H3Africa
Human Heredity & Health in Africa
Newsletter Issue 6
August 2018

A New Dawn for Genomics in Africa

by Dwomoa Adu

First published in Business Times Africa (http://businesstimesafrica.net/)

Body tissues are made up of cells which contain DNA, the unique genetic material that carries the instructions or blueprint for all our body's development and function. A genome is all our genetic material. The human genome is made up of 23 pairs of chromosomes including the sex chromosomes - male XY and female XX. DNA is made up of building blocks called nucleotides and these are wound up in a double helix. What is completely amazing is that these four nucleotides: A, T, G or C in combination provide enough information for the body to make any protein and to transmit information from one generation to the next, thus forming the basis of heredity. For describing and explaining this amazing structure Watson and Crick at the Cavendish Laboratory in Cambridge were awarded the Nobel Prize in 1962. Some 50 years later the whole human genome was sequenced. Of importance, sequencing the genome of Africans showed us to have the most complex arrangements and confirmed that humanity originated from Africa around 60 000 years ago.

We all know about sickle cell disease which causes anaemia and episodes of bone pain. Some 20% of individuals in sub-Saharan Africa (SSA) carry one copy of the sickle cell gene (haemoglobin S). Professor Charles Rotimi and colleagues from the National Institutes of Health in the USA have shown that haemoglobin S (sickle cell trait) evolved some 7 300 years ago in SSA and because it protects against fatal malarial infections increased in frequency. Individuals with two genes for haemoglobin S however develop sickle cell anaemia.

In this issue:

- A New Dawn for Genomics in Africa
- The H3Africa Whole Genome Study
- The Launch of GeneMAP
- Conversation with an Early-Stage Career PI
- Genetics Teacher Workshop
- Young Researchers Forum
- The 11th H3Africa Consortium meeting
- Training Corner
- Publications from the Consortium

Similarly, individuals with variants in the gene for glucose 6 phosphate dehydrogenase (G6PD) are protected from fatal malaria but are also at risk of destroying their red blood cells and developing anaemia. A further example is the Apolipoprotein L1 gene (APOL1) which carries a type of cholesterol in the blood stream. Recent studies show that variants in the APOL1 gene evolved in Africans some 10 000 years ago because they protected our forebears from fatal sleeping sickness (Trypanosomiasis). However, the same APOL1 gene variants increase the risk of developing chronic kidney disease in African Americans and in Africans. Evolution in our genes can lead to protection against infectious diseases but by the law of unintended consequences can also lead to completely unrelated disease. If we can understand how this occurs, then we can develop new ways of treatment.

The ability to rapidly sequence the Ebola virus genome by Professor Christian Happi's group from Redeemer's University in Nigeria provided critical insights that allowed the patterns of transmission of this virus to be tracked. Our genes also shape the ways we handle drugs, and this can lead to either inadequate effectiveness or side effects from the medication. This is called pharmacogenomics. An example of this is the drug Efavirenz which is used to treat HIV infection. Variants in the gene for the enzyme that metabolizes Efavirenz are found at high levels in some African populations and this leads to high levels of the drug and toxicity. Other examples include the drug Codeine which is metabolized into Morphine; variants in the gene of the enzyme that metabolizes Codeine rapidly are found at high levels in North Africans and Ethiopians who are more likely to develop side effects from this drug. It is not known whether the tragedy addiction to Codeine-containing cough syrups recently reported in Nigeria and of the abuse of tramadol in Ghana may also have a genetic basis.

Thus, sequencing of the human genome led to genome-wide studies that have provided crucial information on the causes of disease. Some of these studies suggest new mechanisms for disease causation that can lead to new and improved treatments. Few of these important studies have been carried out in Africans. Currently, researchers and doctors know some of the genetic changes that can cause disease, but they do not know all of the genetic changes that can cause disease.

By studying many different kinds of diseases through genomics we expect to identify some of the genetic changes associated with diseases. Since we also will combine genetic information with information about environmental exposures and responses to drug treatments we can obtain a better understanding of why some people fall ill and respond differently to treatment. With such knowledge, future treatments could potentially become customized to a patient's unique genetic make-up.

An initiative by the USA National Institutes of Health, and the UK Wellcome Trust and the African Society of Human Genetics in 2012 established the Human Heredity and Health in

Africa (https://h3africa.org/) initiative and funded studies on the genetic basis of disease in Africa with over 100 million US dollars. Other funders include the Bill & Melinda Gates Foundation and the Alliance for Accelerating Excellence in Science in Africa (AESA).

The major areas of H3Africa research include stroke, septicemia, cardiovascular disease, diabetes, sickle cell disease, cardiometabolic disorders, trypanosomiasis, kidney disease, nasopharyngeal and respiratory disease, tuberculosis, rheumatic heart disease, schizophrenia and inherited neurologic disorders. These research projects are underpinned by a bioinformatics network and biorepositories in Africa, reflecting the interest of the program in improving research infrastructure in Africa.

