

XI Reunión. Estado del Arte en
INSUFICIENCIA CARDIACA

PRÁCTICA CLÍNICA Y MODELOS ORGANIZATIVOS

Sede: Hotel Meliá MaríaPita, A Coruña

A CORUÑA 27-28 SEPTIEMBRE 2024



XI Meeting. State of the Art in
HEART FAILURE

CLINICAL PRACTICE AND ORGANIZATIONAL MODELS

Venue: Hotel Meliá MaríaPita, A Coruña

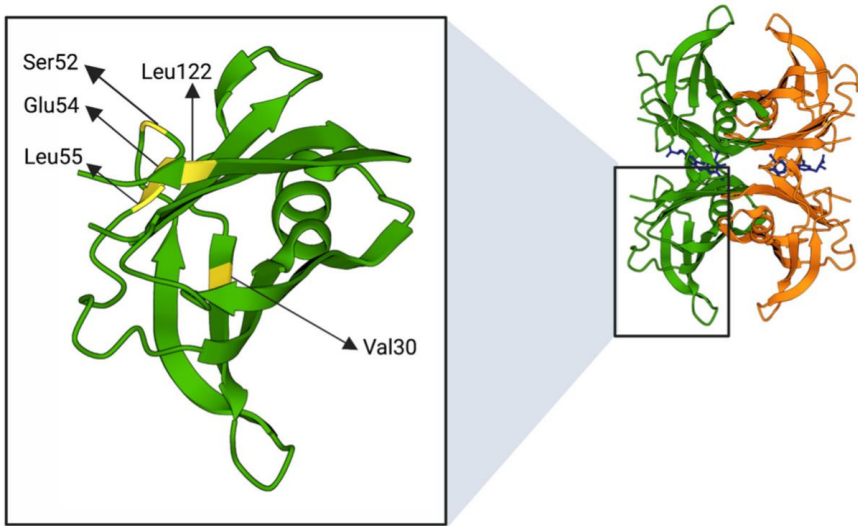
#ACoruñaHF2024

A CORUÑA 27-28 SEPTEMBER 2024

Genetic testing: what to look for, when to do it and what it brings to clinical management.

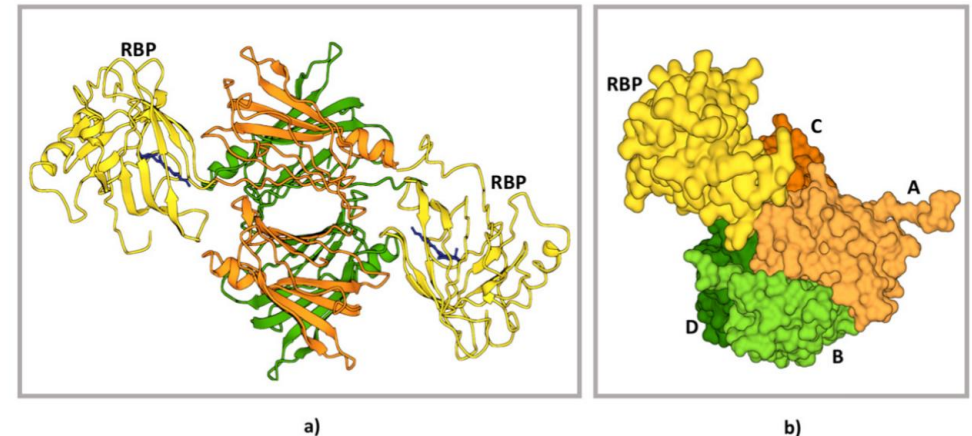
Esteban Martín Álvarez | *Complejo Hospitalario Universitario A
Coruña*

WHAT TO LOOK FOR?

