

Pathogenic cardiomyopathy-associated gene variants inform prognosis in atrial fibrillation

results from exome sequencing in 17000 individuals from the TIMI trials

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Background

- Atrial fibrillation (AF)
 - high morbidity and mortality
 - little personalized medicine
- Rare genetic variants contribute to AF
 - notably, for cardiomyopathy (CMP)
- AHA/ACC guidelines for AF
 - 2B for genetic testing in early-onset
- Clinical implication of rare variant in AF?

Baseline characteristics

- N=17 190 with baseline AF and WES
- N=421 CMP variant carriers
 - 67±10 yrs, 65% male
- N=16 769 non-carriers
 - 70±9 yrs, 64% male
- History of HF: 9 275 (54%)
- HF admissions during FU: 1 365 (7.9%)
- History of ischemic stroke: 2 991 (17.4%)
- Ischemic stroke during FU: 599 (3.5%)
- CVD death during FU: 1 147 (6.7%)

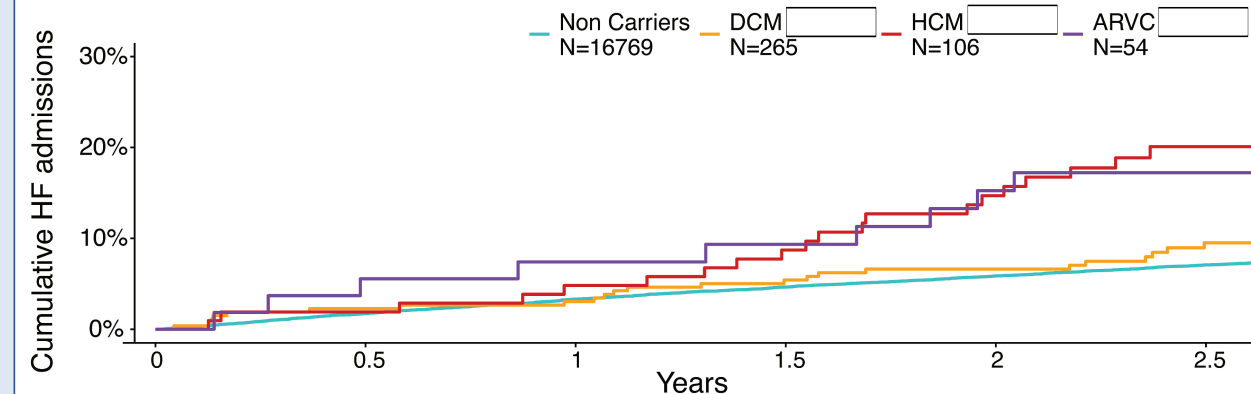
Methods

- Data from 5 large clinical trials from TIMI
 - ENGAGE-AF, PEGASUS, DECLARE, SAVOR, FOURIER
 - all with exome sequencing (WES)
- Curation (likely) pathogenic variants for CMP
 - Loss-of-function and ClinVar variants
 - phenotype-specific, including DCM, HCM, ARVC
- Assoc for heart failure (HF), stroke, CVD mortality
 - Logistic regression for baseline diseases
 - Cox regression for incident events
 - Adj. for sex, age, trial, and ancestry PCs

Results

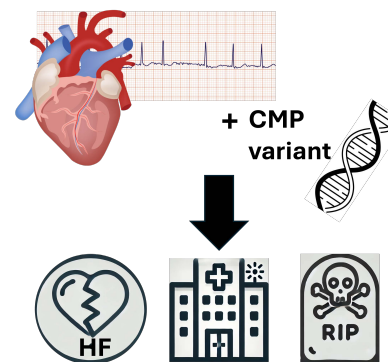
- Association between CMP variants and HF:
 - elevated baseline HF (OR 1.66, $P<0.0001$)
 - elevated HF admissions (HR 1.75, $P<0.0001$)
- between CMP variants and ischemic stroke:
 - not elevated at baseline (OR 0.99, $P=0.96$)
 - not elevated during FU (HR 0.95, $P=0.84$)
- between CMP variants and CVD death:
 - elevated CVD death (HR 1.46, $P=0.02$)
 - notable for DCM variants (HR 1.77, $P=0.003$)

Incident HF admissions by variant group



Conclusions

- CMP-associated variants in AF:
 - ↑ HF and HF admissions
 - ↑ CVD mortality
 - no effect on ischemic stroke
- Based on well-phenotyped trial data
- Support prognostic implication for rare variants
- Support select genetic testing in AF



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