The H3Africa Consortium has already made a huge impact on ways in which the ethical, legal and social implications of genomic research in Africa can be addressed. For example, H3Africa has engaged national research ethics boards of most African countries where there are research projects. This has allowed the establishment of important principles governing the autonomy of the research subject. Similarly, wide-spread engagement of the communities in which research is being undertaken has helped to refine the ethical principles of informed consent, issues of broad consent for secondary studies and data and biospecimen sharing to ensure that local needs and issues relating to genomic research are addressed.

H3Africa also strongly supports collaborations among scientists in Africa and outside. Accordingly, H3Africa scientists have reached out to scientists of African origin in the diaspora to collaborate with their colleagues in developing genomic research on the continent. There has also been a gratifying willingness of scientists in high income countries to collaborate in this endeavor. All of this means that the health of people in Africa will benefit from the rapid advances in genomic medicine that are currently taking place. Crucial to developing and sustaining genomic science in Africa is training and this is occurring at all the levels that allow the development of research.

"…the future wellbeing of our people requires funding from African governments to sustain the achievements made so far"

The platform for genomics research has been established in Africa, but the sustainability of these projects is critically dependent on the willingness of African governments to provide funding for this research. The US Precision Medicine project plans to recruit one million subjects for genomic research. The UK has a 100,000 Genomes Project. The European Union and China all have planned or ongoing genome projects. The important benefits of genomics to the future wellbeing of our people require funding from African governments to sustain the achievements made so far. We foresee a future in which Africa joins the genomic

revolution that promises to transform the way in which we understand and treat diseases that blight our people's health.

The H3Africa Whole Genome Sequence Study

by Ananyo Choudhury and Neil Hanchard

The dataset and history

Despite recent reductions in the cost of whole genome sequencing and the increasing popularity of large-scale genome-sequencing projects, the genomic diversity of Africa - with only a few hundred low coverage genomes in the public domain - remains highly under-represented. Moreover, samples that have been sequenced by large-scale genome sequencing projects, such as the 1000 Genomes and African Genome Variation projects, have a strong geographical bias due to an imbalance in study location. If these datasets were considered together, West Africa would be represented by ~500 genomes, East Africa by ~300 genomes, leaving South Africa to be represented by only ~100 genomes and Central Africa completely unrepresented. Another bias lies in the representation of ethnic groups currently sequenced due to the tremendous ethnolinguistic diversity found in certain regions. For instance, anthropological studies suggest that some ethnolinguistic groups in Nigeria are likely to be very different from the groups that have already been sequenced, despite the country being one of the best studied in respect to African genomics.

As datasets of available whole genome sequences were being assembled for the design of an efficient Africa-centric H3Africa-genotyping SNP array, the chip design team recognized these gaps and pressed for a set of high-coverage whole genome sequences (WGS) from the consortium to facilitate the design process. The Genome Analysis working group in turn contacted H3Africa Principal Investigators for potential samples to fill these gaps. Once the list of potential samples was received, the working group carefully scrutinized the available genomic data and proposed the best samples to be sequenced, focusing on geographic regions and ethnolinguistic groups that have not been surveyed or might differ significantly from existing datasets. The final chosen dataset included 348 individuals, belonging to more than 10 ethnolinguistic groups spanning 8 countries (Zambia, Botswana, Cameroon, Nigeria, Benin,

Ghana, Burkina Faso and Mali) across West, Central-West, Central and Southern Africa **(Figure 1)**. Although all the participants included in the study were Niger-Congo speakers, many were expected to have ancestral contributions from other groups such as Khoisan hunter-gatherer, Rain forest foragers, Nilo-Saharan and Afro-Asiatic due to the history of admixture.

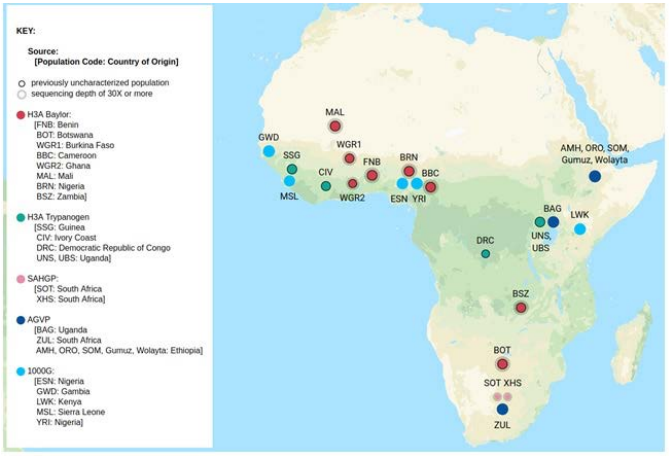


Figure 1. African whole genome sequence data in public domain. The possible locations of populations are marked with circles. The geographies of novel populations included in the H3Africa and Trypanogen studies are shown with green and dark red circles, respectively.

