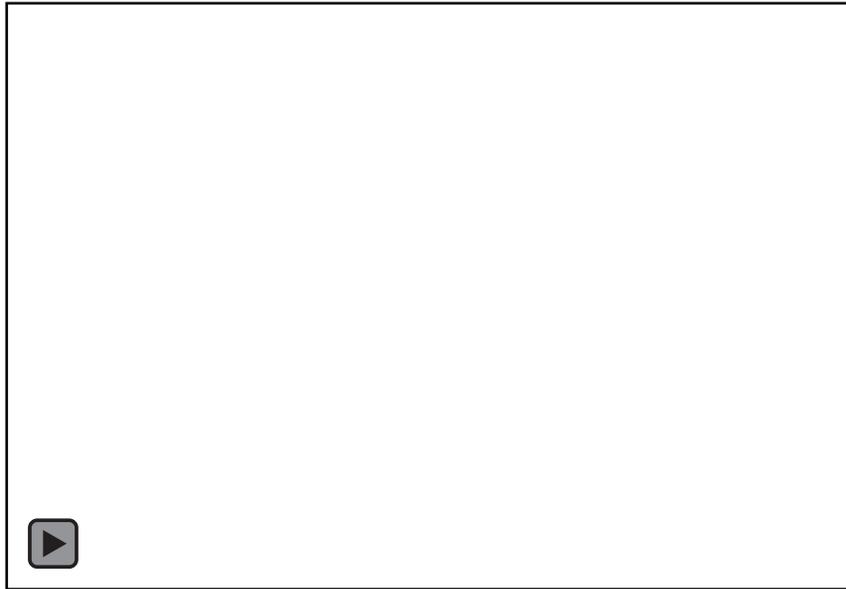
Recommendations	Class <sup>a</sup>	Level <sup>b</sup>	Ref. <sup>c</sup>
Genetic counselling is recommended for all patients with HCM when their disease cannot be explained solely by a non-genetic cause, whether or not clinical or genetic testing will be used to screen family members.	I	B	169–173
Genetic counselling should be performed by professionals trained for this specific task working within a multidisciplinary specialist team.	IIa	C	168–173

Recommendations	Class <sup>a</sup>	Level <sup>b</sup>	Ref. <sup>c</sup>
Genetic testing is recommended in patients fulfilling diagnostic criteria for HCM, when it enables cascade genetic screening of their relatives.	I	B	24,175 178–180
It is recommended that genetic testing be performed in certified diagnostic laboratories with expertise in the interpretation of cardiomyopathy-related mutations.	I	C	168,172,183
In the presence of symptoms and signs of disease suggestive of specific causes of HCM, genetic testing is recommended to confirm the diagnosis.	I	B	36–40, 43–46,67
Genetic testing in patients with a borderline <sup>d</sup> diagnosis of HCM should be performed only after detailed assessment by specialist teams.	IIa	C	168
Post-mortem genetic analysis of stored tissue or DNA should be considered in deceased patients with pathologically confirmed HCM, to enable cascade genetic screening of their relatives.	IIa	C	181,182

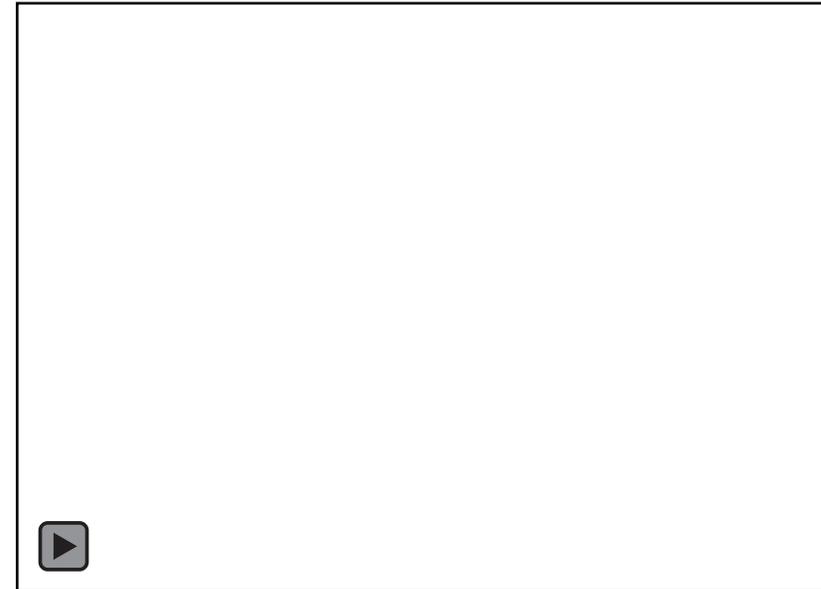




- 18 años
- SIV 15 mm / AI 45 mm / Grad pico 45 mmHg
- MS familiar



- 18 años
- SIV 15 mm / AI 45 mm / Grad pico 45 mmHg
- MS familiar

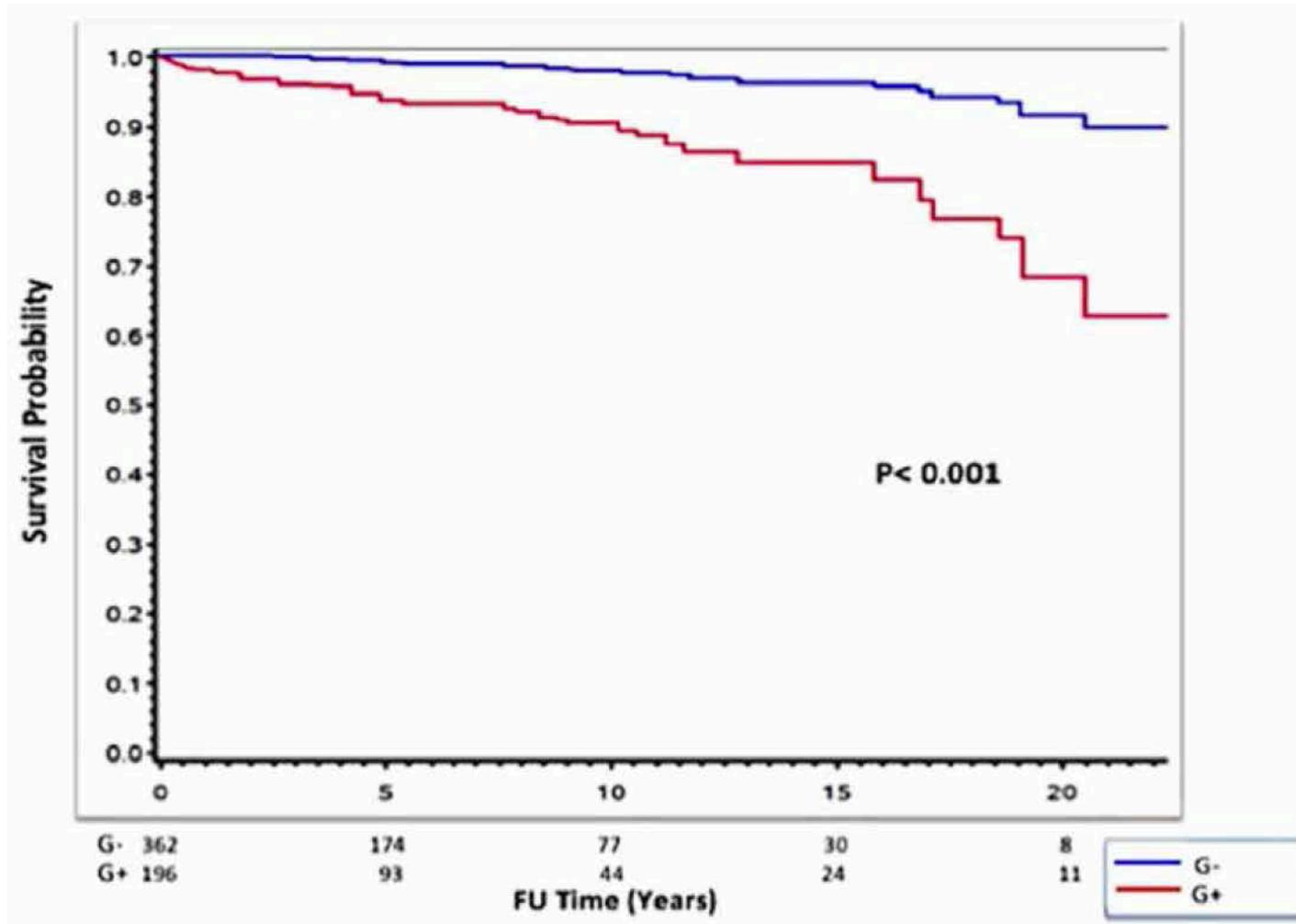


- 18 años
- SIV 15 mm / AI 45 mm / Grad pico 45
- MS familiar

<b>Risk of SCD at 5 years (%):</b> 4.93
<b>ESC recommendation:</b> ICD may be considered



