Key Summary of a Published Article

Validation of a Genetic Risk Score for Atrial Fibrillation: A Prospective Multicenter Cohort Study

Background

- Atrial fibrillation (AF) is a common, and often asymptomatic, cardiac arrhythmia associated with a high risk of stroke.[1]
- Approximately 40% of the risk for AF is attributed to genetic factors.[2]
- A genetic risk score for AF (AF-GRS), composed of 12 single nucleotide polymorphisms (SNPs), was developed and validated in large population-based studies.[3]
- **Objectives:** This study prospectively evaluated whether the previously developed 12-SNP AF-GRS can help identify individuals at risk for AF in a clinical setting.

Methods

- The final study population included 904 adults (341 men and 563 women) who were enrolled from December 2013 to January 2016.
- Participants were >40 years of age, had at least 1 clinical risk factor for AF or presented with AF symptoms, and did not have a previous diagnosis of AF.
- DNA was extracted from blood specimens of study participants and was used to genotype 12 SNPs; a weighted allele-counting approach was used to calculate AF-GRS.
- Participants were monitored for AF events with an ambulatory cardiac rhythm monitor for up to 2 weeks.

Results

- Among the 904 participants in the study population, an AF event was detected in 85 (9.4%).
- The average AF-GRS was higher (p=0.001) for participants with an AF event (0.58) than for those without an AF event (0.44).
- An AF event was more likely in participants with AF-GRSs in the top quintile than in those with AF-GRSs in the bottom quintile.
    - The odds ratio for AF was 3.1 (95% CI=1.3-7.6; p=0.01), after controlling for established risk factors (age, sex, smoking status, body mass index, hypertension, diabetes, heart failure, and myocardial infarction).

Conclusions

- The prospective assessment of AF-GRS can help identify individuals at increased risk of AF.
- Adding this AF-GRS screen to the overall risk assessment of AF may lead to timely cardiac rhythm monitoring.

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