The samples were sequenced at a depth of 30X reads – the highest depth for a systematic study of African genomes to date - at the Baylor College of Medicine sequencing facility in the USA. As the mandate of the chip design team was limited to identification of probable tag-SNPs and evaluation of imputation, only a part of the potential analytic value of the data was explored in the chip design study. Therefore, the H3Africa Genome-Analysis Working Group proposed a separate study to conduct a comprehensive analysis of the data that would focus on the population and medical genetic aspects of the WGS data.

The team and timeline

To facilitate this more detailed study, a core group of team leaders with experience and expertise in population genetic and disease research was convened. Four team leaders were assigned to lead the analyses on population genetics, signatures of selection, rare variants, and disease-associated variants, respectively, together with an editorial team tasked to steer the entire study. To enable all interested researchers in the consortium to participate in the study, a request for volunteer analysts to join the various teams was circulated, and all applicants with requested skills in bioinformatics and medical genetics were assigned to either their group of choice or the group where they could be of most assistance.

In this regard, it is noteworthy to mention that the entire study was conducted through voluntary work with no paid positions. Preliminary plans for the study were finalized during the H3Africa meeting held at Mauritius in October 2016, and these were further developed at the Botswana H3Africa meeting in March 2017. During the initial design of the study, the Trypanogen group, who had sequenced more than 200 genomes at low/moderate coverage, mostly from non-overlapping geographic regions, volunteered their dataset for inclusion. This brought the final WGS dataset to more than 550 whole genomes from across 13 African countries – the largest such study to date. A three-day Jamboree, hosted by Professor Nicola Mulder, took place in Cape Town in August 2017. At this meeting the teams compiled the final datasets, identified the most pressing research questions, and outlines the final analyses. This was followed by over a year of extensive analysis by various teams. During this time, the

teams continued to meet twice a month via conference calls and more often via a very active set of Slack channels.

The Key Questions

The languages belonging to Bantu-language family constitute the most spoken language in sub-Saharan Africa (SSA). The spread of this family of languages across SSA is ascribed to a 5,000 years old migration of Bantu-speaking people, from their homeland, somewhere in present-day Nigeria and Cameroon. This migration and the following admixture events with resident populations in various parts of Africa have played a pivotal role in shaping the genomic landscape of sub-Saharan Africa. Although, research over the years has uncovered piece-meal details, the exact timing and path taken during this migration, especially through central Africa is still not clear. Based on the novel data from populations in Botswana, Democratic Republic of Congo, Zambia and Uganda, a major aim of this study was to identify the possible route and timeline for the migrations. The migration also necessitated rapid adaptation to new diet, disease, environment, and lifestyle. This was achieved by directional selection on existing variants as well as introduction of variants better suited to a particular environment via admixture. Based on the comprehensive whole genome sequence and an assortment of method we aimed to identify the genomic regions under selection in these Bantu-speaker populations, study their variation across Africa and understand their significance in recent/ancient adaptation. The unprecedented high-coverage WGS dataset also enabled us to investigate rare genetic variation, in particular identifying novel variants with high confidence and predicting on the potential for additional novel variant discovery from WGS in other African populations. Moreover, it also yielded an opportunity to study rare variants which occur more than once and are predicted to result in an abnormal, damaged, protein; particularly, we wanted to describe how these variants are shared between populations, and what genes they occur in. Finally, using the variation in frequencies of known disease-associated variants, we wanted to describe the patterns of disease risk across the continent and study the correlation between the distribution of genetic variants and actual disease incidence.

Preliminary insights

The study so far has significantly enhanced our understanding of Bantu-migration by identifying a possible milestone population in Central-Africa. We found geography-specific hunter-gather admixtures in most of the central-African groups reiterating the role of these populations in shaping African genomic diversity. Analysis of mitochondrial DNA and Y chromosome in these populations further hinted at possible gender biases in some of these admixture events. In addition, evidence for a novel-ancestry, incorporated by admixture, in one of the newly surveyed Nigerian populations was detected. The distinguishing levels of homozygosity as well as the distribution of long runs of homozygosity in some of the ethnolinguistic groups from Mali

suggests some level of assortative mating in these populations, especially in recent history.

Several genes associated with immunity, non-communicable diseases, and metabolism were found to be under positive selection. Almost half of these signals were novel, emphasizing the potential for in-depth studies on genomic diversity and signatures of selection using unbiased datasets. Interestingly, some of the signals were restricted to particular populations or geographic regions despite sharing a relatively recent common history, suggesting differences in local selective pressures.