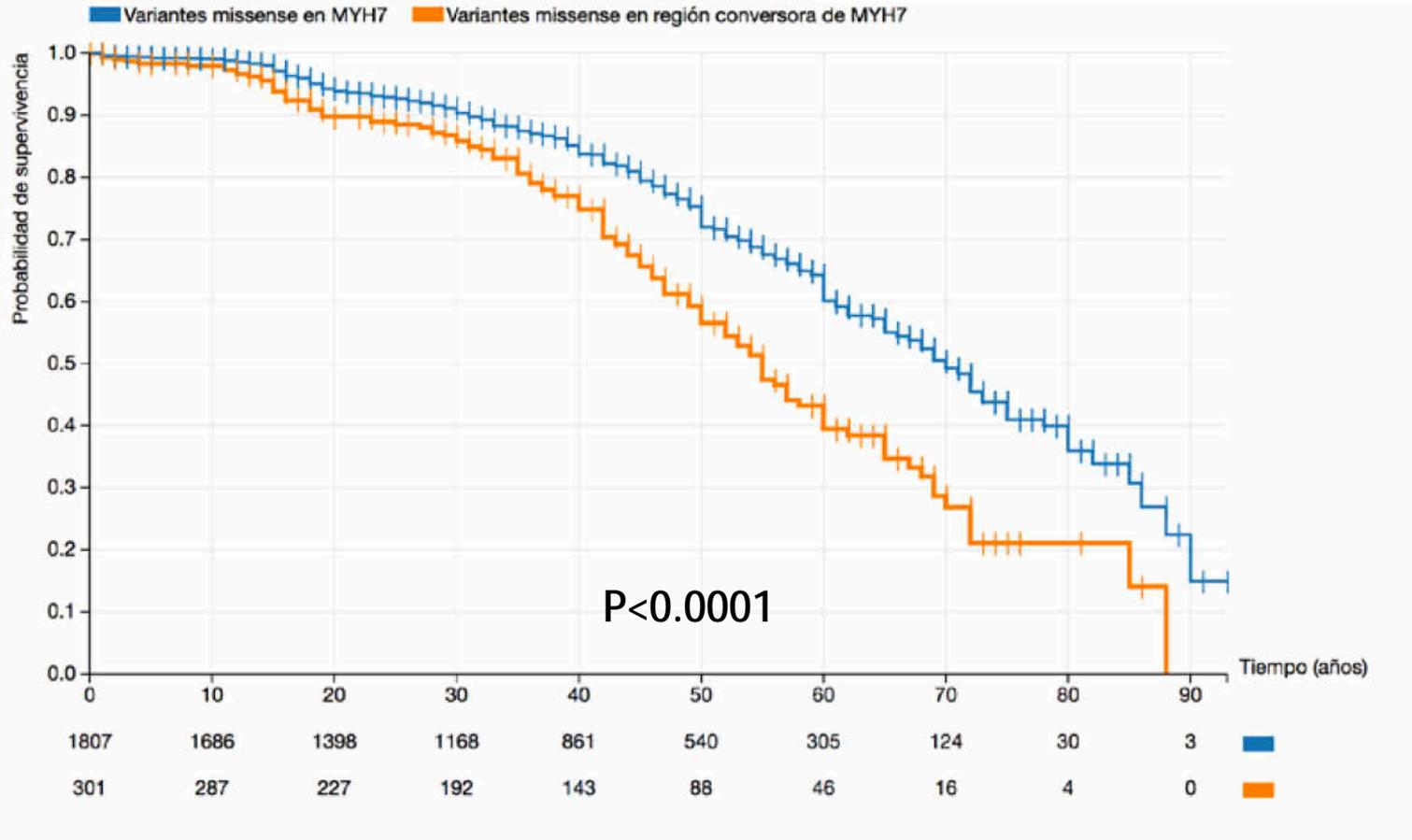
# Miocardiopatía hipertrófica





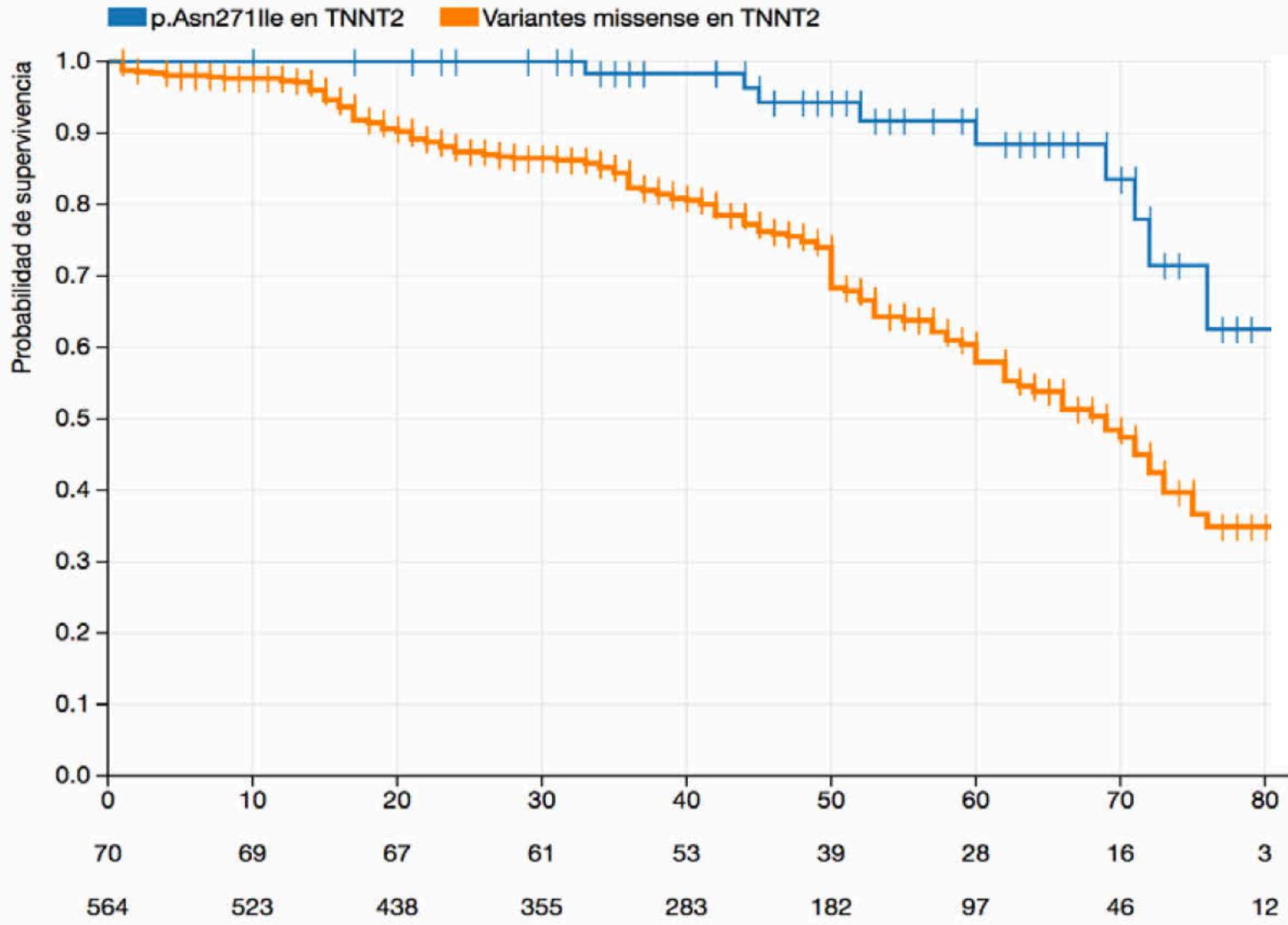
ORIGINAL ARTICLE

# Phenotype and prognostic correlations of the converter region mutations affecting the $\beta$ myosin heavy chain





### Función de supervivencia





# HRS/EHRA Expert Consensus Statement on the State of Genetic Testing for the Channelopathies and Cardiomyopathies

Section # – Disease	Diagnostic	Prognostic
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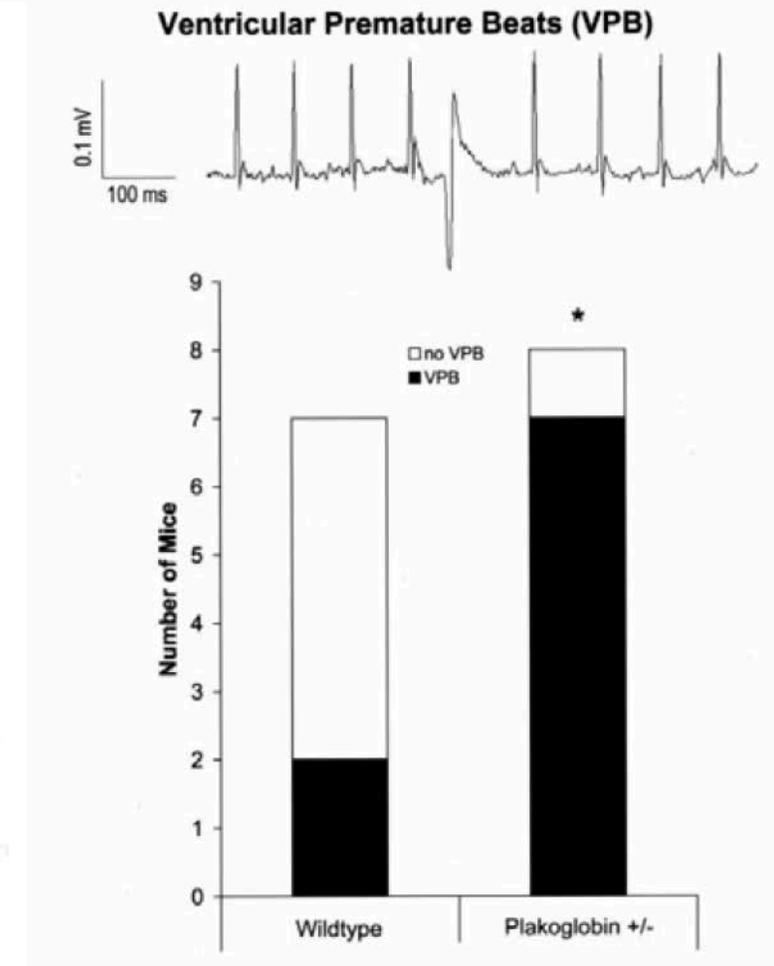
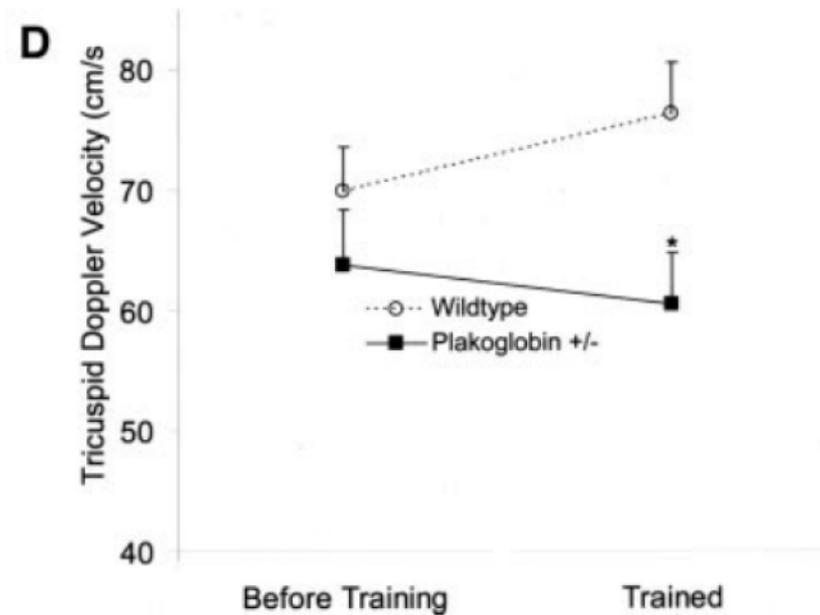
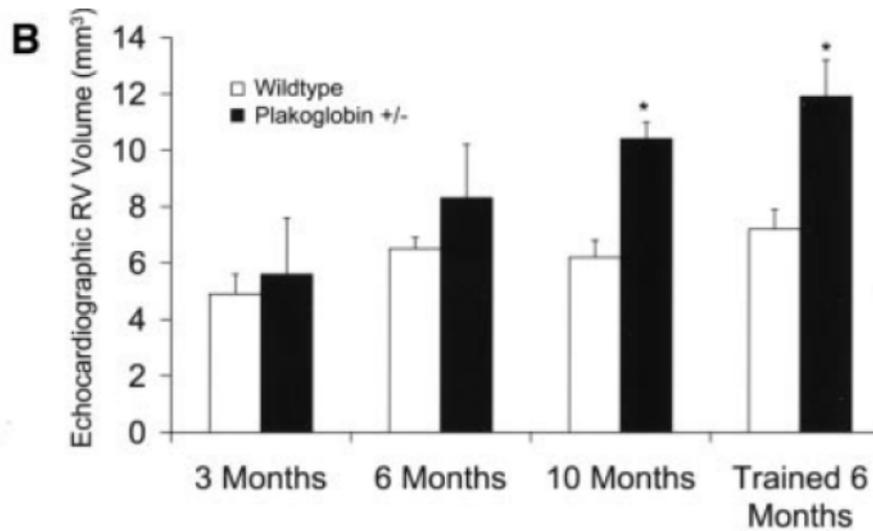
# Diagnosis of arrhythmogenic right ventricular cardiomyopathy/dysplasia

## Major criteria

- ARVC/D confirmed in a first-degree relative who meets current Task Force criteria
