Novel genetic markers improve measures of atrial fibrillation risk prediction

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<td>Published Version</td>
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</table>
Novel genetic markers improve measures of atrial fibrillation risk prediction

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Aims

Atrial fibrillation (AF) is associated with adverse outcome. Whether recently discovered genetic risk markers improve AF risk prediction is unknown.

Methods and results

We derived and validated a novel AF risk prediction model from 32 possible predictors in the Women’s Health Study (WHS), a cohort of 20 822 women without cardiovascular disease (CVD) at baseline followed prospectively for incident AF (median: 14.5 years). We then created a genetic risk score (GRS) comprised of 12 risk alleles in nine loci and assessed model performance in the validation cohort with and without the GRS. The newly derived WHS AF risk algorithm included terms for age, weight, height, systolic blood pressure, alcohol use, and smoking (current and past). In the validation cohort, this model was well calibrated with good discrimination (C-index (95% CI) = 0.718 (0.684–0.753)) and improved all reclassification indices when compared with age alone. The addition of the genetic score to the WHS AF risk algorithm model improved the C-index [0.741 (0.709–0.774); P = 0.001], the category-less net reclassification [0.490 (0.301–0.670); P < 0.0001], and the integrated discrimination improvement [0.00526 (0.0033–0.0076); P < 0.0001]. However, there was no improvement in net reclassification into 10-year risk categories of <1, 1–5, and 5+ % [0.041 (–0.044–0.12); P = 0.33].

Conclusion

Among women without CVD, a simple risk prediction model utilizing readily available risk markers identified women at higher risk for AF. The addition of genetic information resulted in modest improvements in predictive accuracy that did not translate into improved reclassification into discrete AF risk categories.

Keywords

Women • Atrial fibrillation • Genetics • Risk prediction • Epidemiology

Introduction

Atrial fibrillation (AF) is the most common sustained cardiac arrhythmia and is associated with enormous societal costs, including an increased risk of stroke, heart failure (HF), and death.1–3 The prevalence of AF is increasing even among those individuals thought to be at low risk, such as women or those without cardiovascular disease (CVD) or HF.4,5 Treatment of AF remains challenging and associated with risk; therefore, prevention is an important public health objective. Recently, investigators working in the Framingham Heart Study (FHS) and the Atherosclerosis Risk in Communities (ARIC) study derived separate AF risk prediction models among individuals with and without heart disease, but neither study considered routine blood biomarkers or genetic markers for inclusion in those models.6–11 These prediction algorithms also require electrocardiograms (ECGs), which may not be readily available among individuals without clinical heart disease.

The first aim of this study was to derive and validate an AF risk prediction algorithm that could be employed in our healthy population of 20 822 women without prevalent CVD, HF, or ECGs at baseline. The second aim of the study was to determine whether a genetic risk score (GRS) based on recently published risk markers...
Genetic risk score

Twelve single-nucleotide polymorphisms (SNPs) in nine loci reported to associate with AF were included in the GRS. Seven of the SNPs (rs13376333, rs2200733, rs10033464, rs3853445, rs3807989, rs7164883, and rs7193343) were directly genotyped, while the rest (rs3903239, rs17570669, rs10821415, rs10824026, and rs1152591) were imputed. In the primary analysis, a weighted GRS was created by summing the product of the natural logarithm of the published risk ratio for each SNP (Supplementary material online, Table S1) times the gene dose at that SNP for each participant. Because allele weights were calculated by taking the natural logarithm of published risk ratios, alleles with risk ratios >1 had positive weights, while those with risk ratios <1 had negative weights. In order to eliminate bias, risk estimates from replication (rather than discovery) cohorts were used wherever possible. As a secondary analysis, an unweighted GRS was constructed to evaluate the sensitivity of our results to these published risk estimates. For this score, the allele associated with increased AF risk at each SNP was identified, and the measured or imputed allele dose at each of the 12 SNPs was then summed for each participant.

