



University of Colorado
Anschutz Medical Campus

Diagnostic and Prognostic Efficiency of Genotype Versus Phenotype in Genetic Cardiomyopathies

Kristen Medo MS³, Alessia Paldino MD*¹, Matteo Dal Ferro MD*¹, Davide Stolfo MD¹, Ilaria Gandin PhD², Sharon Graw PhD³, Marta Gigli MD¹,
Giulia Gagno MD¹, Denise Zaffalon MD¹, Matteo Castrichini MD^{1,3}, Marco Merlo MD¹, Gianfranco Sinagra MD FESC¹,
Luisa Mestroni MD FACC FAHA³, Matthew RG Taylor MD PhD³

¹ Cardiovascular Department, Azienda Sanitaria Universitaria Giuliano Isontina (ASUGI), University of Trieste, Italy

² Biostatistics Unit, University of Trieste, Italy

³ Cardiovascular Institute and Adult Medical Genetics Program, University of Colorado Anschutz Medical Campus, Aurora, CO, USA

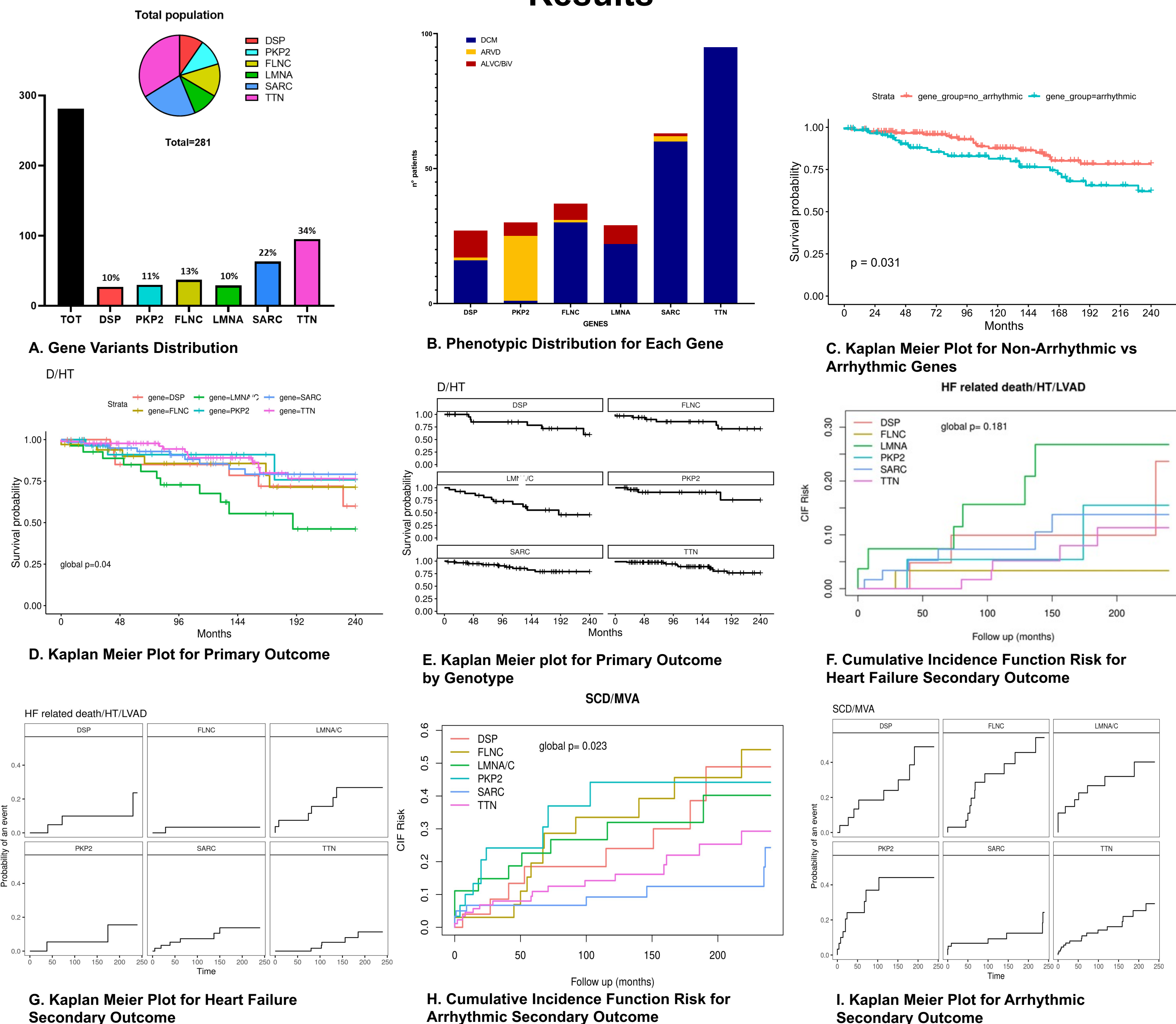
Background

- In cardiomyopathies (CMP), genetic background may show phenotypic heterogeneity.
- We aimed to define the efficiency of the phenotype- versus the genotype-based classification in the diagnostic and prognostic definition of a large cohort of patients with positive genetic testing and different CMPs:
 - Dilated Cardiomyopathy (DCM)
 - Arrhythmogenic Right Ventricular Cardiomyopathy (ARVC)
 - Left Ventricular Arrhythmogenic Cardiomyopathy (ALVC)
 - Biventricular ARVC (BiV).

Methods

- 281 patients (80% DCM) carrying pathogenic or likely pathogenic variants (P/LP) were included in this study.
- Phenotypes were classified as DCM, ARVC, ALVC, and BiV according to current consensus criteria.
- Primary and secondary outcomes included: 1) all-cause mortality/heart transplant (D/HT); 2) heart failure-related death/heart transplant/left ventricular device implantation (DHF/HT/VAD); and 3) sudden cardiac death/life-threatening ventricular arrhythmias (SCD/MVA).
- Statistical tests performed included the analysis of variance (ANOVA) test with the Brown-Forsythe statistic, nonparametric Mann-Whitney test, chi-square test and the Fisher's exact test.

Results



Conclusions

- In genetic cardiomyopathies, the genotype is associated with significant phenotypic heterogeneity.
- Nevertheless, the genotype showed higher accuracy in differentiating patients with CMPs and predicting their outcome compared to the phenotype-based classification.

Implications

- Our findings provide strong evidence of the necessity to include genotype predictors, in addition to phenotypic expression, in the evaluation and clinical management of cardiomyopathies.

Disclosures

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