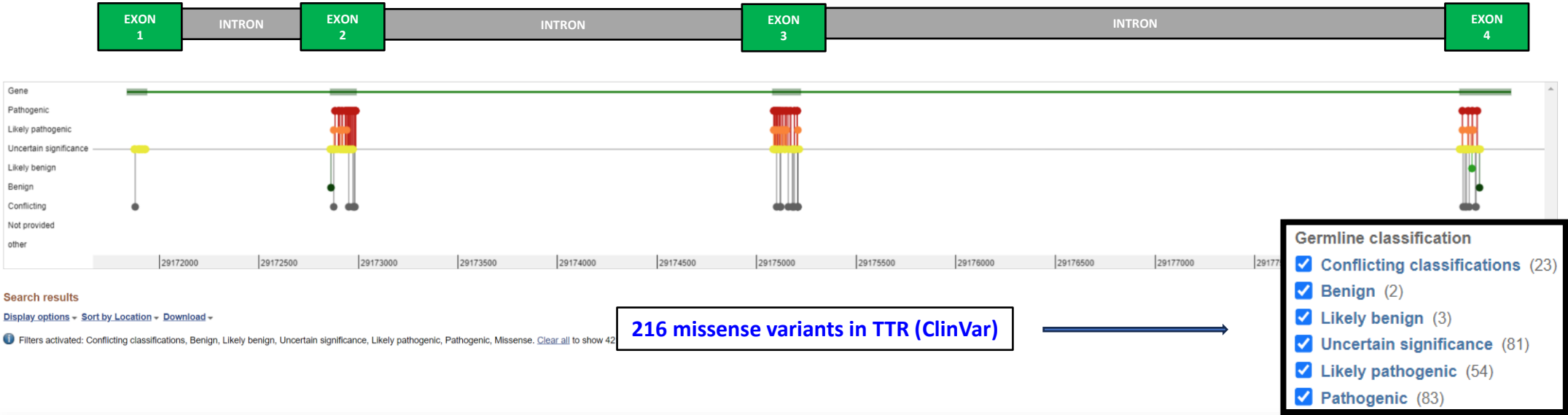


- **Human TTR** is a protein encoded by a single gene located on chromosome 18q.
- **Mature protein has 127 amino acids.** Pro-TTR monomers have 147 amino acids (including a 20-amino acid signal peptide). The current nomenclature, according to the Human Gene Organization, includes this peptide.
- **ATTRv** is caused by **pathogenic variants** in the **TTR gene** that **reduce stability** of the TTR tetramer, leading to **easier dissociation** in pro-amyloidogenic monomers.

Figure 4. Positions of amino acids (highlighted in yellow) subjected to mutations described in Table 1. The figure was created through “www.rcsb.org” and “biorender.com” web sites (license agreement number KJ247URGZS), access date 22 June 2022.



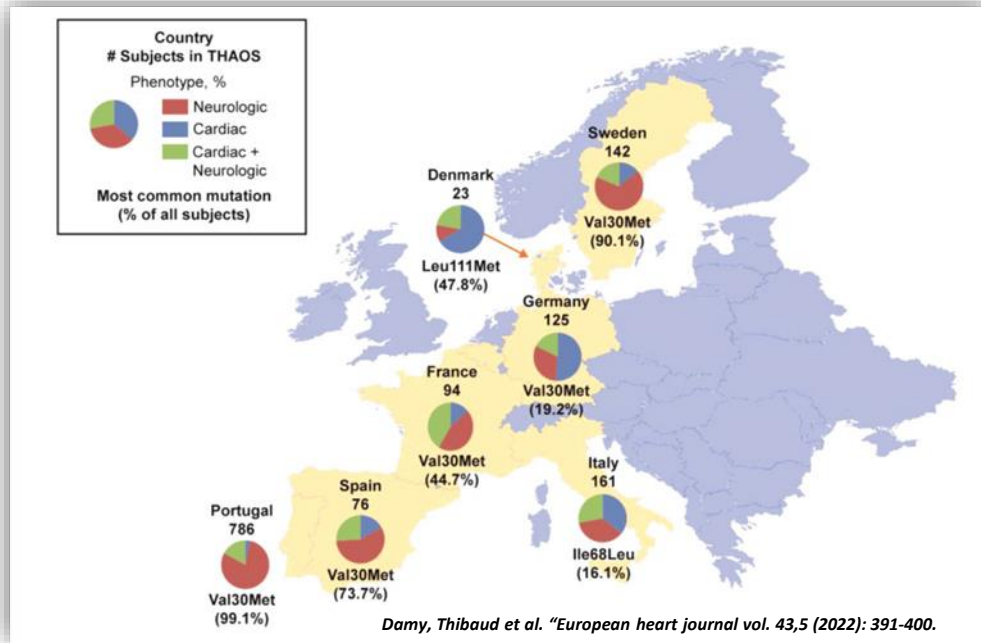
WHAT TO LOOK FOR?



<input type="checkbox"/>	NM_000371.4(TTR):c.133G>T (p.Ala45Ser)	TTR (A45S)	Single nucleotide variant (missense variant)	Cardiovascular phenotype	G Likely pathogenic ★
<input type="checkbox"/>	NM_000371.4(TTR):c.148G>T (p.Val50Leu)	TTR (V50L)	Single nucleotide variant (missense variant)	Familial amyloid neuropathy	G Pathogenic ★
<input type="checkbox"/>	NM_000371.4(TTR):c.148G>C (p.Val50Leu)	TTR (V50L)	Single nucleotide variant (missense variant)	Cardiovascular phenotype +2 more	G Pathogenic ★★
<input type="checkbox"/>	NM_000371.4(TTR):c.148G>A (p.Val50Met)	TTR (V50M)	Single nucleotide variant (missense variant)	Cardiovascular phenotype +7 more	G Pathogenic ★★
<input type="checkbox"/>	NM_000371.4(TTR):c.149T>G (p.Val50Gly)	TTR (V50G)	Single nucleotide variant (missense variant)	Familial amyloid neuropathy	G Pathogenic ★
<input type="checkbox"/>	NM_000371.4(TTR):c.149T>C (p.Val50Ala)	TTR (V50A)	Single nucleotide variant (missense variant)	Familial amyloid neuropathy	G Pathogenic ★★
<input type="checkbox"/>	NM_000371.4(TTR):c.155T>C (p.Val52Ala)	TTR (V52A)	Single nucleotide variant (missense variant)	Cardiovascular phenotype +1 more	G Likely pathogenic ★★

