Salon XV: Genomics, representation, and equity
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Recent large-scale initiatives in genome sequencing have aimed to expand genomic analysis to diverse global populations. With more data, the thinking goes, the genomic medicine can cover and benefit historically underrepresented groups. This session will examine issues of representation and equity in genomic medicine. Who benefits from the "mining" of genomic data? Does this turn in genomic medicine mark a new age in global health, or a new wave of colonialism?

Specifically, we will be discussing the conception and progress of a relatively new initiative in Africa called "Human Heredity and Health in Africa" (**H3Africa**). This project was formally launched in October 2012, and has focused on the development and expansion of genomics research and medicine across the African continent. As described in the official mission statement, **"The core goal of the H3Africa program is to enhance the capacity of African researchers to undertake cutting edge research to advance understanding of the genetic and environment determinants of common diseases and use this knowledge to improve the health of African populations."**

In this session, we will discuss some of the key goals of H3Africa, as outlined in their mission statement and early prospective papers, and whether these have been upheld.

1. State of Genetics and Genomics medicine in Africa

- Minimal level of medical genetics clinics
- Practice of medical genetics limited to very few cases (e.g. sickle cell disease)
- Genetic "literacy" of communities and practitioners is limited
- Diseases of focus in H3Africa
    1. Role of genetic variability on interaction between disease-causing micro-organisms and the human host
    2. Genetic variability and connection to non-communicable diseases such as hypertension, stroke, heart disease, diabetes, cancer. Understand the interaction between genes and environment (such as diet) that may be leading to the increased incidence of these diseases.

2. H3Africa Policy Framework

- African Leadership
    - Leadership by scientists on the African continent, grants awarded to and managed by African institutions
    - Majority of funds have to be spent in Africa
    - "South-to-South network"
- Data-sharing
    - H3Africa researchers must make data globally available
    - H3Afria granted a minimum of 11 mo before data are publicly released
    - Further 12 mo publishing embargo after data release
    - Applicants wishing to access the data need to describe how their proposed use will contribute to capacity building and health improvement in Africa
- Sample-sharing
    - Sample movement across borders raises concerns over exploitation and fairness
    - For 3 yrs, samples can only be used for research that strengthens African research capacity (by researchers resident in Africa, or their close collaborators)
- Data and biospecimen access committee

- Committee to decide on access requests
- Committee will be comprised primarily of researchers from Africa, but will also include researcher outside Africa with experience working in Africa

3. Difficulties in Implementing H3Africa

- Building critical mass for genomic research in Africa
  - Retention of scientific leadership to conduct and maintain research and institutions
  - Lack of strong history of collaborative scientific endeavor
  - Infrastructure to collect, house, and disseminate data/samples
- Acquiring broad consent for participation
  - Fears of exploitation with no immediate benefit
  - Legislative policies hamper data sharing across national boundaries
  - Large cultural differences between urban and rural communities with shared genetic ancestry affecting:
    - Beliefs about sample donation
    - Ability to return individual genomic results
    - Ability to give informed consent
- Balancing the need for:
  - "African first" priority for analysis and publishing
  - The benefit of global access to H3Africa data
- Funding
  - Principle funding sources are:
    - National Institute of Health (US)
    - Wellcome Trust (UK)

4. H3Africa Progress

- $38 Million initial investment into H3Africa by NIH and Wellcome Trust (2012), $76 million for period of 2012-2016
- Increase in proportion of NIH and Wellcome Trust awards made directly to African scientists and institutions (~40% Wellcome Trust, 63% NIH funding for research in Africa)
- Ebola outbreak in West Africa, 2014 → rapid sequencing and genomic surveillance
- April 2015, 1st Annual African Symposium on Genome-wide association studies for complex disease
- "The consortium has grown and now includes eight collaborative centers, seven research projects, six ethics projects, three H3Africa biorepository sites and a pan-African bioinformatics network. The research is performed by 26 research groups in 27 African countries and includes over 500 investigators who will be studying over 75,000 participants in Africa." -2015 update on H3Africa program

Suggested Readings:

H3Africa homepage: http://h3africa.org/
H3Africa Ethics and Governance: http://h3africa.org/about/ethics-and-governance
H3Africa Publications (by year): http://h3africa.org/links/publications

Hegel M. **Incidental Findings Challenges Point to Need for Better Databases, Population Specific References**. Genomeweb. 2015. https://www.genomeweb.com/clinical-sequencing/incidental-findings-challenges-point-need-better-databases-population-specific
"Jarvik said that because there is much less data on individuals not from European descent, calling variants as pathogenic or not is more difficult. 'One of the most helpful things in determining if a variant is disease causing or not is how commonly you see that variant… variants that we rarely see in one population may turn out to be common in another population. That information is helpful, because it means it probably doesn't cause disease' "

Paula P. **Funding Research in Africa**. The Scientist. 2014. http://www.the-scientist.com/?articles.view/articleNo/41427/title/Funding-Research-in-Africa/
"Most of the African researchers are mainly focusing on getting resources, publishing their papers in collaboration, but are not in the position to lead the research that will solve the continent's problems… The problem is resources. There is no Pan-African research funding agency."

de Vries J., Tindana P., Littler K., Ramsay M., et al. **The H3Africa policy framework: negotiating fairness in genomics.** Trend in Genetics. 2015. http://www.cell.com/trends/genetics/pdf/S0168-9525(14)00196-6.pdf
"Here, we outline four key components of that policy framework that together seek to establish more 'fair' ways of working together, most notably by advocating preferential access to funding, samples, and data for African researchers."

Landouré G., Samassékou O., Traoré M., Meilleur K. G., Guinto C. O., Burnett,B. G., Sumner C. J. and Fischbeck K. H. **Genetics and genomic medicine in Mali: challenges and future perspectives**. Mol Genet Genomic Med. 2016. http://onlinelibrary.wiley.com/doi/10.1002/mgg3.212/full
"Although Africa harbors a majority of infectious diseases, studies on the genetic susceptibility to infectious diseases or resistance to treatment have been scarce on the continent. While searching for resistance variants in the treatment of HIV/AIDS and tuberculosis has become a standard practice in developed countries, in Mali, as in several parts of Africa, genetics and genomic medicine of infectious diseases is still limited to few research laboratories."

Gire S., Goba A., Andersen K., Sealfon R., Park D., et al. **Genomic surveillance elucidates Ebola virus origin and transmission during the 2014 outbreak**. Science. 2014.
http://science.sciencemag.org/content/345/6202/1369.full
"Gire *et al.* describe Ebola epidemiology on the basis of 99 whole-genome sequences, including samples from 78 affected individuals. The authors analyzed changes in the viral sequence and conclude that the current outbreak probably resulted from the spread of the virus from central Africa in the past decade. The outbreak started from a single transmission event from an unknown animal reservoir into the human population. Two viral lineages from Guinea then spread from person to person into Sierra Leone."