- ARVC/D confirmed pathologically at autopsy or surgery in a first-degree relative
- Identification of a pathogenic mutation<sup>†</sup> categorized as associated or probably associated with ARVC/D in the patient under evaluation

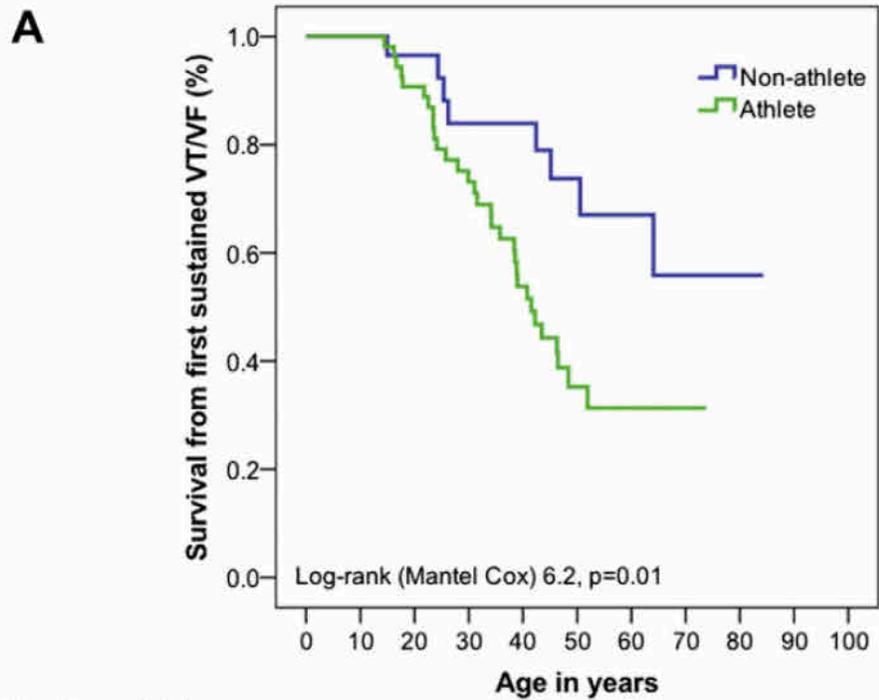


# Age- and Training-Dependent Development of Arrhythmogenic Right Ventricular Cardiomyopathy in Heterozygous Plakoglobin-Deficient Mice



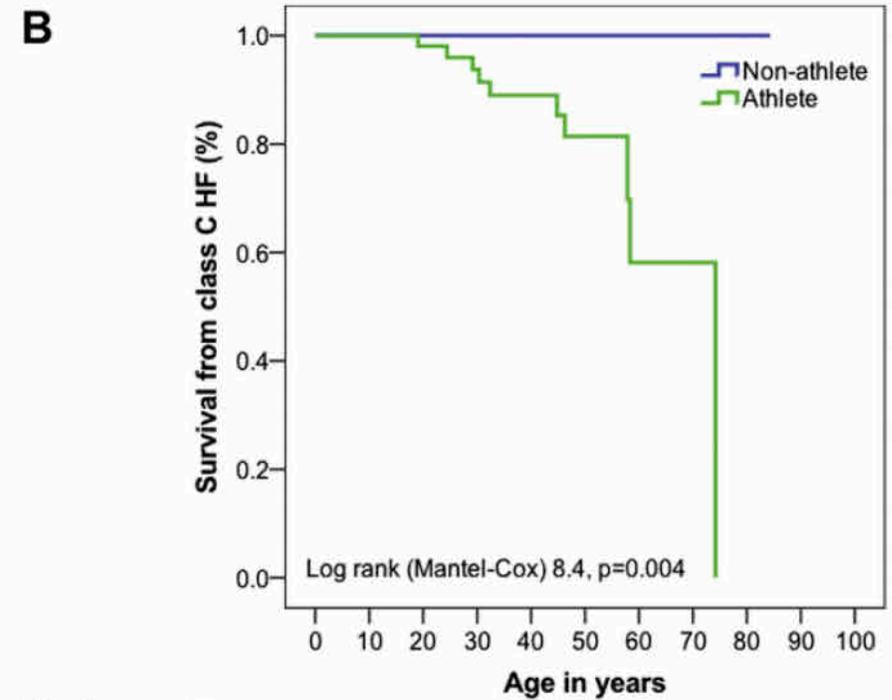


# Exercise Increases Age-Related Penetrance and Arrhythmic Risk in Arrhythmogenic Right Ventricular Dysplasia/Cardiomyopathy-Associated Desmosomal Mutation Carriers