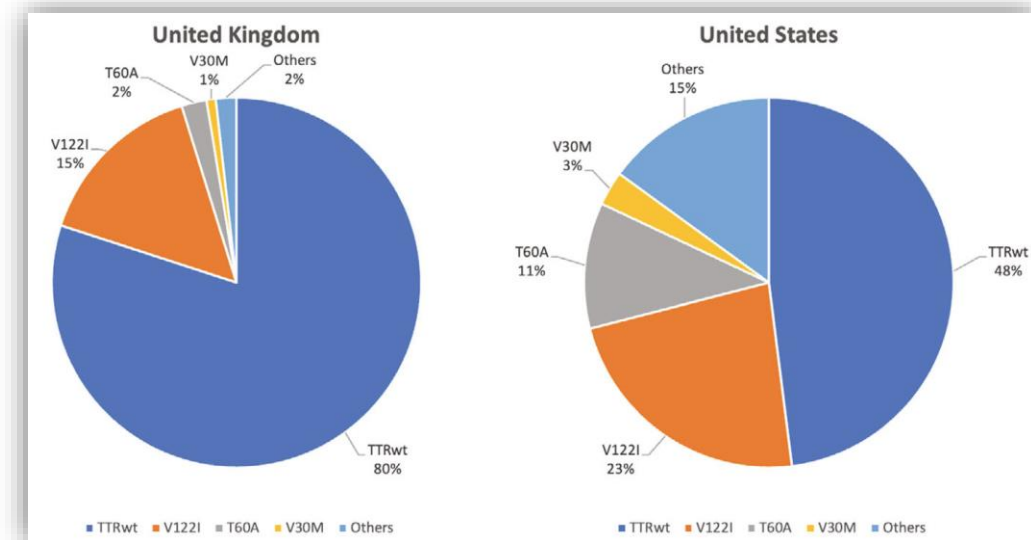
ATTRv around the world

- Estimated **prevalence** of **1/1.000.000**.
- **Endemic foci**: Portugal (almost 1/500), Sweden, Brazil, Japan and 2 regions in Spain (Mallorca and Huelva).
- **Typical phenotype** for specific **variants**, but **geographical area** also matters.



p.Val50Met

- Most common pathogenic variant worldwide
- Most frequent in Europe, South America and Japan.
- **Early-onset** phenotype in endemic areas in Japan and Portugal.
Late-onset in the rest.



Porcari, Aldostefano et al. European journal of heart failure vol. 25,4 (2023): 515-524.

p.Val142Ile

- Most frequent in USA y UK, mainly in people with black ancestry.
- Predominantly cardiac phenotype.

ATTRv in Spain

Mutaciones	
Val50Met	120 (67,8)
Val142Ile	22 (12,4)
Glu109Lys	14 (7,8)
Ser97Tyr	6 (3,4)
Val122Del	4 (2,2)
Ser43Asn	2 (1,1)
Asp38Asn	2 (1,1)
Val71Ala	1 (0,5)
Glu89Gln	1 (0,5)
Ala65Thr	1 (0,5)
Thr80Ala	1 (0,5)
Leu32Pro	1 (0,5)
Glu74Gln	1 (0,5)
Ala128Val	1 (0,5)



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The most frequent variant in **Spain** is **p.Val50Met**, not only in the two endemic areas, but in the others.
The typical form in Spain is the **late-onset phenotype** (vs Portugal).

WHEN TO DO A GENETIC TEST?

- As soon as **ATTR-CM** has been confirmed, the presence of **pathogenic variants** in the TTR gene should be evaluated and **genetic counseling** should be given.
- ATTRv** and **ATTRwt** are two different diseases. **100% of ATTRwt affect the heart**, but **not all ATTRv do so** (30-100%).
- Genetic testing should be done **regardless of age**.