Clinical reclassification of atrial fibrillation prediction models

The models developed in the derivation set were used to estimate the 10-year risk of AF in the validation set (n = 6879) and improvement in measures of discrimination and calibration with the addition of clinical and/or genetic covariates were calculated in this cohort. While there is no broad consensus on what risk categories are clinically informative, 10-year clinical risk categories of <1, 1 to <5, and 5% and higher were utilized on an a priori basis given the low-risk nature of this healthy population. To test whether the WHS score and/or the addition of genetic information improved clinical risk classification across categories, the net reclassification improvement (NRI) and the reclassification calibration test were calculated. To address potential finer increments in reclassification, the continuous NRI and the integrated discrimination improvement (IDI) were calculated for each base model with and without genetic information. Modifications appropriate for survival data were used. Bootstrap resampling was used to calculate confidence intervals and P-values for each discrimination and reclassification statistic. As a sensitivity analysis, changes in WHS AF risk prediction algorithm performance after the addition of genetic information were calculated in all available women in the WGHS cohort with complete information on all model covariates (n = 20 222). Statistical analyses were performed using SAS version 9.1 (SAS Institute Inc., Cary, NC, USA).

Results

Study characteristics

The derivation and validation cohorts were similar with respect to the baseline characteristics and variables considered for inclusion in the AF risk prediction algorithm (Table 1). Established AF risk factors such as age, body mass index, weight, height, hypertension, and alcohol use were similar in the two cohorts. Levels of biomarkers previously associated with AF such as markers of inflammation, haemoglobin A1c, creatinine, and lipids were similar in the two cohorts.
In the derivation cohort, 32 potential variables outlined in Table 1 were evaluated for model inclusion. Univariable association between each potential variable and incident AF in the derivation cohort are presented in Supplementary material online, Table S2. Of these, the inclusion of terms for the natural logarithm of age, weight, height, systolic blood pressure, ≥ 2 alcoholic drinks per day, and a history of either current or past smoking (ever smokers) resulted in the best fitting prediction model with the smallest BIC (7319.7). Model coefficients from the derivation cohort for these variables are presented in Table 2. The BIC for a model including the body mass index instead of height and weight was 7347.8, and the BIC for a model including age instead of the natural logarithm of age was 7321.8. Although none of the blood-based biomarkers were included in the final model, high-sensitivity C-reactive protein (hsCRP) would have been the next variable included (P = 0.02), but inclusion resulted in a small increase in the BIC (BIC = 7320.7 with hsCRP).

We then tested this AF prediction model in the validation cohort. Using coefficients calculated in the derivation set, the c-index (95% CI) for the WHS predictive model [0.718 (0.684–...]

Table 1  Baseline characteristics and covariables considered for inclusion in the atrial fibrillation risk prediction algorithm among women in the derivation and validation cohorts