We discovered more than 3 million novel variants in the 350 genomes, demonstrating that additional sequencing in carefully selected African ethnolinguistic groups is likely to yield significant novel variants that are highly relevant to human disease despite the limited number of African whole genomes available in the public domain. This underlines the necessity and incentives for future studies on the continent. Additionally, the clear concurrence between disease incidence and frequencies of disease-associated variants for some diseases such as influenza, illustrates the significance of similar studies in disease research.

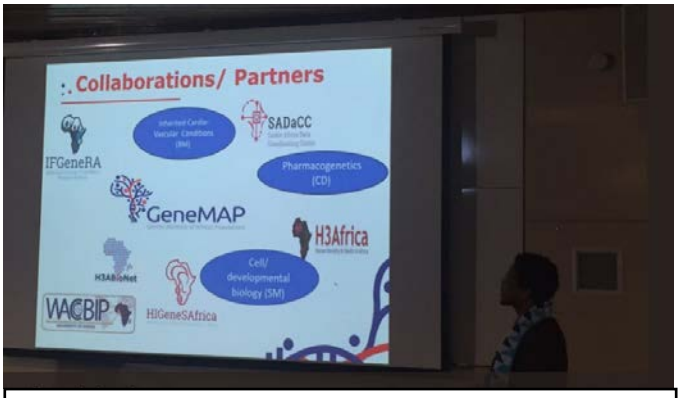
Where are we now?

These preliminary results were presented at the H3Africa Uganda (March 2018) meeting. We are planning to present a more comprehensive session to discuss these results in the upcoming H3Africa meeting to be held in Kigali this September. The analyst team is also busy preparing a first draft for circulation within the consortium.

The Launch of GeneMAP

by Rolanda Julius

The Genetic Medicine of African Populations (GeneMap) project was launched on June 7th, 2018. The late Prof. Bongani Mayosi (Dean of the Faculty of Health Sciences, University of Cape Town, South Africa) opened the event, welcoming the new research projects and inter-institutional collaboration. Prof. Ambroise Wonkam, the director of GeneMAP, presented an overview of GeneMAP and reiterated that the genomic diversity of the African population holds promise to fully engage genetic and genomic medicine which would also be relevant to other world populations. The guest speakers then continued to introduce the projects in specific disease areas with genetic associated causes.



Prof. Ambroise Wonkam introducing GeneMAP

Key results from long term studies on Sickle Cell Disease (SCD) and Fragile X Syndrome were highlighted, emphasising the pronounced effects of such genetic associated diseases in the African population.

One of the new projects, Hearing Impairment Genetic Studies in Africa (HIGENES-Africa) will focus on the research, diagnosis and care of people living with hearing impairment (HI) of which there is a high burden in Africa. Prof. Guida Landouré (University of Science, Technique and Technology of Bamako, Mali) pointed out that different degrees of hearing impairment are quite common but underdiagnosed. Moreover, up to 50% of congenital HI is of genetic etiology.

Another project, Individual Findings in Genetic Research in Africa (IFGeneRA) will explore the complexities and implications for receiving a diagnosis of a genetic disorder using Fragile X as a case study. IFGeneRA subjects participating in HIV, psychosis and neurodevelopmental conditions research will also be included to determine the appropriateness of the type of feedback participants could expect. Concurrently, the project will assess the effectiveness of communication channels and the public awareness of genomic research. To this end, Prof. Jantina de Vries (University of Cape Town, South Africa) showcased an in-progress re-enactment of the book *The Drama of DNA,* by Karen Rothenberg and Lynn Bush. Similarly, Prof. Mogomotsi Matshaba (Baylor College of Medicine, Botswana) presented the comic series "Genome Adventures", which introduces genomics and genetics to non-scientists. These findings inform the need of capacity building in genetic counselling and acceptability of genomic medicine.

Next, Prof. Nicola Mulder (University of Cape Town, South Africa) introduced the concept of building ontologies for SCD. Ontology development is a bioinformatics initiative to facilitate data sharing and ease of analyses as it is recognized by data analysis software programmes. Currently, there is a necessity to coordinate all the concepts and categories and their relationships associated with SCD. This project will address this need and deposit the information in a database.

The launch of the project re-emphasised that there is still a dearth of information on African population genomics and heritable diseases and that data and sample sharing and collaboration is key to boost this research.

Conversation with an Early-Stage Career PI

by Savannah Mwesigwa

Dr David Kateete, acting chair of the Department of Immunology and Molecular Biology, College of Health Sciences at the University of Makerere in Uganda, was recently interviewed by Savannah Mwesigwa, a PhD candidate with the Collaborative African Genomics Network (CAfGEN) project at Makerere University.