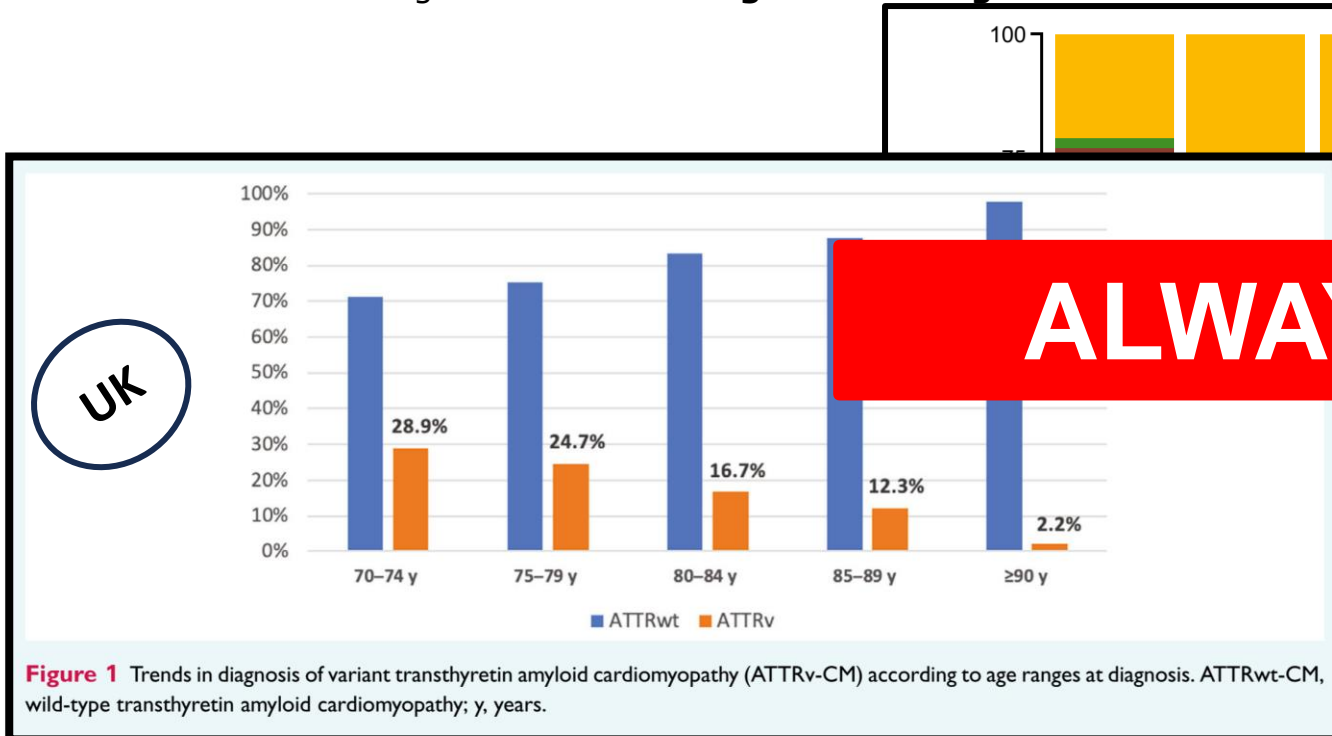


Figure 1 Trends in diagnosis of variant transthyretin amyloid cardiomyopathy (ATTRv-CM) according to age ranges at diagnosis. ATTRwt-CM, wild-type transthyretin amyloid cardiomyopathy; y, years.

Porcari, Aldostefano et al. "Prevalence, characteristics and outcomes of older patients with hereditary versus wild-type transthyretin amyloid cardiomyopathy." *European journal of heart failure* vol. 25,4 (2023): 515-524.