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Derivation cohort (n = 13 061)</th>
<th>Validation cohort (n = 6879)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Events/person-years of follow-up</td>
<td>404/181 350</td>
<td>212/95 253</td>
</tr>
<tr>
<td>Incidence rate, per 1000 person-years of observation</td>
<td>2.23</td>
<td>2.23</td>
</tr>
<tr>
<td>Age [median (IQR), years]</td>
<td>52.9 (48.9–58.8)</td>
<td>52.9 (48.9–58.8)</td>
</tr>
<tr>
<td>Body mass index [median (IQR), kg/m²]</td>
<td>24.8 (22.5–28.3)</td>
<td>24.9 (22.5–28.3)</td>
</tr>
<tr>
<td>Weight [median (IQR), kg]</td>
<td>67.1 (59.9–77.1)</td>
<td>68.0 (59.9–77.1)</td>
</tr>
<tr>
<td>Height [median (IQR), cm]</td>
<td>165.0 (159.9–167.5)</td>
<td>165.0 (159.9–167.5)</td>
</tr>
<tr>
<td>Systolic blood pressure [median (IQR), mmHg]</td>
<td>125 (115–135)</td>
<td>125 (115–135)</td>
</tr>
<tr>
<td>Diastolic blood pressure [median (IQR), mmHg]</td>
<td>80 (70–80)</td>
<td>80 (70–80)</td>
</tr>
<tr>
<td>Physical activity [n (%)]</td>
<td></td>
<td></td>
</tr>
<tr>
<td>1–3 times per week</td>
<td>4193 (32.1)</td>
<td>2263 (32.9)</td>
</tr>
<tr>
<td>4+ times per week</td>
<td>1520 (11.6)</td>
<td>798 (11.5)</td>
</tr>
<tr>
<td>Ever smoker [n (%)]</td>
<td>6375 (48.8)</td>
<td>3338 (48.5)</td>
</tr>
<tr>
<td>Alcohol use, ≥ 2 drinks/day [n (%)]</td>
<td>527 (4.0)</td>
<td>289 (4.2)</td>
</tr>
<tr>
<td>History of hypertension [n (%)]</td>
<td>3143 (24.1)</td>
<td>1640 (23.9)</td>
</tr>
<tr>
<td>History of treatment for high blood pressure [n (%)]</td>
<td>1618 (12.4)</td>
<td>874 (12.7)</td>
</tr>
<tr>
<td>History of treatment for high cholesterol [n (%)]</td>
<td>387 (3.0)</td>
<td>246 (3.6)</td>
</tr>
<tr>
<td>History of diabetes [n (%)]</td>
<td>314 (2.4)</td>
<td>163 (2.4)</td>
</tr>
<tr>
<td>History of menopause [n (%)]</td>
<td>7005 (53.6)</td>
<td>3729 (54.3)</td>
</tr>
<tr>
<td>Hormone therapy use [n (%)]</td>
<td>5827 (44.6)</td>
<td>3008 (43.8)</td>
</tr>
<tr>
<td>Aspirin use [n (%)]</td>
<td>6533 (50.2)</td>
<td>3458 (50.3)</td>
</tr>
<tr>
<td>Vitamin E use [n (%)]</td>
<td>6502 (49.8)</td>
<td>3500 (50.9)</td>
</tr>
<tr>
<td>Beta carotene use [n (%)]</td>
<td>6525 (50.1)</td>
<td>3450 (50.2)</td>
</tr>
<tr>
<td>Cholesterol [median (IQR), mmol/L]</td>
<td></td>
<td></td>
</tr>
<tr>
<td>Total</td>
<td>5.39 (4.74–6.11)</td>
<td>5.39 (4.77–6.09)</td>
</tr>
<tr>
<td>Low-density lipoprotein</td>
<td>3.13 (2.59–3.72)</td>
<td>3.14 (2.61–3.74)</td>
</tr>
<tr>
<td>High-density lipoprotein</td>
<td>1.35 (1.13–1.62)</td>
<td>1.35 (1.12–1.62)</td>
</tr>
<tr>
<td>Non-high-density lipoprotein</td>
<td>3.98 (3.33–4.69)</td>
<td>3.99 (3.34–4.71)</td>
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<tr>
<td>Triglycerides [median (IQR), mmol/L]</td>
<td>1.33 (0.94–1.95)</td>
<td>1.33 (0.95–1.97)</td>
</tr>
<tr>
<td>Apolipoprotein B100 [median (IQR), g/L]</td>
<td>0.995 (0.834–1.208)</td>
<td>1.001 (0.841–1.207)</td>
</tr>
<tr>
<td>Apolipoprotein A-I [median (IQR), g/L]</td>
<td>1.494 (1.329–1.683)</td>
<td>1.498 (1.325–1.684)</td>
</tr>
<tr>
<td>Lipoprotein(a) [median (IQR), µmol/L]</td>
<td>0.37 (0.15–1.13)</td>
<td>0.37 (0.15–1.15)</td>
</tr>
<tr>
<td>hsCRP [median (IQR), mg/L]</td>
<td>2.0 (0.8–4.4)</td>
<td>2.0 (0.8–4.2)</td>
</tr>
<tr>
<td>s-ICAM-1 [median (IQR), µg/L]</td>
<td>341.2 (300.2–393.0)</td>
<td>343.2 (302.8–394.5)</td>
</tr>
<tr>
<td>Fibrinogen [median (IQR), µmol/L]</td>
<td>10.29 (9.02–11.77)</td>
<td>10.21 (8.97–11.75)</td>
</tr>
<tr>
<td>Homocysteine [median (IQR), µmol/L]</td>
<td>10.4 (8.7–12.9)</td>
<td>10.5 (8.7–12.8)</td>
</tr>
<tr>
<td>Creatinine [median (IQR), µmol/L]</td>
<td>54.1 (48.0–61.0)</td>
<td>53.9 (48.2–60.7)</td>
</tr>
</tbody>
</table>

