THE BioVU Investigator

Volume 3, Issue 1

Save the Date: BioVU User Q & A Session

May 16, 2017 | 1 - 2 pm | 415 RLH

Please plan to join us for the ***BioVU User Q&A session***. We will field questions, provide a forum for feedback from our investigator community, & review the results from the Investigator Survey. **The team will also be discussing future updates to BioVU -- don't miss it!**

Let Us Know You're Coming - Here!

In February, the BioVU Progam celebrated its 10th Birthday!

Relation of Obstructive Sleep and a Common Variant at Chromosome 4a25 to Atrial Fibrillation

Atrial fibrillation (AF or AFib) is the most common of irregular heart beat disorders. It can cause blood clots, stroke or heart failure. It is important to identify patients with higher risk of developing AF because the death rate from AF is fast rising. Obstructive sleep apnea (OSA) is an often overlooked confounding factor for developing AF. OSA is a common sleep disorder in which patients' upper airway gets partly or completely blocked during sleep. The relative risk of AF in patients with OSA can be as high as 2.8.

Now in a study published in *The American Journal of Cardiology*, using BioVU resources at Vanderbilt, **Neel J. Patel, MD**, pictured above, has shown that there is a significant association between AF and OSA severity, and a chromosome genotype 4q25 SNP can predict AF status independent of clinical risk factors.

Although older age, high blood pressure, diabetes, or existing heart disease are among risk factors for developing AF, genetics and race also play important roles. There is a strong association between single nucleotide polymorphisms (SNPs) on chromosome 4q25, adjacent to the PITX2 gene, for four fold increased risk of developing AF during one's

BioVU Counts

Adults	205,155
28,836	Children
GWAS	40,211

SD User Support

5/24 RLH 412 from 1-2p

For information on future SD User Support meetings click here!

lifetime.

The relationship between AF, OSA, and genetics has been actively investigated at Vanderbilt by Ken Monahan, MD. Monahan has previously shown that OSA and the SNPs at 4q25 reduce the effectiveness of AF treatment. They have also shown that the severity of OSA influences the effect of genotype on response to anti-arrhythmic drug therapy for AF.

Following these studies, Patel said, his "hypothesis for this study was to assess whether knowledge of OSA severity and 4q25 genotype in addition to traditional risk factors would increase the ability to predict the presence of atrial fibrillation in patients."

Patel and his team identified 674 adults among those who had undergone polysomnography (sleep study) and compared the genotypes in the 4q25 region. They correlated the SNP prevalence among individuals who had previously shown symptoms of AF or OSA in their EMR against subjects not yet identified for AF. They found that common AF susceptibility SNP at chromosome 4q25 is associated with AF, independent of other AF risk factors.

The study highlights that knowledge of AF-related SNPs may enhance AF risk identification for patients undergoing sleep study. Although, Patel cautioned, "one of the limitations of our study (was) we had a relatively small sample size and our data is from a single center, therefore our population may not be representative of the general population."

Patel said, "The next step would be to perform larger prospective studies at multiple centers to validate our findings. With a larger patient population we also would like to evaluate other associated SNPs to see if the predictive ability of the model increases."

Article Citation: *Patel, N. J., Wells, Q. S., Huang, S., Upender, R. P., Darbar, D., & Monahan, K. (2017). Relation of Obstructive Sleep Apnea and a Common Variant at Chromosome 4q25 to Atrial Fibrillation. The American Journal of Cardiology, 119(9), 1387-1391.*

Article Submitted By: Sanjay Mishra, Chemical & Physical Biology PhD Candidate

The BioVU Team recently celebrated National DNA Day with the VICTR department with a helix building activity! The day celebrates the discovery of DNA's double helix in 1953 and the completion of the Human Genome

BioVU MEGA

MEGA-ex array data is available for ~22,500 BioVU subjects! Submit your data application today (click here)!

iLab Training

The iLab team will be having a training session orienting new users to the system.

VUMC Employee Training

- 5/16 | 10 - 11am

VU Employee Training

- 5/16 | 2 - 3pm

SD Data Update:

External Death Data

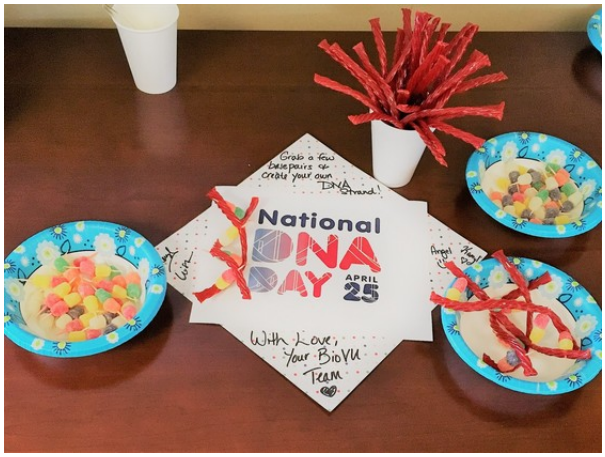
Due to changes in the National Technical Information Service policies, dates of death in the SD will only contain death data from VUMC until futher notice.

Recently Complete a BioVU Project?

Report a Publication

Report Awarded Grants

Project in April 2003. To learn more about National DNA Day, click here!



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