

MORTE CARDIACA IMPROVVISA, CANALOPATIE E CARDIOMIOPATIE GENETICHE

A recurrent *LMNA*:c.949G>A variant associated with shared cardiomyopathic and arrhythmic features in a series of unrelated affected patients

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AIM OF THE STUDY

LMNA pathogenic variants
Lamin A/C protein

Unmet need

To determine whether a recurrent variant identified in apparently unrelated families gives rise to a recognizable clinical profile that may be useful for risk stratification, follow-up, and family screening.

Dilated / arrhythmogenic cardiomyopathy

Conduction disease

Malignant ventricular arrhythmias

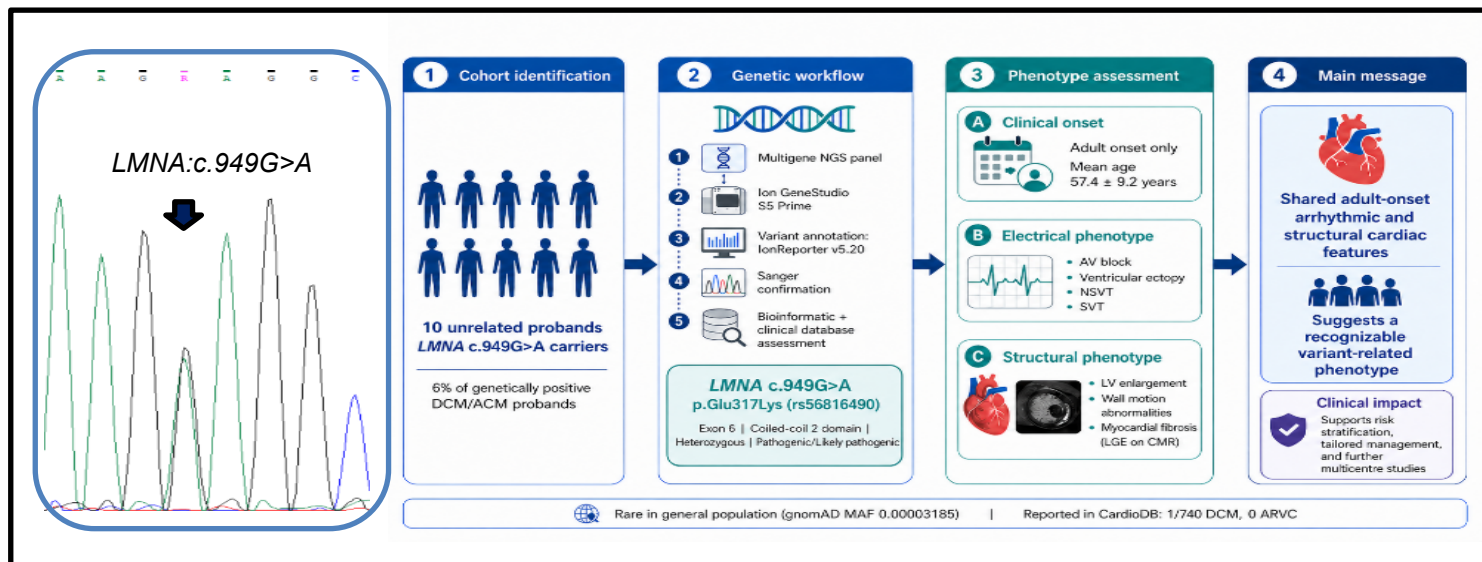


AIM OF THE STUDY

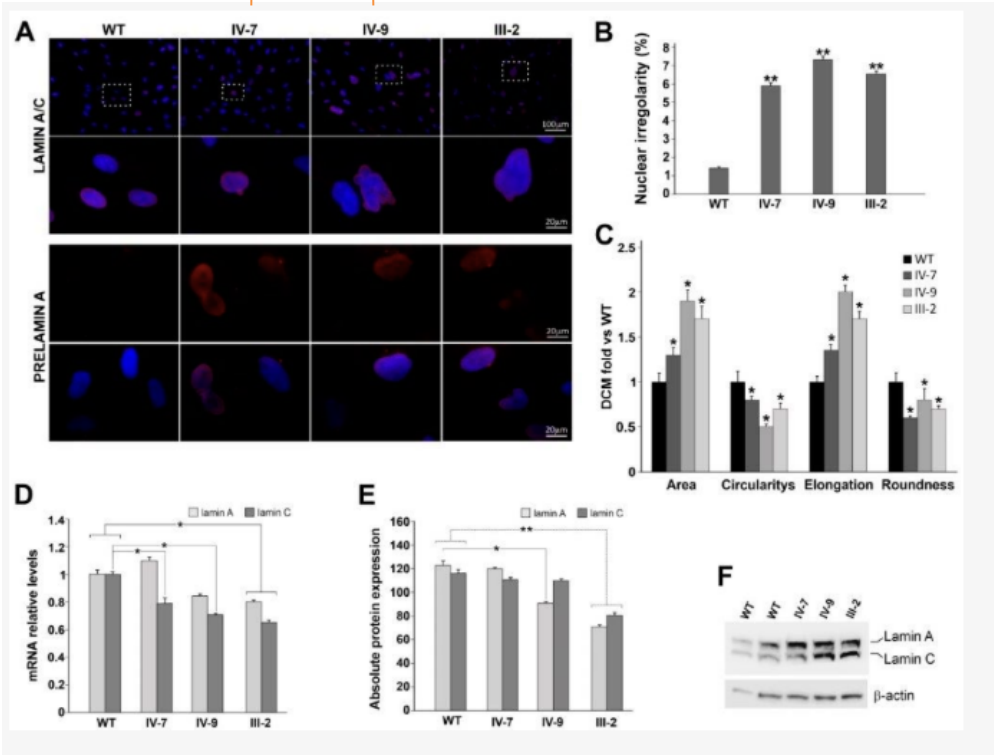
to characterize the phenotypic spectrum of unrelated probands carrying the pathogenic *LMNA*:c.949G>A, p. (Glu317Lys) variant (rs56816490) and to identify potential shared clinical features.

Key hypothesis

