Ellinor - Identification of Common Genetic Variants for Atrial Fibrillation and PR Interval - Atrial Fibrillation Genetics Consortium (AFGen)

Updated 10/30/2018

Introductory slides from the June 4, 2015 Steering Committee/EAP meeting (requires log-in). [1]

AFGen Consortium Early-Onset Atrial Fibrillation WGS Study

Our study will consist of whole genome sequencing in 2,799 cases with early-onset atrial fibrillation (**EOAF**) from members of the AFGen Consortium and 3,375 referents from the Framingham Heart Study. EOAF cases will be drawn from 10 studies including the Massachusetts General Hospital AF Study, Framingham Heart Study, Vanderbilt University AF Study, Heart and Vascular Health Study, Cleveland Clinic AF Study, Atherosclerosis Risk in Communities Study, Women's Genome Health Study, University of Massachusetts AF Study and the Partners Healthcare Biorepository. By focusing on a young, relatively healthy population we have the advantage of being able to study AF without the confounding effects of other major comorbidities. WGS for the EOAF cases and referents from Framingham will be performed at the Broad Institute. Our initial analytic efforts will focus on identifying risk variants at known AF loci followed by genome wide analyses of single nucleotide variants, structural variation, loss of function variants, and the integration of WGS data with other genetic, expression and regulatory datasets.

Source URL (modified on 10/30/2018 - 6:45pm):<u>https://topmed.nhlbi.nih.gov/group/afgen</u> Links

[1]

https://topmed.nhlbi.nih.gov/system/files/meetings/ellinor_AF_WGS_Project_Update_06042015%20%5BCompatibili ty%20Mode%5D.pdf