Numbers at risk

Non-athlete	31	31	24	20	18	11	9	3	1	0	0
Athlete	56	56	49	36	24	9	3	2	0	0	0

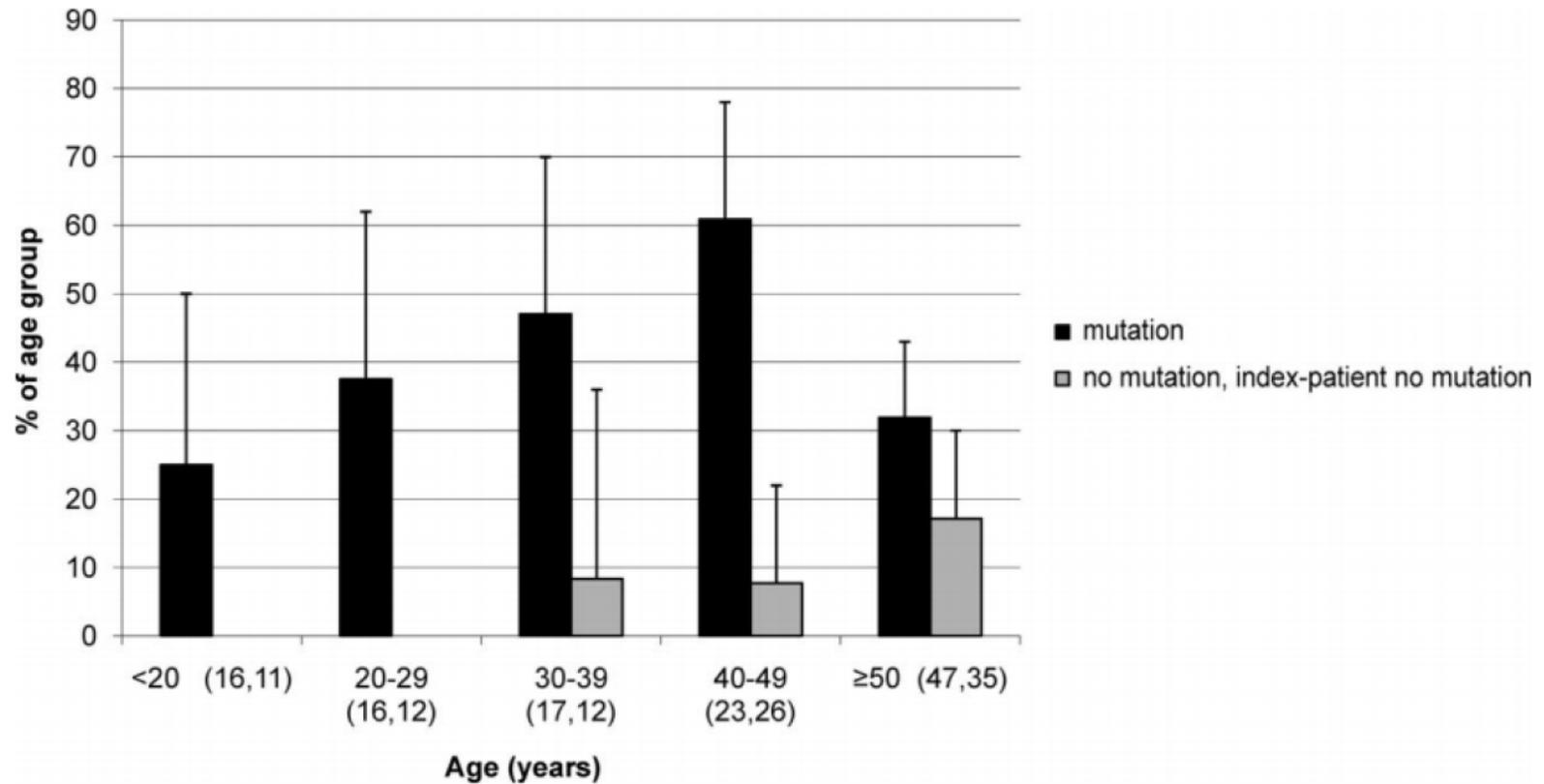


Numbers at risk

Non-athlete	31	31	24	22	18	11	9	4	1	0	0
Athlete	56	56	50	41	32	14	4	2	0	0	0

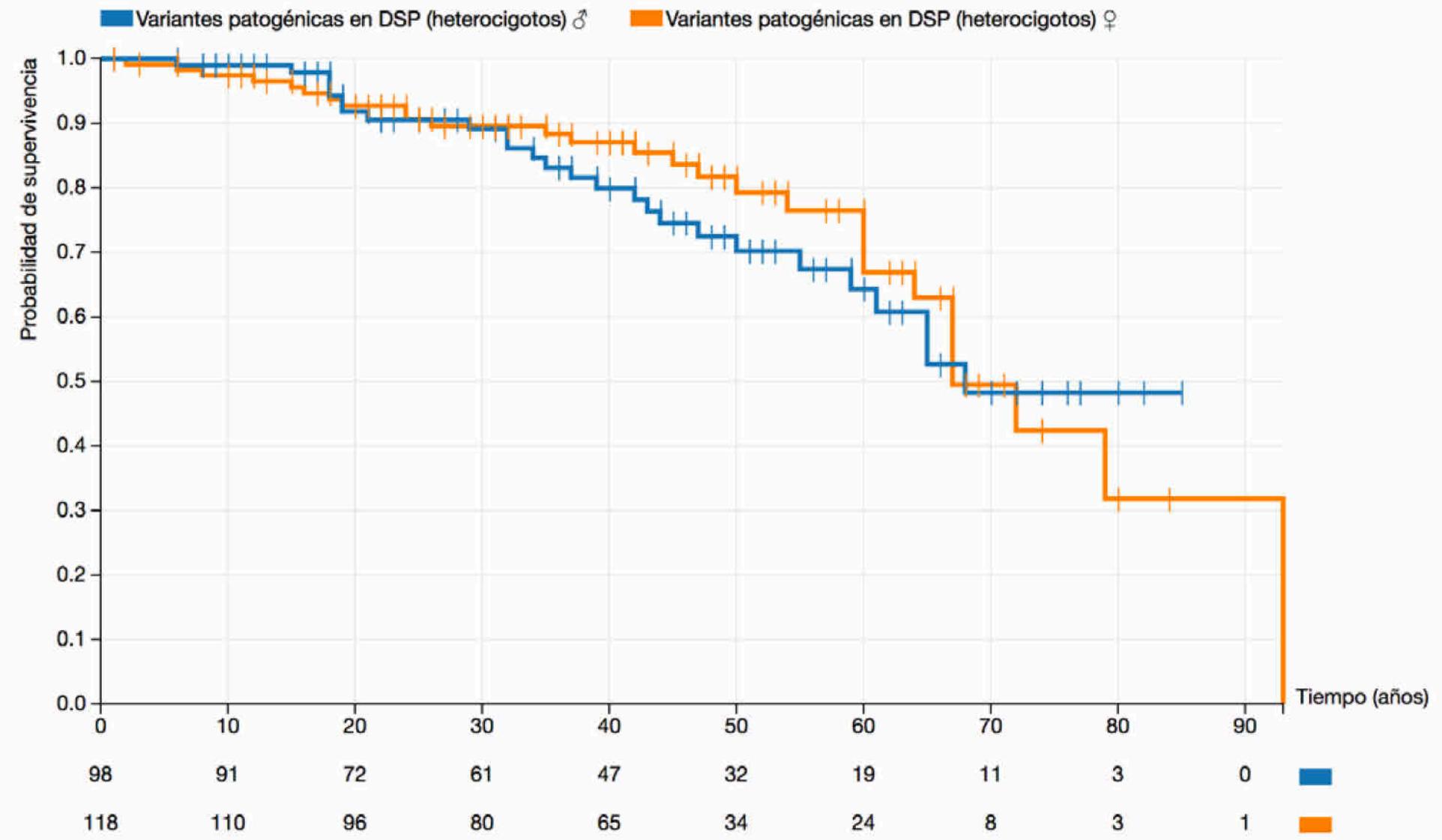


# Arrhythmogenic Right Ventricular Dysplasia/Cardiomyopathy Pathogenic Desmosome Mutations in Index-Patients Predict Outcome of Family Screening: Dutch Arrhythmogenic Right Ventricular Dysplasia/Cardiomyopathy Genotype-Phenotype Follow-Up Study