Dr. David Kateete, acting chair of the Department of Immunology and Molecular Biology, Makerere University and PI of BRecA

***Savannah**: Tell us about your background, focusing on significant events that have shaped your career.*

Dr Kateete: I trained in Veterinary Medicine then trained intensively in Molecular Biology before attaining a master's degree in the same field. I was one of the pioneer trainees of the Molecular Biology program here in Uganda, as well as being a forerunner in the area of research at the veterinary school in the early 2000s. In the late 2000s the Medical School became extremely interested in the implementation of molecular biology techniques. This coincided with the return of Prof. Moses Joloba to Makerere University from Case Western Reserve University, having completed his PhD. He was tasked by the Medical School to implement the molecular disciplines to see how they could support or improve the school. That's how I became a member of Prof. Joloba's research group. We had a re-entry grant from the NIH for the purpose of studying signalling genes in *Mycobacterium tuberculosis*. With my master's degree in hand, I began working on this research in 2003. My focus was to characterize the signalling genes. We were successful in securing an R01 grant for this research, which then supported my PhD work in combination with a Fogarty grant for basic research. Around 2006, I was recruited to become a faculty member in the Department of Microbiology. I worked hard to implement molecular biology with the team and we established these molecular techniques, the use of which then spread into various labs; molecular diagnostics lab, the Immunology lab and TB culture lab, to name a few. This effort was supported by multiple funding agencies and an enlarged personnel group. In 2011, we started a program in Immunology and Molecular Biology. We then began a dialogue with the university regarding these skills, which culminated in the approval of the Department of Immunology and Molecular Biology within Makerere University in 2016. At that time, I was chosen to be the acting chair of the department.

***Savannah**: What are the best and worst aspects of your job position?*

Dr Kateete: I will begin with the worst aspects; as the department chair, I spend a significant amount of my time in administration. The job description is very broad and covers mobilizing resources for the unit, governing human resources, meeting with different partners, reviewing the curriculum, community service, managing the public research output of the department and grant applications, to name

but a few. It's a delicate task balancing between developing the department and developing one's career, because the university applies the same criteria to measuring productivity of both the department and of individuals. I find it's easy to get caught up in progressing the department, frequently at the cost of one's personal development.

The best aspect I've experienced as chair of the department is really the feeling that I am providing a service to the community. I find fulfilment in the knowledge that I am part of laying a foundation that the next department chair and their team can build upon.

***Savannah**: Can you elaborate on the BRecA project that you are working with?*

Dr Kateete: Nurturing Genomics and Bioinformatics Research Capacity in Africa (BRecA) is a training program supported by Fogarty International Centre as part of the H3Africa initiative. BRecA extends from an H3Africa-supported initiative at Makerere University in Uganda to the Collaborative African Genomics Network (CAfGEN) and the Integrated Biorepository of H3Africa Uganda (IBRH3AU), which two programs, including the H3ABioNet at the Uganda Virus Research Institute (UVRI), actually gave birth to BRecA. Prior to that, there were already other partners supporting the growth of bioinformatics in Uganda, including the THRiVE Consortium for Health Research Capacity Building and Makerere University E-Learning Environment (MUELE). All these existing activities, strengthened by the development of CAfGEN and the biorepository, gave birth to BRecA. The primary goal of BRecA is to establish degree programs at Makerere University; as in, MSc and PhD in Bioinformatics which would both be by coursework and dissertation. Both these programs are awaiting approval by the University Council. The PhD would the first doctoral program in Bioinformatics here in Uganda. We also have a postdoctoral training program, which is meant to support CAfGEN trainees and launch them as independent researchers as they complete their degrees; 2 positions are available, one each for a trainee from Botswana and Uganda. So, it is evident that as much as BRecA is based at Makerere, we also have a responsibility to partner with our African collaborators in Botswana and support them as they build similar programs in Bioinformatics.

***Savannah**: Clearly, you're a busy man and you juggle multiple projects. What do you wish you had known about science management before you took your first management role?*

Dr Kateete: Science management is, to use very technical language, huge! It's very important that we conduct science in the correct manner and are availed adequate support. We need to have appropriately trained people managing science because those are the people who will ensure that a vibrant research and educational training culture is grown and maintained across Africa. Lacking the right people, with the right vision, in positions of leadership and management, I believe it will be difficult for Africans to

continue to catch up in technology and research development to our peers abroad.

***Savannah**: If you could make one change about the way we perform research in Africa, what would it be?*

Dr Kateete: One change. If I had the power, the one change would be to increase local funding, from our African governments, from industry and from our research institutions. The best way to drive research in any setting is to have adequate funding, especially from our national governments. Many individuals have exceptional research proposals but not all of them can be supported within the highly-competitive, foreign, extra-mural support that embodies the current funding mechanisms available to most African researchers. This is where government can begin to fill the gap. I believe this would be most relevant at the post-graduate level within Uganda.