Women’s Health Study atrial fibrillation model derivation and validation

In the derivation cohort, 32 potential variables outlined in Table 1 were evaluated for model inclusion. Univariable association between each potential variable and incident AF in the derivation cohort are presented in Supplementary material online, Table S2. Of these, the inclusion of terms for the natural logarithm of age, weight, height, systolic blood pressure, ≥ 2 alcoholic drinks per day, and a history of either current or past smoking (ever smokers) resulted in the best fitting prediction model with the smallest BIC (7319.7). Model coefficients from the derivation cohort for these variables are presented in Table 2. The BIC for a model including the body mass index instead of height and weight was 7347.8, and the BIC for a model including age instead of the natural logarithm of age was 7321.8. Although none of the blood-based biomarkers were included in the final model, high-sensitivity C-reactive protein (hsCRP) would have been the next variable included (P = 0.02), but inclusion resulted in a small increase in the BIC (BIC = 7320.7 with hsCRP).

We then tested this AF prediction model in the validation cohort. Using coefficients calculated in the derivation set, the c-index (95% CI) for the WHS predictive model [0.718 (0.684–...]
The association with incident AF across quintiles of the weighted and unweighted GRS in the entire WHS (n = 20,347) is displayed in Figure 2. As shown, women in the top quintile of the weighted and unweighted score had a 2.25-fold (95% CI: 1.75–2.90, P-trend < 0.0001) and a 2.85-fold (95% CI: 2.18–3.73, P-trend < 0.0001) increase in the risk of AF, respectively, after adjustment for the WHS prediction model covariates. The per-allele relative risks for each of the individual SNPs included in the GRS are displayed in Supplementary material online, Table S3. When modelled as continuous variables, both the weighted and the unweighted GRS were significantly associated with incident AF in the validation and entire cohort (each P < 0.0001). When either the weighted or unweighted score was included among the candidate AF risk predictors considered for inclusion in a secondary, exploratory AF risk prediction model, each score was chosen for inclusion.

Clinical reclassification of atrial fibrillation with and without genetic information

When tested in the validation set, the addition of the weighted GRS to a model including age alone improved the C-index [0.704 (0.667–0.739), P = 0.0006], the NRI [0.107 (0.0286–0.1830), P = 0.006], the continuous NRI [0.578 (0.406–0.751), P < 0.0001], and the IDI [0.0064 (0.0045–0.0088), P < 0.0001] (Table 4). The addition of the weighted GRS to the WHS AF risk prediction algorithm improved AF risk prediction as measured by the C-index [0.741 (0.709–0.774), P < 0.0001], the continuous NRI [0.490 (0.301–0.670), P < 0.0001], and the IDI [0.00526 (0.00625–0.00759), P < 0.0001]. However, reclassification into our pre-specified clinical risk categories did not improve after the addition of the weighted

### Table 2 Beta-coefficients and multivariable adjusted hazard ratios for atrial fibrillation for each covariate selected for inclusion in the WHS atrial fibrillation risk prediction model

<table>
<thead>
<tr>
<th>Base model covariables</th>
<th>Beta (SE)</th>
<th>Adjusted HR (95% CI)</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Age</td>
<td>0.0924 (0.0060)</td>
<td>1.10 (1.08–1.11)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>WHS model</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Ln(age)</td>
<td>5.480 (0.40)</td>
<td>239.79 (109.96–522.94)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Weight (per 10 kg)</td>
<td>0.157 (0.035)</td>
<td>1.17 (1.09–1.25)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Height (per 10 cm)</td>
<td>0.306 (0.082)</td>
<td>1.36 (1.16–1.60)</td>
<td>0.0002</td>
</tr>
<tr>
<td>Systolic blood pressure, (per 10 mmHg)</td>
<td>0.155 (0.037)</td>
<td>1.17 (1.09–1.26)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>2+ drinks per day</td>
<td>0.491 (0.20)</td>
<td>1.63 (1.10–2.43)</td>
<td>0.015</td>
</tr>
<tr>
<td>Ever smoker</td>
<td>0.254 (0.10)</td>
<td>1.29 (1.06–1.57)</td>
<td>0.01</td>
</tr>
</tbody>
</table>

Coefficients displayed here were calculated in the derivation cohort and were used to test the model in the validation cohort.

*For context, a 10-year increase in age (e.g. from age 50 to 60) would be associated with a 2.72-fold increase in atrial fibrillation risk.