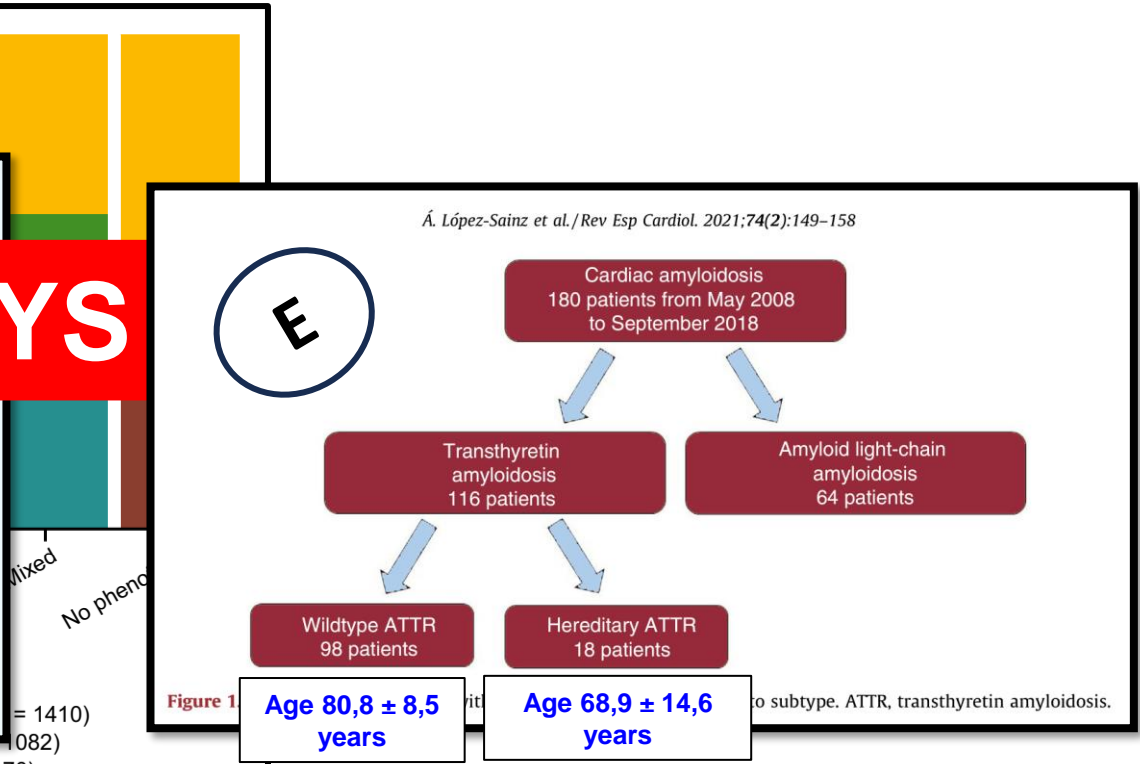
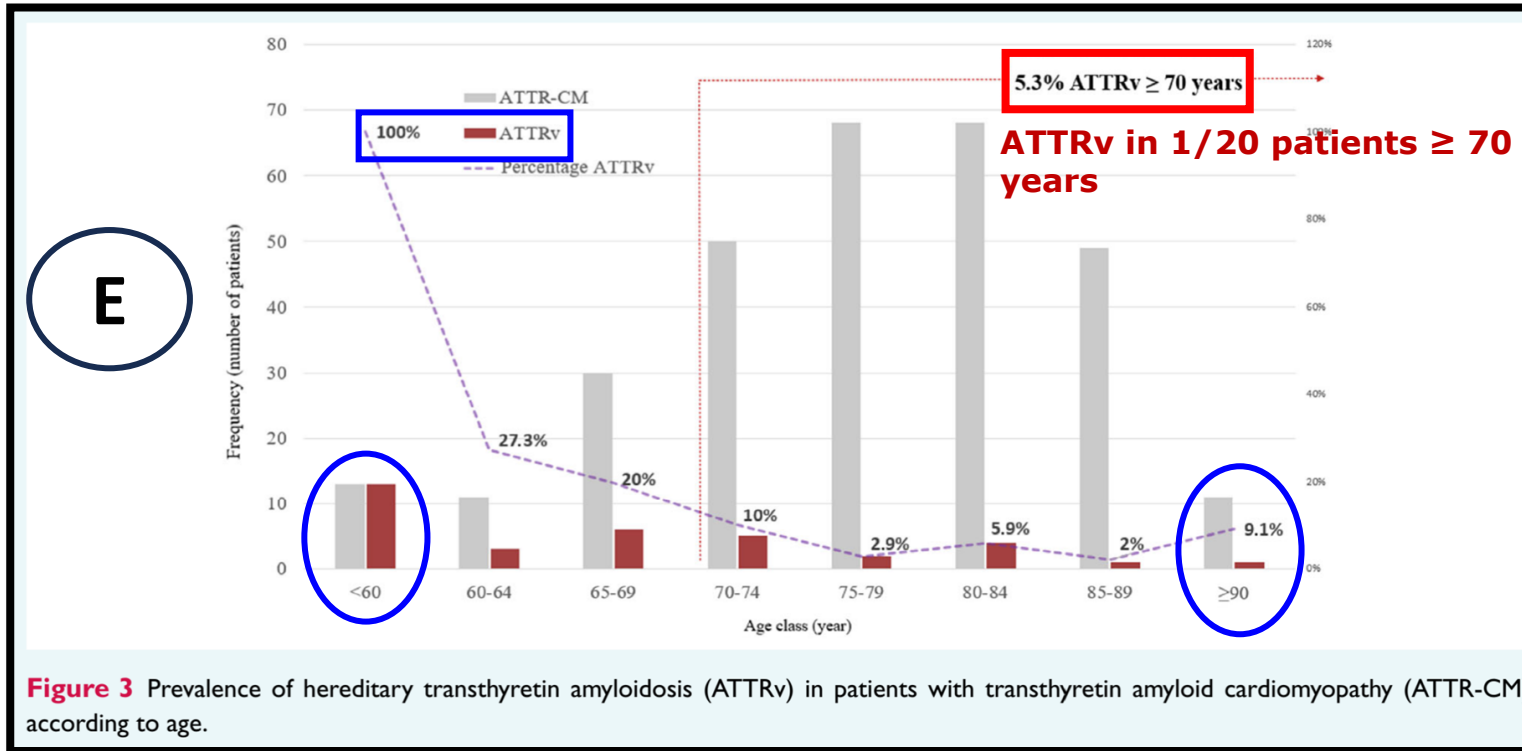


Fig. 4 Distribution of phenotype at enrollment in symptomatic patients according to genotype category. The proportions of patients with each phenotype are shown by genotype. ATTRwt amyloidosis = wild-type transthyretin amyloidosis

López-Sainz, Ángela et al. "Clinical profile and outcome of cardiac amyloidosis in a Spanish referral center." *Revista española de cardiología (English ed.)* vol. 74,2 (2021): 149-158.

- Genetic testing should be done **regardless of age**.



- Overall**, the prevalence of **ATTRv** among 300 patients with ATTR-CM was **12%**.
- In the cohort of ATTR-CM patients **≥ 70 years**, 13/246 had **ATTRv (5.3%)**.
- Prevalence of **ATTRv** among **elderly female** patients with ATTR-CM was **13%**.
- Eldest ATTRv patient was 93-year-old Caucasian female with the p.Val142Ile variant.
- Prevalence in <60 years was 100%.
- Implications of ATTRv diagnosis: **transthyretin-specific** drug treatment, genetic screening in **relatives**, identification of **asymptomatic carriers**.