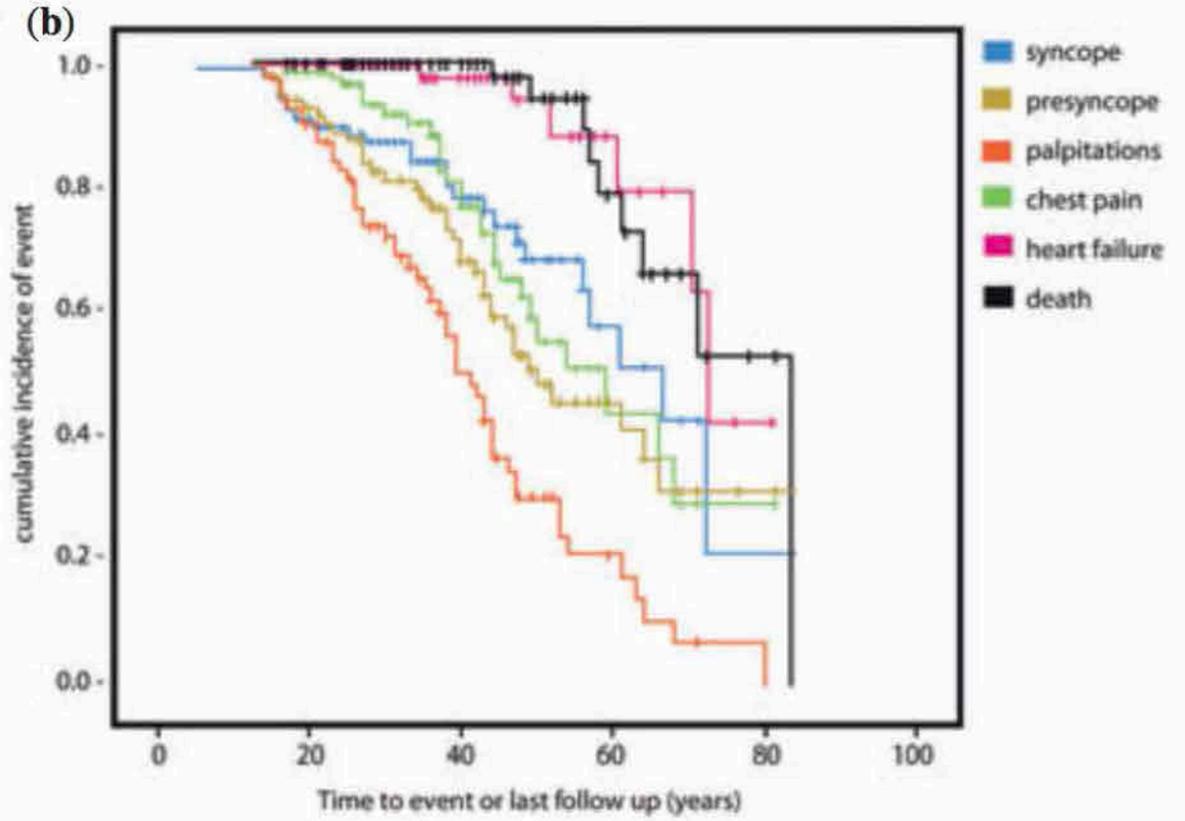
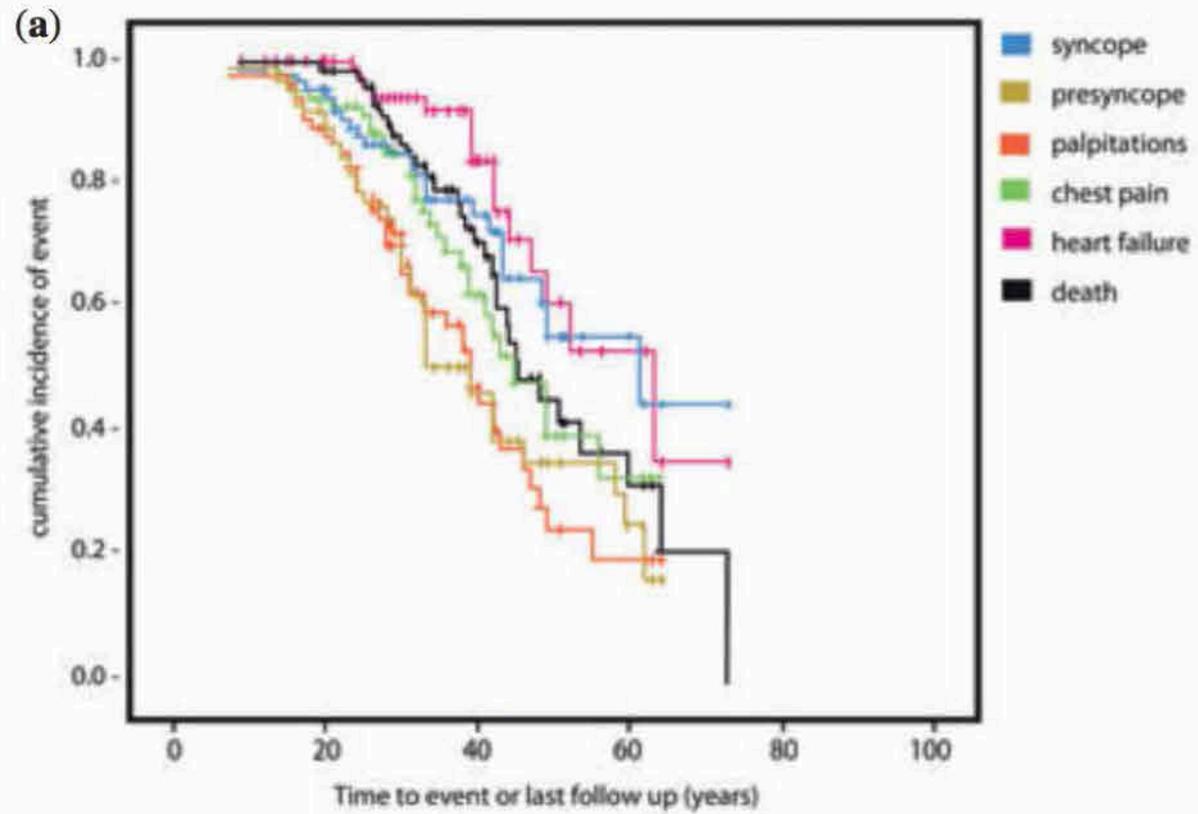


### Función de supervivencia





# The natural history of a genetic subtype of arrhythmogenic right ventricular cardiomyopathy caused by a p.S358L mutation in TMEM43





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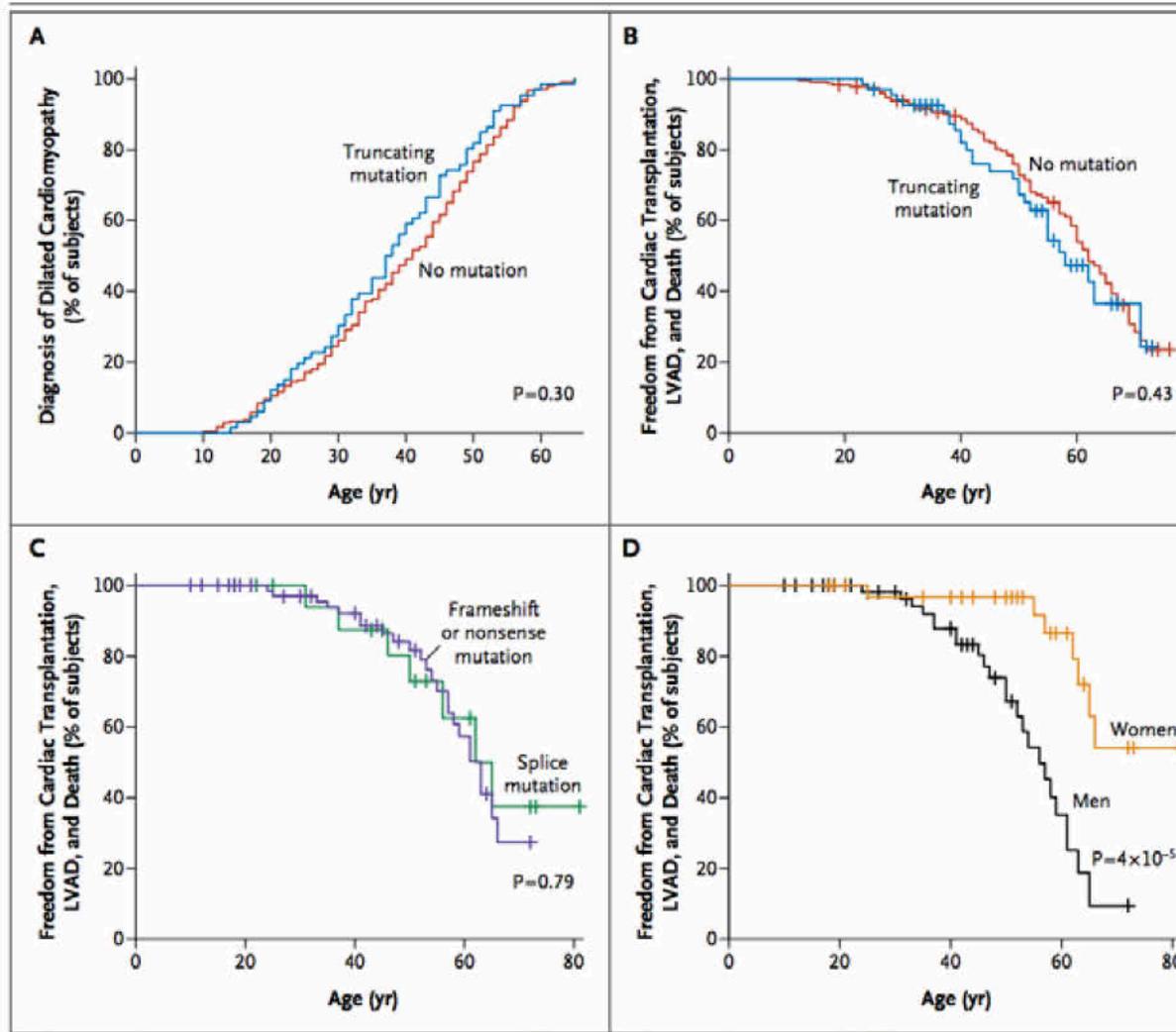
- Varón 40 años
- Disfunción ventricular izquierda severa
- Antecedentes familiares de muerte súbita