The recurrence of the same rare variant in a geographically defined population may reflect a founder effect or a specific clinical profile.



LMNA:c.949G>A



Article

Clinical Features of LMNA-Related Cardiomyopathy in 18 Patients and Characterization of Two Novel Variants

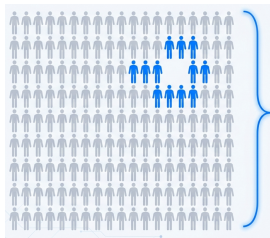
Valentina Ferradini ¹, Joseph Cosma ², Fabiana Romeo ², Claudia De Masi ¹, Michela Murdocca ¹, Paola Spitalieri ¹, Sara Mannucci ¹, Giovanni Parlapiano ¹, Francesca Di Lorenzo ¹, Annamaria Martino ³, Francesco Fedele ⁴, Leonardo Calò ³, Giuseppe Novelli ^{1,5,6}, Federica Sangiulio ^{1,4} and Ruggiero Mango ²

- Increased percentage of abnormal nuclei, irrespective of the type of nuclear malformation correlating with nuclear architecture instability
- Lamin C expression is statistically significantly reduced if compared to WT ones



STUDY COHORT

11 Unrelated patients



6% of unrelated probands with DCM/ACM-like features who tested positive for genetic variants

