Risk prediction of atrial fibrillation in the community combining biomarkers and genetics

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On behalf: BiomarCaRE

Topic(s):
Genetic Causes of Atrial Fibrillation

Citation:
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Background: Classical cardiovascular risk factors (CVRF), biomarkers and genetic variation have been suggested for risk assessment of atrial fibrillation (AF).

Purpose: To evaluate their clinical potential, we analysed their individual and combined effectiveness in AF prediction.

Methods: In N=6945 individuals of the FINRISK 1997 cohort, we assessed the predictive value of CVRF, N-terminal pro B-type natriuretic peptide (NT-proBNP) and 145 recently identified single nucleotide polymorphisms (SNPs) for incident AF.

Results: Over a median follow-up of 17.8 years, N=551 participants (7.9%) developed AF. In multivariable-adjusted Cox proportional hazard models, NT-proBNP (hazard ratio (HR) per standard deviation (SD) 1.90, 95% confidence interval (CI): 1.71–2.11, P<0.001) and the polygenic risk score (PRS) (HR per SD 1.66, 95% CI: 1.51–1.84, P<0.001) were significantly related to incident AF. The discriminatory ability improved asymptotically with increasing numbers of SNPs. Compared to a clinical model, AF risk prediction was significantly improved by addition of NT-proBNP and the PRS. The C-statistic for the combination of all CVRF, NT-proBNP and the PRS reached 0.82 compared to 0.77 for CVRF only (P<0.001). Comparing the highest versus lowest quartile, age remained the strongest risk factor with a 15-fold increased risk of AF. The highest quartiles of NT-proBNP and the PRS both showed an approximately 3-fold increased AF risk compared to the lowest quartiles.

Conclusions: The PRS and the established biomarker NT-proBNP predicted incident AF comparably. Both provided incremental predictive value over standard clinical variables. Further improvements for the PRS are likely with the discovery of additional SNPs.
Abstract:

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C-Index for AF prediction

C = 0.77
C = 0.80
C = 0.80
C = 0.82