- Varón 40 años
- Disfunción ventricular izquierda moderada
- Sin antecedentes familiares de muerte súbita

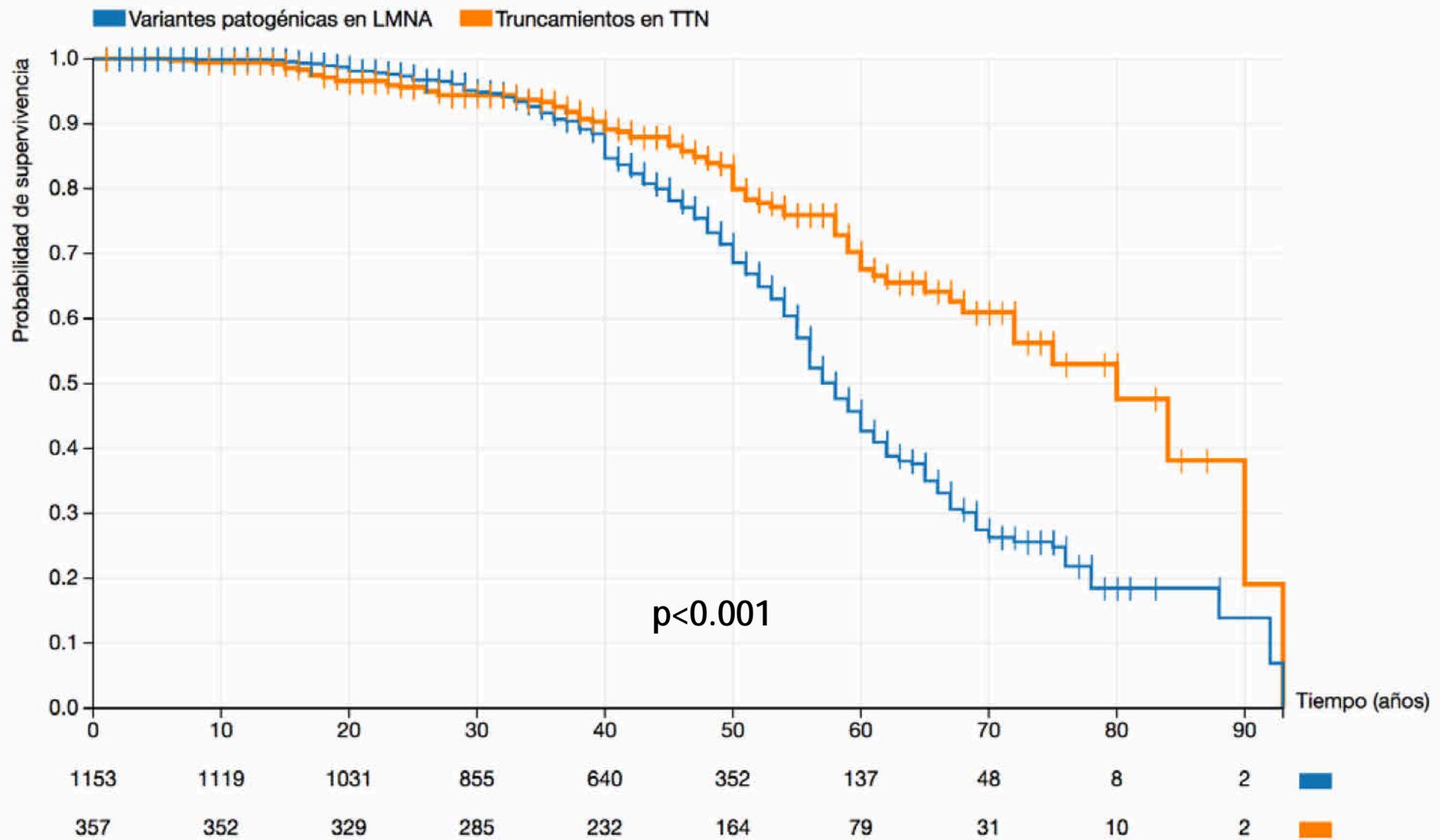


# Truncations of Titin Causing Dilated Cardiomyopathy





# Función de supervivencia

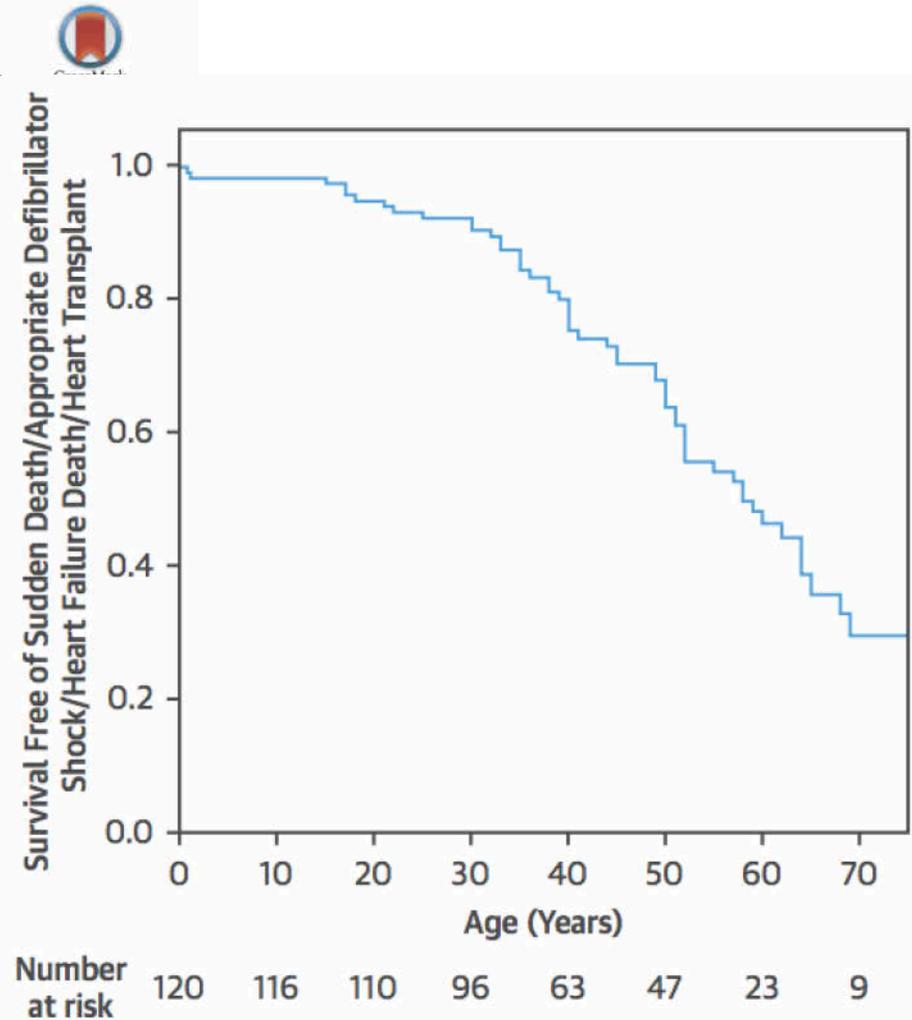




# Truncating *FLNC* Mutations Are Associated With High-Risk Dilated and Arrhythmogenic Cardiomyopathies

**CONCLUSIONS** Truncating mutations in *FLNC* caused an overlapping phenotype of dilated and left-dominant arrhythmogenic cardiomyopathies complicated by frequent premature sudden death. Prompt implantation of a cardiac defibrillator should be considered in affected patients harboring truncating mutations in *FLNC*.