RELEVANCE IN CLINICAL MANAGEMENT

ATTRv is a **multisystem autosomal dominant disease**. **Phenotypic expression** differs between different **variants**, and even for the **same variant** (**early-onset p.Val50Met** vs. **late-onset p.Val50Met**)

"Cardiac variants":
Val142Ile, **Leu131Met**,
Thr80Ala, **Ile88Leu**

Most patients with ATTRv show a mixed phenotype. **Neurologic evaluation is mandatory.**

TABLE 1 Demographic, Genetic, and Phenotypic Characteristics of ATTRv-CM

Average age, y (range)
Male, %
Race/ethnicity/country of origin
Genetics
Phenotype

^aDepends on endemic vs nonendemic regions

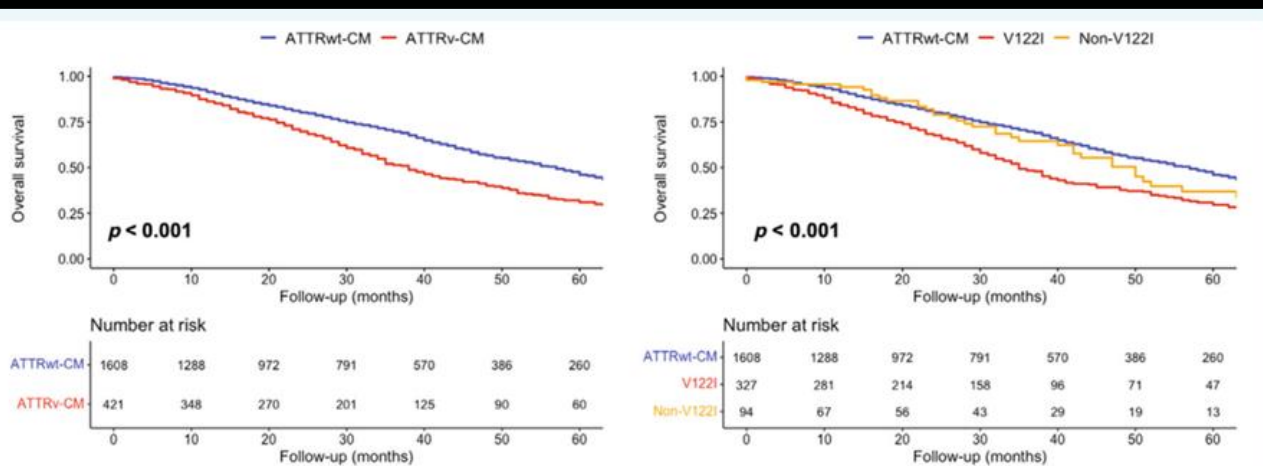
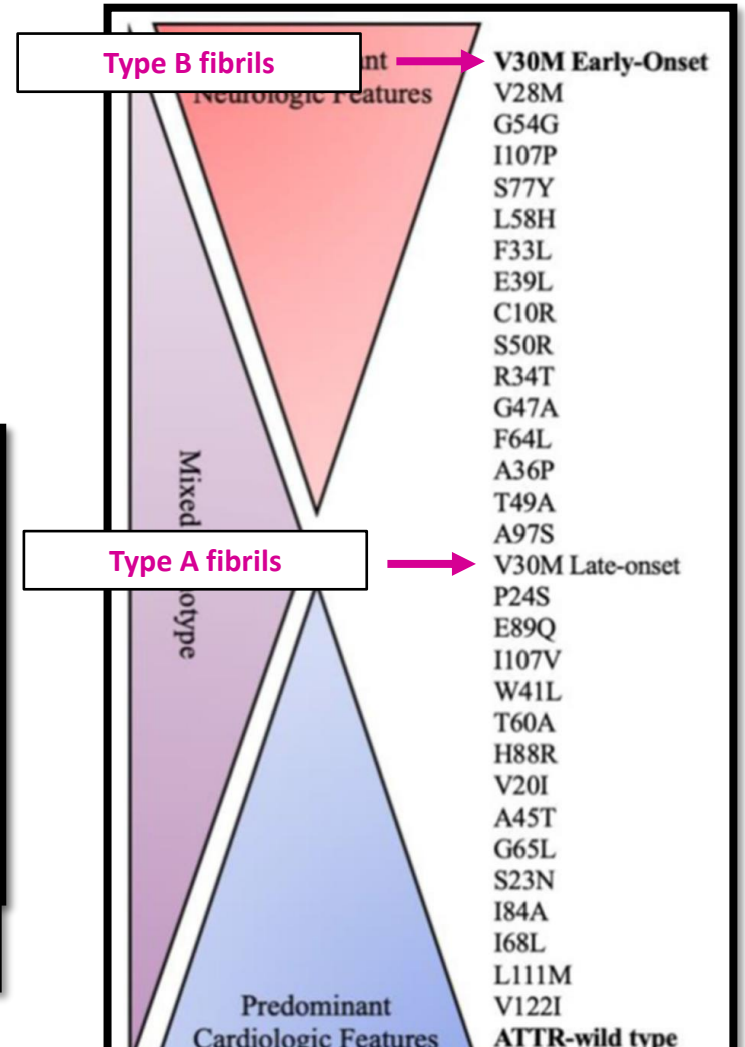


Figure 2 Prognostic impact of variant transthyretin amyloid cardiomyopathy (ATTRv-CM) and specific transthyretin variant on overall survival compared to wild-type transthyretin amyloid cardiomyopathy (ATTRwt-CM). V122I, valine-to-isoleucine substitution at position 122.