### Table 3 Fit, calibration, and discrimination statistics for the age and WHS atrial fibrillation risk prediction models in the validation cohort

<table>
<thead>
<tr>
<th>Risk prediction algorithm</th>
<th>Age alone</th>
<th>WHS</th>
<th>P-value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Model fit (χ²)</td>
<td>55.3</td>
<td>87.9</td>
<td>—</td>
</tr>
<tr>
<td>Model calibration [χ²(P-value)]</td>
<td>7.01 (0.54)</td>
<td>8.07 (0.43)</td>
<td>—</td>
</tr>
<tr>
<td>C-index (95% CI)</td>
<td>0.671 (0.636–0.710)</td>
<td>0.718 (0.684–0.753)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>NRI (95% CI)</td>
<td>0.211 (0.117–0.303)</td>
<td>0.578 (0.406–0.751)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Continuous NRI (95% CI)</td>
<td>0.064 (0.0045–0.0088)</td>
<td>0.0064 (0.0045–0.0088)</td>
<td>&lt;0.0001</td>
</tr>
</tbody>
</table>

CI, confidence interval; IDI, integrated discrimination improvement; NRI, net reclassification improvement; WHS, Women’s Health Study.

*Each likelihood ratio χ² statistic was highly significant (P < 0.0001).

*P-value of <0.01 required to reject the hypothesis that a model is well calibrated.
Figure 1  Clinical reclassification of participants in the validation cohort for the age alone model when compared with the novel Women’s Health Study atrial fibrillation risk prediction algorithm (WHS Model). In total, 1546 participants were reclassified, 1546 (100%) correctly. Reclassification $\chi^2$ calibration statistics calculated from this table were 25.3 ($P = 0.0001$) for the age alone model and 4.51 ($P = 0.48$) for the novel Women’s Health Study atrial fibrillation risk prediction algorithm.

Figure 2  Adjusted relative risk of incident atrial fibrillation for increasing quintiles of the weighted and unweighted genetic risk scores in the entire Women’s Health Study cohort ($n = 20,437$). Estimates of relative risk and 95% confidence intervals are adjusted for the covariates included in the Women’s Health Study atrial fibrillation risk prediction algorithm [$\ln$(age), weight, height, systolic blood pressure, alcohol use ($\geq 2$ drinks per day) and ever smoking status].
genetic score to the WHS AF risk prediction algorithm [NRI: 0.041 (−0.0444–0.123), P = 0.33]. Nevertheless, many (591, 58.5%) of the 1011 reclassified participants were reclassified correctly on the basis of the genetic information (Figure 3).

In a secondary analysis, we observed similar results for the unweighted GRS when it was added to the WHS AF risk prediction algorithm (Supplementary material online, Table S4 and Figure S1). Finally, in a sensitivity analysis conducted in the entire WGHS, we observed similar changes in the indices of reclassification after the addition of the GRS to the WHS AF risk prediction algorithm (Supplementary material online, Table S5 and Figures S2 and S3).
Discussion

In this prospective cohort of 20,822 women without CVD at baseline, we derived and validated a novel WHS AF risk prediction algorithm, which despite being relatively simple, demonstrated good discrimination, calibration, and improved reclassification into 10-year risk categories when compared with age alone. We then tested whether our ability to predict incident AF was improved by the addition of a weighted or unweighted GRS to the risk prediction algorithm. The addition of either GRS improved the c-index and other continuous measures of risk discrimination, but did not appreciably improve the ability to classify participants into pre-specified 10-year risk categories.

Our AF risk prediction model derived among women without pre-existing CVD shares many AF risk predictors with those derived in the FHS and ARIC populations, which included men and women with and without established CVD. The exceptions included physical exam findings and electrocardiographic variables, which were unavailable in this cohort. Despite the absence of this information, our model performed well and was able to reclassify 22.5% of women in a separate validation cohort. The six variables selected for inclusion in the AF risk prediction model—age, weight, height, systolic blood pressure, alcohol use, and past or current smoking—are readily available in nearly every primary prevention population. In addition, several of these variables are modifiable through lifestyle interventions. Therefore, patients can be counselled regarding lifestyle changes that might lower their 10-year risk of AF. Potential future clinical applications of this simple AF risk prediction algorithm could include identification of populations where targeted screening for asymptomatic AF might be cost-effective and/or where interventions designed to lower AF risk might be tested in randomized trials. Given the expanding indications for anticoagulation in lower risk populations and advances in rhythm monitoring devices, targeted screening for asymptomatic AF may have clinical utility in the near future.