(J Am Coll Cardiol 2016;68:2440-51) © 2016 by the American College of Cardiology Foundation.





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Section X – LVNC	+	-
Section XI – RCM	+	+

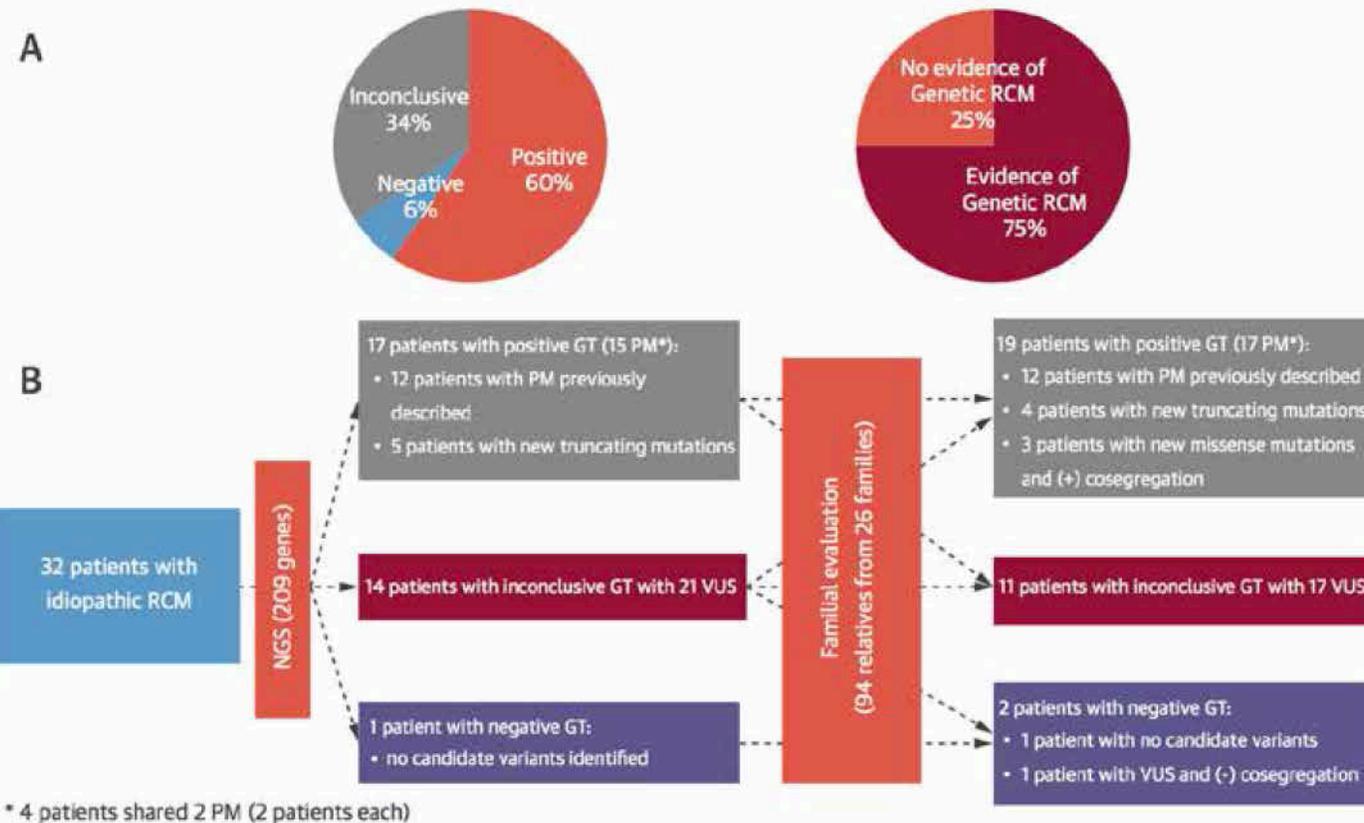


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Section X – LVNC	+	-
Section XI – RCM	+	+



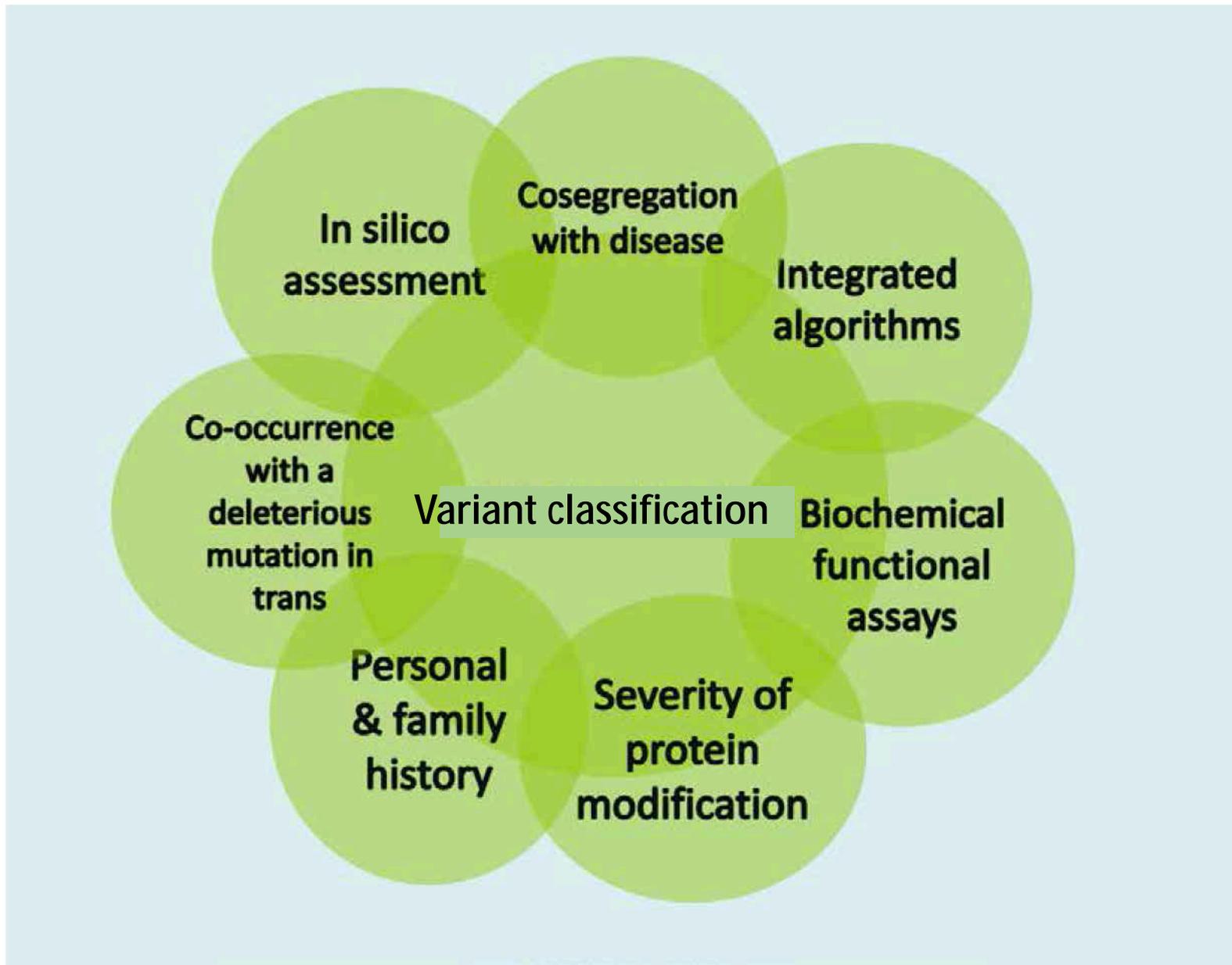
# Idiopathic Restrictive Cardiomyopathy Is Primarily a Genetic Disease

**FIGURE 1** Global Genetic Testing Results and Genetic Evaluation Flowchart in 32 Individuals With Idiopathic RCM





Pedir un estudio genético es muy sencillo...  
Lo importante es darle una interpretación





Nephrol Dial Transplant (2008) 23: 4044–4048  
doi: 10.1093/ndt/gfn370  
Advance Access publication 2 July 2008

**NDT**  
Nephrology Dialysis Transplantation

*Original Article*

## **Two-tier approach for the detection of alpha-galactosidase A deficiency in kidney transplant recipients**

Gert De Schoenmakere<sup>1,2,\*</sup>, Bruce Poppe<sup>3,\*</sup>, Birgitte Wuyts<sup>4</sup>, Kathleen Claes<sup>3</sup>, David Cassiman<sup>5</sup>, Bart Maes<sup>6,2</sup>, Dierik Verbeelen<sup>6,7</sup>, Raymond Vanholder<sup>1</sup>, Dirk R. Kuypers<sup>8</sup>, Norbert Lameire<sup>1</sup>, Anne De Paepe<sup>3</sup> and Wim Terry<sup>1,9,\*</sup>