Griffin, Jan M et al. JACC. Ca

Porcari, Aldostefano et al. "Prevalence, characteristics and outcomes of older patients with hereditary versus wild-type transthyretin amyloid cardiomyopathy." *European journal of heart failure* vol. 25,4 (2023): 515-524.



In general, variants with a predominantly **cardiac** phenotype have a **worse prognosis**

Family Study and Asymptomatic Carriers of Pathogenic Variants

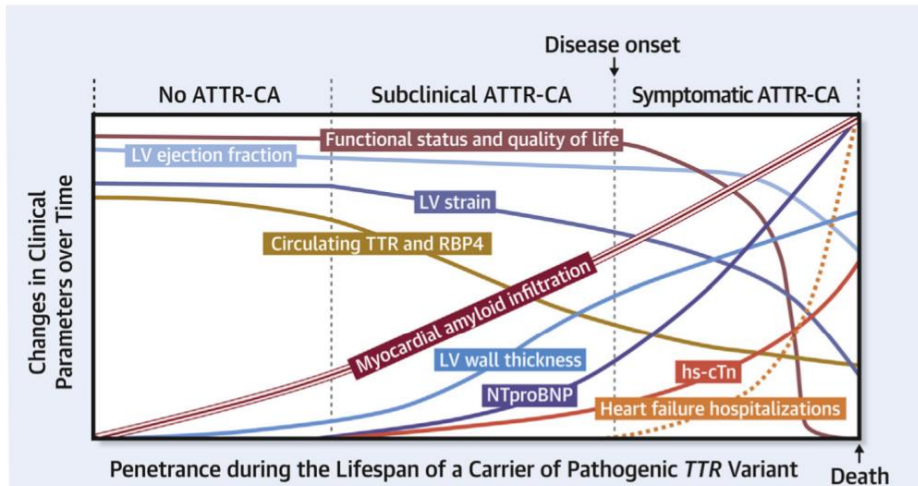
- In hereditary TTR amyloidosis, we do not see isolated patients, but **families**.
- The **age of presentation, phenotype, penetrance, and progression** depend on the particular variant.
- To decide when to initiate penetrance assessment in carriers, we are guided by the **specific variant** and the **age of onset in affected relatives (PADO)**.

Table 2. Estimating the predicted age of disease onset in patients with ATTR amyloidosis.

Phenotype group	Genotype	Penetrance	Typical age of onset	Rate of progression
Neurologic	V30M early onset	>90%	<40 years	++++++
Neurologic/mixed	V30M late onset	>60%	>50 years	++++++
Cardiac	V122I	Unknown	55 years	++
	L111M	>90%	35–40 years	++
	T60A	>90%	55 years	++
	I68L	>90%	55 years	++
Mixed	S77Y	>90%	55 years	++++
	E89Q	>90%	50 years	++++
	G47E	>90%	30 years	++++++

The number of “+” provides an indication of how fast the disease progresses, with “+” representing slow progression of ATTR amyloidosis.

FIGURE 2 Proposed Natural History of Penetrance in Carriers of Pathogenic TTR Variants



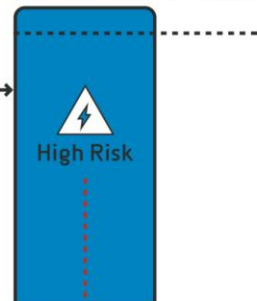
Griffin, Jan M et al. JACC. CardioOncology vol. 3,4 488-505. 19 Oct. 2021

Establishing the follow-up and frequency

10 years before the age of debut in family members. **Sooner**, if you have suspicious symptoms or signs.

Educate the carrier to understand the early clinical signs associated with the specific mutation and increase frequency of surveillance if signs suspected

Increased frequency of follow-up, particularly in those genotypes associated with rapidly progressing disease



Predicted age of disease onset } Typical age of onset for the specific genotype
 · Family history
 · Proband age of onset

Baseline assesment 10 years prior to predicted age of onset

Figure 1. Establishing the start and frequency of follow-up of carriers of a TTR mutation.

Genetics are a must in ATTR!!

DIAGNOSIS (ATTRv vs ATTRwt)