***Savannah**: What major challenges have you seen young African scientists in the field of Bioinformatics facing? And what career advice would you give to young persons who want to become involved in this science?*

Dr Kateete: (Big sigh). That's a tough question. The biggest challenge I've seen young scientists in general, not just those in Bioinformatics, struggle with is the question of career path and employment following achievement of their post-graduate degree. Uganda currently has a population of 42 million, which only highlights the scarcity of job openings for young graduates. But on the other hand, I think the pooled brain resources from such a large population also provides a great opportunity to come up with ideas to turn the situation around. On a positive note, I haven't encountered many graduate students within our local setting who have failed to find meaningful employment. My career advice to young scientists who are wondering what to do post-graduation, is to focus on their current research. We have a tremendous need for research in Africa as we battle the disease burden prevalent over the continent as whole. I believe this is really the best time to produce Bioinformaticians and other young African scientists who can engage in this work. The future is very bright for them and I think embarking on a career in bioinformatics is a risk well worth taking.

***Savannah**: Think back 5 years. Has your career progressed as you had envisaged back then?*

Dr Kateete: That's a great note to close on! In actual fact, my career progression has exceeded what my expectations were back then. Similar to young scientists today, when I completed my PhD in 2013, I wasn't sure what I wanted to do with all the knowledge I'd accumulated. It's clear now that my PhD training opened many opportunities that led me to my current position. I believe that the same trajectory remains true for today's graduates.

***Savannah**: Thank you so much, David. We wish you all the best moving forward in your career.*

Dr Kateete: Thank you, Savannah. I look forward to interviewing you as chair of department in future (laughter)!

Genetics Teacher Workshop

by A Kleinsmidt

Teaching genetics to high school learners

Genetics forms a significant component of the grade 12 life sciences curriculum in South Africa, but university lecturers are concerned about the superficial level of knowledge of students entering 1st year medicine and science studies. Grade 12 teachers struggle to teach genetics using traditional pedagogy. Genetics lends itself to group learning, interactive timelines, taking family histories, quizzes and ethical debates. The current syllabus is outdated and for example, lacks content on genomics and 'nextgen' sequencing. As part of its community engagement in biobanking research projects, the Centre for Medical Ethics and Law, Stellenbosch University, South Africa developed activity books on genetics for life sciences Grade 12 learners and has started a process of participating in curriculum development of genetics content for Grade 12 learners.

Life sciences teacher workshop

In February, the Centre hosted a very well-attended teacher workshop for Grade 12 life sciences teachers, where they were exposed to three lectures followed by a panel discussion.

A lecture by Prof Himla Soodyall on Genetics and Society commenced with 2 participants winning free genetic ancestry tests to great applause, a generous gift from Prof Soodyall. Dr Farha Cassim gave a presentation titled 'Teaching genetics in the biology curriculum: New educational tools' on the development of pamphlets, a biobanking DVD and the genetics activity booklets. These colourful booklets teach about genetics in an engaging style with cartoons, word searches and crossword puzzles. Dr Cassim described the workshops undertaken with matric life sciences learners and explained the learning that was measured before and after the activities. Scientist Dr Craig Kinnear then took a detailed look at the matric genetics syllabus in his talk 'New vision for genetics in the biology curriculum' and discussed with the teachers, his recommendations for updating the syllabus and equipping matric learners to enter university science and medicine studies. These talks were followed by a panel discussion and Q&A session.

Dr Kinnear, Dr Cassim and Ms A. Kleinsmidt, together with matric life sciences teachers are enthralled by Prof. Soodyall (off camera).

Updating the matric genetics curriculum

The life sciences curriculum advisor for the Western Cape, Mr. Jean Goliath, was present and stressed the need for further engagement between the Centre for Medical Ethics & Law and the education department, given the success of the teacher workshop. The revision of the curriculum along the lines suggested by Dr Kinnear has since been raised at national level in the department of education. The teachers present at the workshop are looking forward to using the genetics activity books in their matric revision sessions as the knowledge is conveyed in an accessible way through games and fun activities.

Young Researchers Forum

by Rahaman Ademolu

The African Society of Human Genetics (AfSHG) in collaboration with H3Africa organized the Young Researchers Forum on November 15th, 2017 at the National Research Center (NRC) in Cairo, Egypt prior to the annual AfSHG conference. The program was planned for young scientists in the field of human genetics across the continent to meet, showcase their research findings, and promote collaborations amongst themselves.

The program commenced with an opening speech by Prof. Samia El Temtamy, a renowned mentor and pioneer of the NRC Human Genetics and Genome Research Department (HGGRD) in Egypt. She presented a brief, motivating biography followed by a chronicle of her contributions to the development of HGGRD in Egypt, a department which already over half a century old. Emphasizing the importance of teamwork and collaboration in research, Prof. Temtamy described her projects in the Computational, Evolutionary and Human Genomics (CEHG), mentioning some of her most fruitful collaborations and various awards and achievements of the group. She concluded with a quote by Francis Collins (2003); "Make big plans; aim high in hope and work remembering that a notable, logical diagram once recorded will not die but long after will be living thing, asserting itself with ever-green insistency".