278 hombres – 395 mujeres  
1 caso (varón) – Ala143Thr

ily members has AFD-related signs or symptoms. Despite the delayed diagnosis, treatment with recombinant human AGALA is planned for the index patient. The results of



Lenders *et al.* *Orphanet Journal of Rare Diseases* (2016) 11:54  
DOI 10.1186/s13023-016-0441-z

Orphanet Journal of  
Rare Diseases

RESEARCH

Open Access



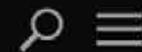
# Alpha-Galactosidase A p.A143T, a non-Fabry disease-causing variant

Malte Lenders<sup>1</sup>, Frank Weidemann<sup>2,3</sup>, Christine Kurschat<sup>4</sup>, Sima Canaan-Kühl<sup>5</sup>, Thomas Duning<sup>6</sup>, Jörg Stypmann<sup>7</sup>, Boris Schmitz<sup>8</sup>, Stefanie Reiermann<sup>1</sup>, Johannes Krämer<sup>2,9</sup>, Daniela Blaschke<sup>10</sup>, Christoph Wanner<sup>2</sup>, Stefan-Martin Brand<sup>8</sup> and Eva Brand<sup>1\*</sup>



Health » Misdiagnoses: A hidden risk of genetic testing

International Edition +



# Misdiagnoses: A hidden risk of genetic testing

By Jacqueline Howard, CNN

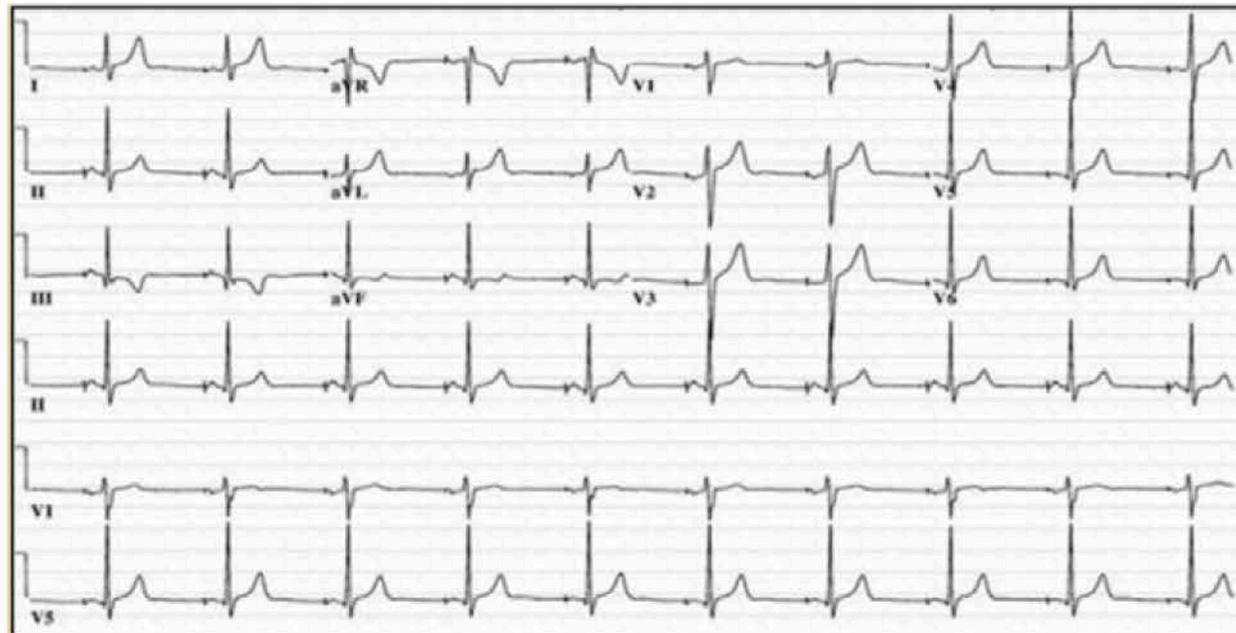
🕒 Updated 1448 GMT (2248 HKT) October 31, 2016

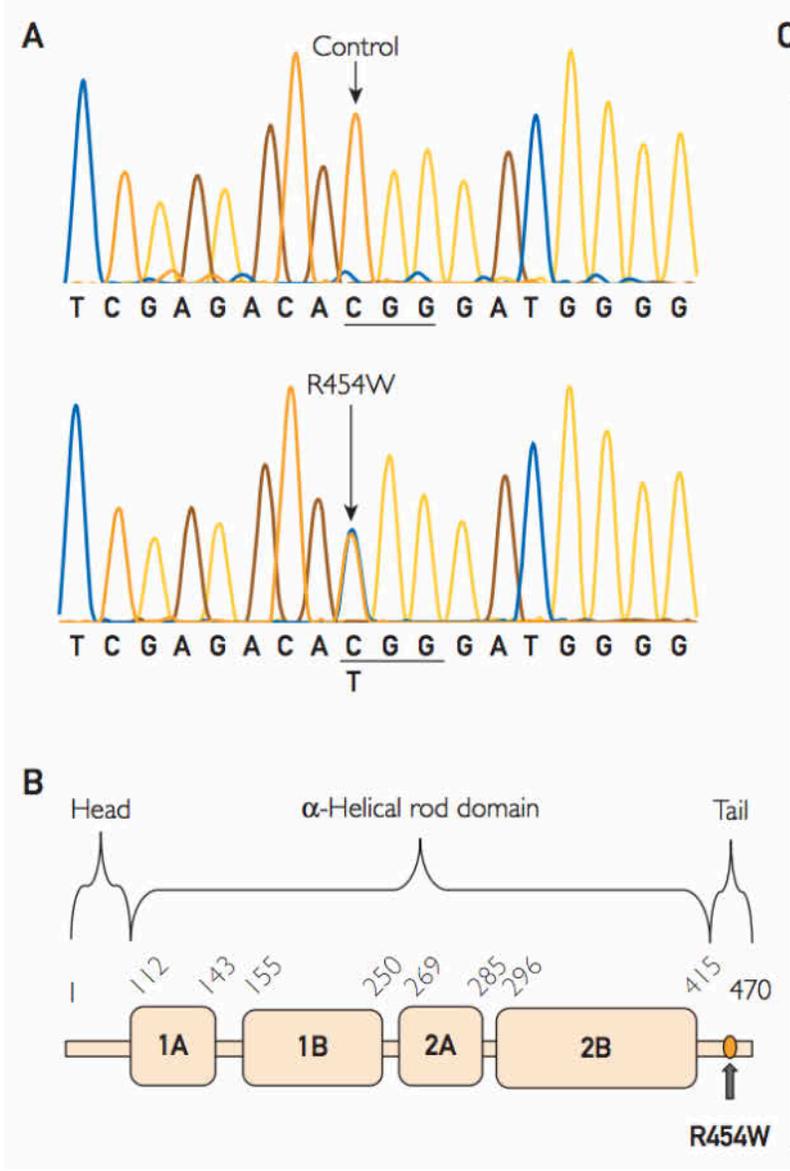




# The Promise and Peril of Precision Medicine

Jaeger P. Ackerman, BA; Daniel C. Bartos, PhD; Jamie D. Kapplinger, BS;  
David J. Tester, BS; Brian P. Delisle, PhD; and Michael J. Ackerman, MD, PhD





**C**

	Pathogenic			
	Supporting	Moderate	Strong	Very strong
<b>Population data</b>		Absent in 1000G and ESP	Prevalence in affected individuals statistically significantly increased over controls	
<b>Computational and predictive data</b>	Multiple lines of computational evidence support a deleterious effect on the gene/gene product	Novel missense change at an amino acid residue where a different pathogenic missense change has been seen before In-frame INDELs in a nonrepeat region or stop-loss variants	Same amino acid change as an established pathogenic variant	Truncating variant in a gene where LOF is a known mechanism of disease
<b>Functional data</b>	Missense in gene with low rate of benign missense variants and pathogenic missense common		Well-established functional studies show a deleterious effect	
<b>Segregation data</b>	Co-segregation with disease in multiple affected family members	→ Increased segregation data →		
<b>De novo data</b>		De novo (without paternity and maternity confirmed)	De novo (paternity and maternity confirmed)	
<b>Allelic data</b>		For recessive disorders, detected in trans with a pathogenic variant		
<b>Other database</b>	Reputable database = pathogenic			
<b>Other data</b>	Patient's phenotype highly specific for gene			



SPECIAL ARTICLE

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Jaeger P. Ackerman, BA; Daniel C. Bartos, PhD; Jamie D. Kapplinger, BS;  
David J. Tester, BS; Brian P. Delisle, PhD; and Michael J. Ackerman, MD, PhD



# Conclusiones

- El abordaje genético es mucho más que el estudio genético
- El estudio genético es útil a nivel diagnóstico, pronóstico, terapéutico y de aproximación a la familia
- La interpretación genética es compleja, requiere un abordaje multidisciplinar y alta especialización

# ¡GRACIAS!



**GENETICS**  
This is how it works