

## Supplementary Online Content

Chang SH, Kuo CF, Chou IJ, et al. Association of a family history of atrial fibrillation with incidence and outcomes of atrial fibrillation: a population-based family cohort study. *JAMA Cardiol*. Published online July 5, 2017.

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**eAppendix.** Supplemental Appendix

**eFigure 1.** The Distribution of Diagnosis Age of AF in Those With Family History of AF and in Those Without

**eFigure 2.** The Distribution of Phenotypic Variance of AF Estimated by the Threshold Liability Model

**eFigure 3.** MACE-Free Survival of Newly Diagnosed AF Patients With or Without FDR Affected by AF

This supplementary material has been provided by the authors to give readers additional information about their work.

## **eAppendix.** Supplemental Appendix

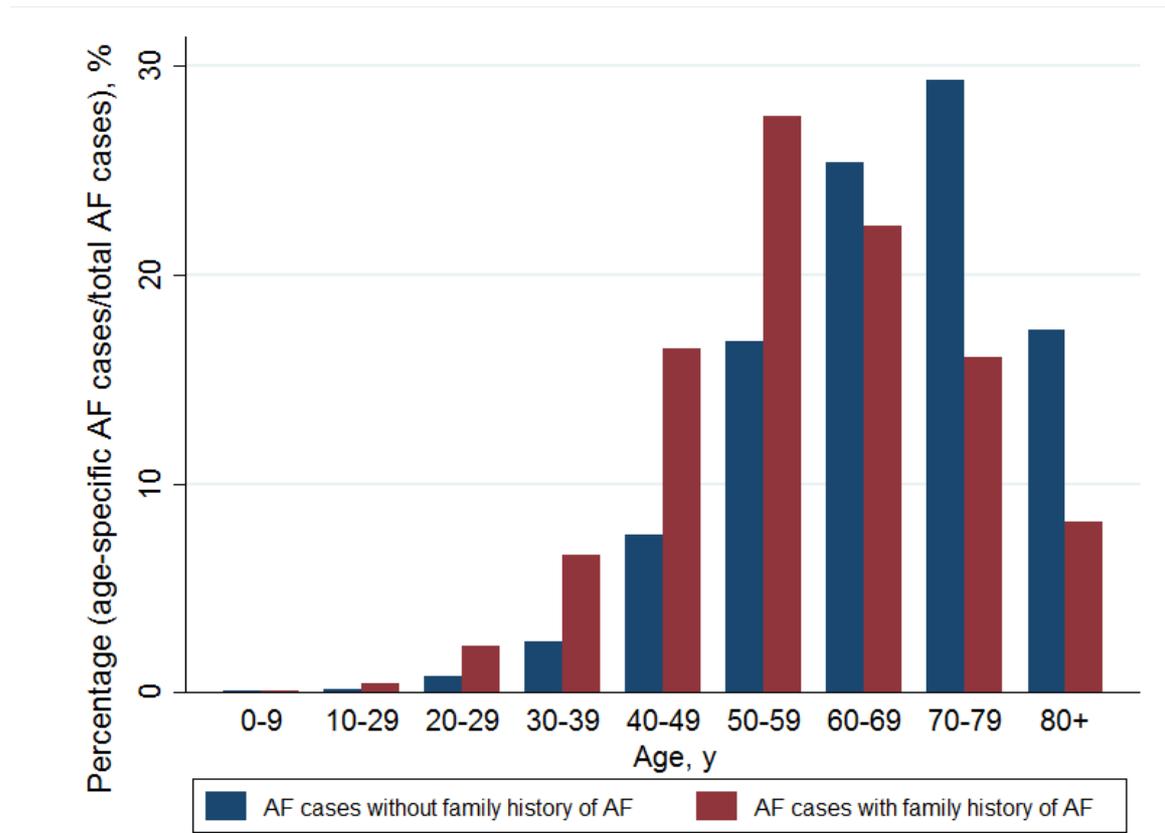
We used the standard “ACE” model to examine the influence of additive genetic (A), common environmental factors shared by family members (C) and non-shared environmental factors (E) accounting for variance in a phenotype (P). This model can be expressed as:

$$\sigma_P^2 = \sigma_A^2 + \sigma_C^2 + \sigma_E^2$$

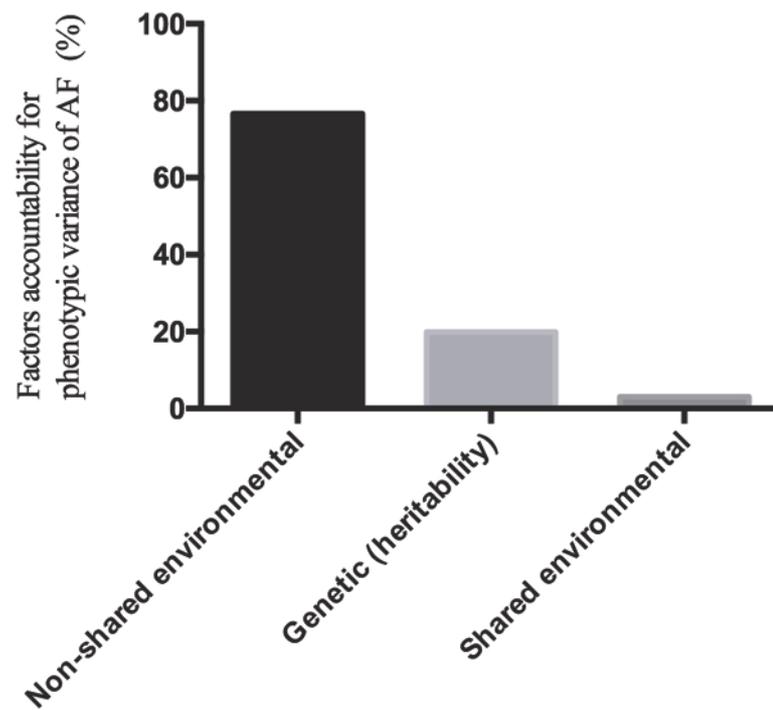
where  $\sigma_P^2$  = total phenotypic variance;  $\sigma_A^2$  = additive genetic variance;  $\sigma_C^2$  = common environmental variance; and  $\sigma_E^2$  = non-shared environmental variance.

Heritability was defined as the proportion of phenotypic variance attributable to genetic factors, and was expressed as  $\sigma_A^2 / \sigma_P^2$  with the familial transmission being expressed as  $(\sigma_A^2 + \sigma_C^2) / \sigma_P^2$ , which is the sum of heritability and common environmental variances.<sup>1</sup> We used the polygenic liability model to calculate both measures. A 2-sided p value of 0.05 was taken to indicate statistical significance.

**eFigure 1.** The Distribution of Diagnosis Age of AF in Those With Family History of AF and in Those Without



**eFigure 2.** The Distribution of Phenotypic Variance of AF Estimated by the Threshold Liability Model. The shared environmental factors account the major portion of variance. The genetic factor, in the other hand, explained trivial phenotypic variance of AF.



**eFigure 3.** MACE-Free Survival of Newly Diagnosed AF Patients With or Without FDR Affected by AF