Some young researchers with Prof. Michele Ramsay at the Forum

Oral presentations by young scientists were spread over two sessions, each comprising ten speakers, with poster presentations between the sessions. Some of the presentations included "*Novel Genome-Wide susceptibility loci for cardiometabolic traits in Africa*" (Segun Fatumo) where a novel association unique to African population was reported with

serum bilirubin on the X chromosome for variant rs14647488.

"…genetic substructure for western African populations …markedly different from southern and eastern African populations"

Yosr Hamdi presented on "*Etiology of Breast Cancer in North Africa*". She reported 3 families identified with a double heterozygous BRCA2 deleterious mutations and four polymorphisms specific to the Tunisian populations. Romuald Palwende Boua reported on the findings and future steps on "*Genetic and Epidemiological Diversity in Africa GWAS studies*", an association study on a risk factor of cardiovascular disease which was investigated with genotyping data generated using the H3Africa array. This study identified a genetic substructure for western African populations which was markedly different from southern and eastern Africa populations.

Following presentations, the forum was open for discussion on challenges and expectations of young researchers in creating a sustainable human genetic research in Africa. The responses were tremendous, commending the organizers and focused on seeing the continent adequately equipped with the resources required to develop human genetic research in Africa. The program ended with networking between researchers from different part of the continent over a sumptuous meal.

Looking back: The 11th H3Africa Consortium meeting

by Haddijatou Mbye, Dhriti Sengupta and Rasheed Taiwo

The 11th H3Africa Consortium meeting was held on the grounds of the beautiful Serena Lake Victoria Hotel in Entebbe, Uganda from March 21 – 25, 2018.

The Fellows Research Day was held on March 21st, the first day of the meeting. It was a great opportunity for selected fellows to present the exciting research they were engaged in. This gave a broad overview of the diverse research being performed in Africa. Local organizers had bussed in graduate students from Makerere University, which enabled stimulating discussions between young researchers from varied backgrounds. Poster presentations by fellows were held over the lunch session.

During the afternoon, a trip was organised to the zoo in Entebbe, Uganda where Fellows received the opportunity to socialise with each other in a more relaxed setting. This fun atmosphere was extended into a Fellows Pizza session later that evening.

Meeting participants assembled for a group photo at the 11th H3Africa Consortium Meeting in Entebbe, Uganda.

The second day of the meeting, March 22nd, commenced with an early-morning PI introductory session where project PIs new to the Consortium had the opportunity to meet existing PIs. Welcome and introductions to meeting participants were performed by Professors. Moses Joloba and Charles Ibingira from the College of Health Sciences, Makerere University. These were followed by a formal opening of the meeting by the Ugandan Minister of Science and Technology, the Hon. Dr. Elioda Tumwesigye. PI sessions focused on ELSI in genomics research and included presentations from the INDIGENE and IFGeneRa studies. The afternoon saw Consortium members break up into various Working Groups, where Chairs of the WGs reported back on the progress made by their group since the last Consortium meeting.

Key topics of of the morning of day three of the meeting, March 23rd, were Bioinformatics and Training. Presentations from projects such as H3ABioNet, WASLITBRE and BRecA clearly communicated the need for expanded infrastructure and increased training programs in these disciplines across the continent. Tea was followed by a second Working Group session. The afternoon program consisted of presentations centred on the genetics of sight, hearing and developmental disorders, whilst the later part of the afternoon was mainly infectious-disease oriented, featuring research updates on Sickle Cell Disease, Trypanogen and Tuberculosis. The day ended on a high note with a formal dinner at the hotel's Coliseum Garden, the highlight of which was the amazing performance by a local dance troupe.

March 24th marked the fourth day of the Consortium meeting. Presentation subjects were eclectic and ranged from investigating stroke to the epidemiology of Malaria. A Working Group session just before lunch gave the three continent-encompassing biorepository groups an opportunity to confer face-to-face. The afternoon saw meeting participants convene for the final assembly of the program as each Working Group reported back to the Consortium at large on their progress towards their primary goals and terms of reference.

The final day of the meeting, March 25th, had meeting participants rising super-early as some headed for the airport and others rushed to catch the busses dispatched for the 7am excursion to Makerere University! Those who had opted to go on the trip were treated to a comprehensive tour of two campuses; the College of Health Sciences in Mulago located

north-east of Kampala and the laboratories at the main Makerere campus in Kampala. Visitors were impressed by the liquid nitrogen set-up at the main campus laboratories and the sophistication of the TB laboratories hosted in the same building as the Integrated Biorepository of H3Africa Uganda (IBRH3AU). The tour ended with a street-shopping expedition for the passengers of each bus. The vibrant city life of Kampala and the constant presence of 'boda-bodas', small motorbikes which form the local transport network, provided those from outside east Africa with a fasinating glimpse into local life.