When compared with the traditional AF risk factors described above, none of the 14 blood biomarkers we considered met our pre-specified criteria for inclusion in the WHS AF risk prediction algorithm, even though several, such as CRP and haemoglobin A1c, have previously been associated with AF in this or other cohorts. While our inclusion of these biomarkers in the model derivation process is a strength of our study, B-type natriuretic peptide levels were not available for analysis. B-type natriuretic peptide levels have been strongly associated with incident atrial enlargement, and left ventricular hypertrophy, which have been included in other risk prediction algorithms would add to AF risk prediction among women without CVD. Thus, we were unable to compare our model performance to that of the FHS and ARIC scores. We also did not perform screening ECGs during follow-up and some asymptomatic cases of AF may have gone undetected. Third, we did not collect information on the family history of AF at baseline and thus were unable to compare the predictive value of this information to that provided by the GRS. Fourth, as mentioned above, although we were able to test numerous blood biomarkers for inclusion in our model, we were not able to test all biomarkers that have been associated with AF in our study population.

In conclusion, in this large-scale, prospective cohort of initially healthy women of European ancestry, we derived and validated a novel, simple AF risk prediction algorithm utilizing six easily measured AF risk factors (age, weight, height, systolic blood pressure, alcohol use, and smoking). Beyond this information, a GRS based on recently published risk alleles showed potential for improving the ability to identify individuals at higher risk for AF; however, we did not find definitive evidence that the currently identified AF risk alleles can be utilized as a clinically meaningful risk.
stratification tool at present. Discovery of additional genetic variants and/or application to targeted populations may improve the clinical performance of GRSs. At the same time, research directed at developing effective AF screening and prevention strategies will increase the clinical impact of AF risk prediction scores.

**Supplementary material**

Supplementary material is available at European Heart Journal online.

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**Conflict of interest:** B.M.E. reports receiving investigator-initiated research grants from the American Heart Association, the Brigham and Women’s Hospital, and Roche Diagnostics. N.R.C. has no relevant conflict of interest to report. D.C. reports receiving research grants from the Swiss National Science Foundation (PP00P3_133681) and the University of Basel. D.I.C. reports receiving investigator-initiated research grants from the NIH. P.M.R. reports receiving investigator-initiated funding from the National Institutes of Health, the Leducq Foundation, Roche Diagnostics, Amgen, Inc., AstraZeneca, Novartis, Merck, Abbott, and sanofi-aventis; consulting fees from AstraZeneca, Novartis, Merck Schering-Plough, sanofi-aventis, Isis, Siemens, and Vascular Biogenics. P.M.R. is listed as a co-inventor on patents held by the Brigham and Women’s Hospital that relate to the use of inflammatory biomarkers in cardiovascular disease that have been licensed to Siemens and AstraZeneca and has served as a consultant to AstraZeneca. C.M.A. reports receiving investigator-initiated grant support from the National Institutes of Health/National Heart, Lung, and Blood Institute (NHLBI), American Heart Association, Siemens Healthcare Diagnostics, and St Jude Medical, consultancy fees from Novartis and GlaxoSmithKline. No other conflict of interest disclosures were reported.

**References**


CARDIOVASCULAR FLASHLIGHT

Granulomatous mass adherent to a patent foramen ovale occluder

Yann Ancedy*, Anne Bernard Brunet, Laurent Quilliet, Alain Mirza, and Laurent Fauchier

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A 70-year-old woman with a history of repeated cerebrovascular events and patent foramen ovale (PFO) closure with PREMERE occluder (St Jude Medical, St Paul, MN, USA) had a recurrence of transient left hemiparesis. Transoesophageal echocardiography (TOE) revealed an intracardiac mass on the left side of the PFO closure system (8 × 8 mm) (Panel A). Despite oral anticoagulation, TOE performed 2 months later found persistent mass (Panel B). Surgical removal of the PFO occluder with the linked mass (Panel C, arrow) and the closure of the atrial communication were, therefore, performed. Histology concluded to a granulomatous formation. Exogenous structures (Panel D) that may come from the occluder were found in the tissue and participated to an inflammatory reaction associated with fibrosis. To our knowledge, this is the first report of a granulomatous mass which needed removal of a PFO occluder. Beyond its debated indication, this highlights that the PFO closure may have rare but still unknown and not negligible complications.

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