LMNA:c.949G>A, p.(Glu317Lys) · rs56816490

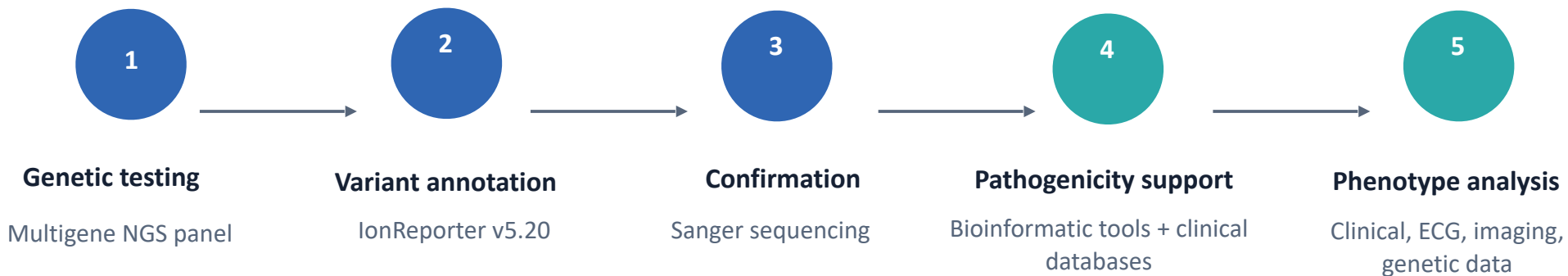
Rare in public databases

Classified as pathogenic

Geographic clustering



METHODS



**Integrated
retrospective
analysis**

Combination of molecular confirmation and multidomain phenotypic reconstruction

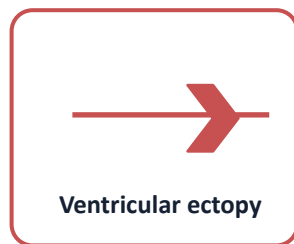
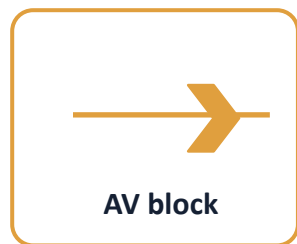


RESULTS

Shared prominent electrical involvement....

Clinical onset (mean + ds)

55.5 ± 8.9 years

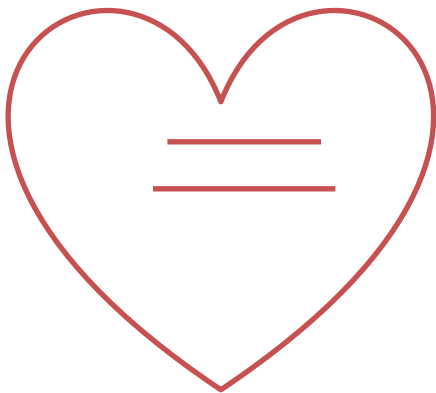


Adult-onset disease with conduction abnormalities and both ventricular and supraventricular arrhythmias.



RESULTS

...and shared structural involvement



> 50%

Altered imaging

Left ventricular enlargement

LV remodeling

Wall motion abnormalities

regional dysfunction

Myocardial fibrosis

tissue injury substrate

The phenotype is not confined to arrhythmias, but also includes morpho-functional and tissue abnormalities consistent with LMNA-related cardiomyopathy.



CONCLUSIONS

- *LMNA*:c.949G>A, although rare in public databases, is a recurrent variant in the observed cohort.
- The variant appears to be associated with a homogenous phenotype
- Recurrence in unrelated probands supports founder-effect assessment and multicentre expansion

A rare variant, a shared geography, and a recurrent cardiac signature.



PERSPECTIVES

Follow-up of genotype-positive relatives



To define penetrance, age at onset, and disease progression.

Founder-effect assessment



To determine whether recurrence reflects a common ancestor.

Multicentre expansion



To increase sample size and strengthen phenotypic robustness.

Clinical refinement



Arrhythmic surveillance, serial imaging, family screening.



***THANK YOU FOR
YOUR ATTENTION!***

U.O.C Genetica Medica, Policlinico Tor Vergata

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Dr.ssa Giorgia D'Ortenzi

Dr. Alessio Ludovico Del Popolo

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