

CIAHD March 12, 2009 Research Meeting

(Summary Minutes)

Convened: 3:00 p.m. (Eastern)

Attendees: Sandra Albrecht, Ana Diez-Roux, Amanda Dudley, Nancy Fleischer, DeMarc Hickson, James Jackson, Jonetta Johnson, Aydin Nazmi, Kiarri Kershaw, Briana Mezuk, Jane Rafferty, Whitney Robinson, Del Rodrigo, Daniel Sarpong, Amy Schulz, Yan Sun, Herman Taylor, Marc Turenne, Monique Willis, Shun Yi Wu

Administrative Items

Ana- Stimulus supplements may be available for the Center. Nothing officially announced but will be soon. Internal supplements that should be relatively small and must be within the scope.

Sharon- interested in bringing the ARIC cohorts environmental data social data with their genome wide association data. Should probably start making inquires using a two prompt approach. Sharon will contact the genetic people in ARIC, Ana will contact Eric Folsum with ARIC Steering Committee. Todd to remind Ana by email.

Challenge Grants, some available under the area of Health Disparities.

Presentations

Continued Discussion on Project 2. Sharon Kardia, "Genetic and Social Factors in Blood Pressure Control in Hypertensives."

Members Comments:

Review on candidate gene GWAS and how are people bringing in the environment to both designs. Each one of us has 10-15 trillion cells, each of which have the same DNA. Chromosomes are labeled biggest to littlest down to X, Y. 3.1 billion base pairs when put together. The genomic approach took off 5 or 6 years ago with the development of SNP chips defined as a single nucleotide polymorphism, which have to be at 1% or greater in a population. Approximately 15 million SNP s exist. 99.9% of base pairs are the same. Every mutation starts in a single individual. Each individual carries about 100-200 unique mutations that comes from the mitotic process from both parents. In order to reach 1% each particular mutation had to keep tracking along until reaching a pretty significant fraction. Epidemiologically Population can be defined as small as 100 people. Therefore, 1 in 100 people. In other populations can be defined geographically. We each differ from one another by 3-4 million SNP s.

Two companies Alumina and Afrometrics have chosen 1 SNP s based on principles based on coverage, and frequency/correlation.

Population stratification is a really classic confounding case. One of the main field center locations located in Rochester, MN. Lots of people with non-region immigrant background work, live, and participate.

In candidate genes tag SNPs are a pretty complicated concept that have to do with marking variation within a gene that is not redundant and actually spans the gene.

Genowa study has about 256 candidates and what is happening is that there is a whole new set

Questions:

How many total base pairs do we each have? 3.1 billion base pairs.

How are people defining genes these days? Genes are defined as things that code.

“3P21” is like an address? Yes, and at that address you could have any combination of A, T, or CG with that outcome.

Are Affymetrix and Illumina different from one another? Yes, they are very different. Some overlap does exist. Depending on if you could see how strong the SNPs are.

How did the companies come up with two largely different sets of one million? This was done by sequencing. Affymetrix in the beginning ignored ethnic variations and made a very Caucasian sensitive selection of SNPs. Did a better job in the million SNP chip.

Is there more or less an agreement that states that these two companies do a good job at capturing variability across different ethnic groups? Pretty strong sense in the genetics community that they are only casting a coarse net to capture ethnic variability.

Is there a sense that the private mutations could be important for common diseases? No, however in looking over the literature and biology in recent research, this could make a difference. Could be more clinically relevant.

Principle components are summaries of SNP variations that travel together? Yes, and distinguish people. A component will utilize and maximize the explained variable outside.

Candidate genes are called so because they are hypothesized to play a role in the biology of something we are interested in? Yes, they are considered biological candidates for causing disease.