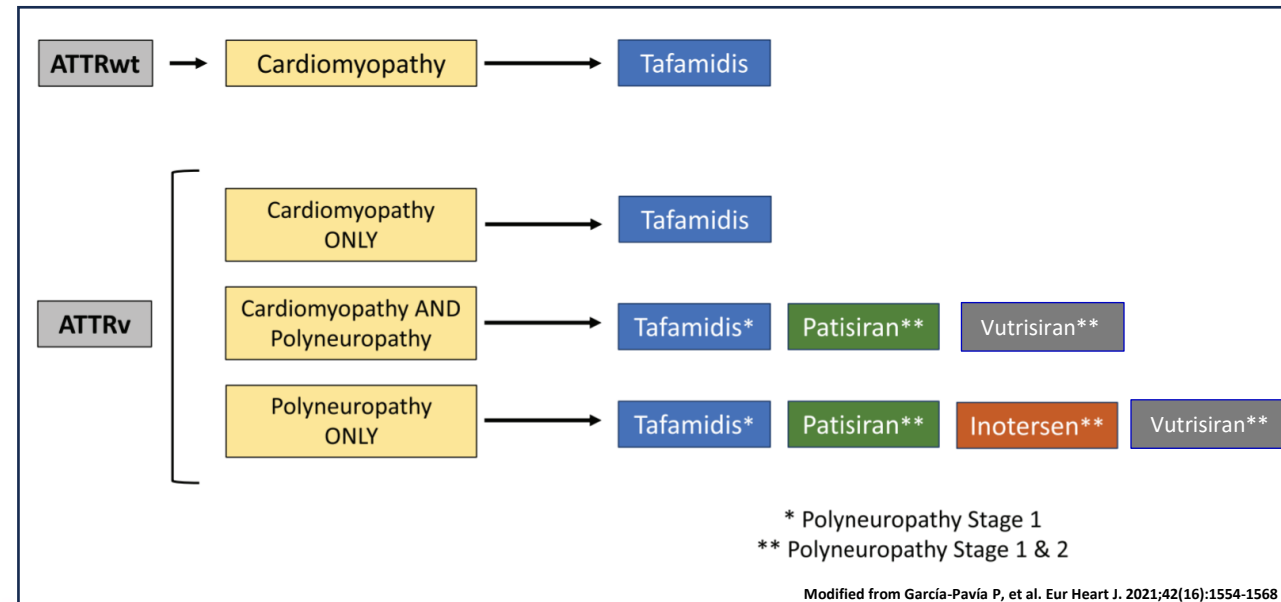
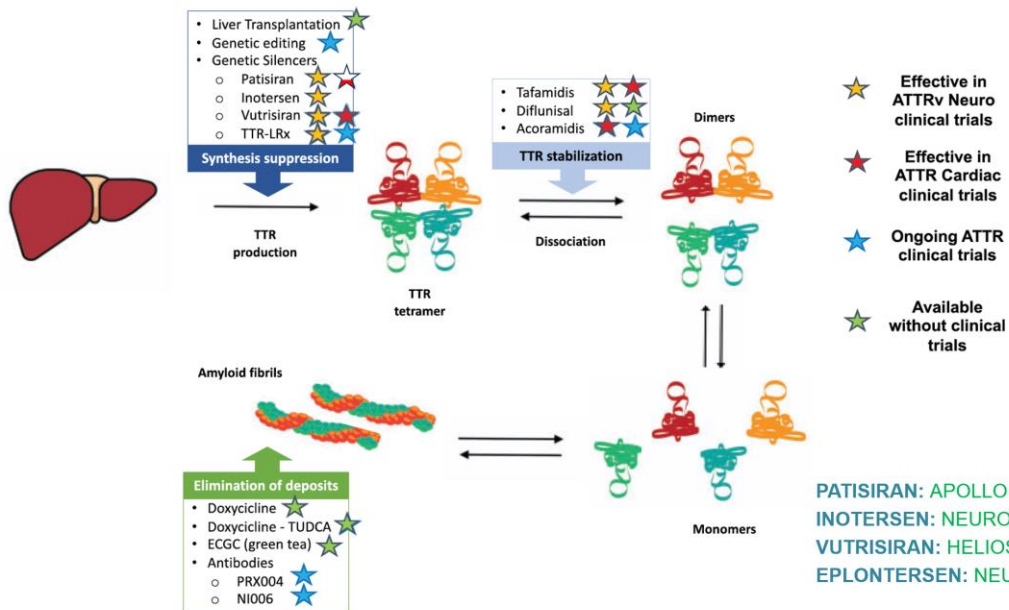
CARRIERS

PROGNOSIS

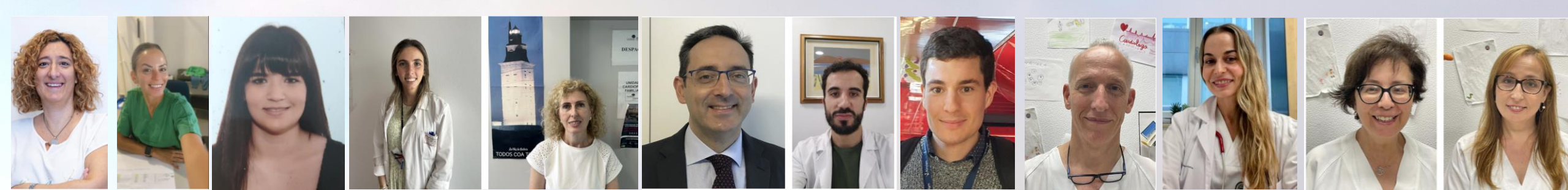
TREATMENT

GENETIC COUNSELING

FOLLOW-UP



Modified from García-Pavía P, et al. Eur Heart J. 2021;42:1554-1568.



¡MUCHAS GRACIAS POR LA ATENCIÓN!



**Complexo Hospitalario Universitario
A Coruña**