The Fellows in attendance found the 11th H3Africa Consortium meeting a rewarding experience. On behalf of all H3Africa Fellows, we would like to thank the organizers (Dr. Michelle Skelton and the H3ACC, and Dr. Joloba and his team in Uganda) for organizing yet another well-executed meeting.

"The mystery of life isn't a

problem to solve, but a reality

to experience."

- Frank Herbert

New Deputy Dean of Faculty Health Sciences, University of Cape Town

We wish to congratulate Prof. Ambroise Wonkam on his appointment on July 1st, 2018 to the post of Deputy Dean: Research, Division of Human Genetics, Faculty of Health Sciences, University of Cape Town. The late Prof. Bongani Mayosi, in introducing the new incumbent, hailed Prof. Wonkam as a highly accomplished leader of multiple studies; SADaCC, HIGENES-Africa and IFGeneRA, to name but a few, and emphasized his leadership roles in various international organizations: on the steering committees of the H3Africa Consortium and the Global Genetic Medicine Collaborative; as secretary of the African Society of Human Genetics, as board member of the International Federation of Human Genetics Societies; as council member of the Human Genome Organization, and as Associate Editor of the American Journal of Medical Genetics.

Prof. Ambroise Wonkam

Training Corner by the ECTWG

In this edition of the H3Africa Newsletter, the training corner is highlighting some achievements by the H3Africa Trainees. Congratulations!

Presentation and Poster Award Recipients from the 11th H3Africa Consortium meeting

Yasmine Ochi, a first-year fellow at the Institut Pasteur of Tunis was awarded 1st prize for her oral presentation in Uganda and was awarded a trip to the H3Africa meeting in Kigali, Rwanda.

Runners-up for the oral presentation award were Romuald Palwende Boua, Haddijatou Mbye and Samuel Mawuli Adadey.

The poster presentation winners were Haddijatou Mbye, Dhriti Sengupta and Rasheed Taiwo.

"Celebrate whenever you achieve each milestone towards your goals. "

- Carmita Prieto

Graduations

Priscilla Akyaw (Kidney Research Network) Priscilla from NMIMR, University of Ghana, recently graduated with an MPhil in Molecular Biology from the University of Ghana.

Ernestine Kubi (Kidney Research Network) Ernestine from NMIMR, University of Ghana, recently attained an MPhil in Molecular Biology from the University of Ghana.

(Please send us your achievements or awards for inclusion in this section!)

Priscilla and Ernestine at their graduation

Publications from the Consortium

2018:

Biobanking in a Challenging African Environment: Unique Experience from the SIREN Project; Akinyemi et al. PMID: 29733683

Whole-Exome Sequencing Reveals Uncaptured Variation and Distinct Ancestry in the Southern African Population of Botswana; Retshabile et al. PMID: 29706352

H3Africa: current perspectives. Mulder et al. PMID:29692621

Different adiposity indices and their association with blood pressure and hypertension in middle-aged urban black South African men and women: findings from the AWI-GEN South African Soweto Site. Pisa et al. PMID:29673339

Renewing Felsenstein's phylogenetic bootstrap in the era of big data. Lemoine et al. PMID:29670290

Stroke Among Young West Africans: Evidence From the SIREN (Stroke Investigative Research and Educational Network) Large Multisite Case-Control Study. Sarfo et al. PMID:29618553

Including all voices in international data-sharing governance. Kaye et al. PMID:29514717

Dominant modifiable risk factors for stroke in Ghana and Nigeria (SIREN): a case-control study. Owolabi et al. PMID:29496511

Rules of engagement: perspectives on stakeholder engagement for genomic biobanking research in South Africa. Staunton et al. PMID:29482536

The development and application of bioinformatics core competencies to improve bioinformatics training and education. Mulder et al. PMID:29390004

Insights into the genetics of blood pressure in black South African individuals: the Birth to Twenty cohort. Hendry et al. PMID:29343252

Implementation of genomics research in Africa: challenges and recommendations. Adebamowo et al. PMID:29336236

The epidemiology of stroke in Africa: A systematic review of existing methods and new approaches. Owolabi et al. PMID:29228472

Clinical and genetic factors are associated with pain and hospitalisation rates in sickle cell anaemia in Cameroon. Wonkam et al. PMID:29205277

APOL1, CDKN2A/CDKN2B, and HDAC9 polymorphisms and small vessel ischemic stroke. Akinyemi et al. PMID:28975602

HUMA: A platform for the analysis of genetic variation in humans. Brown & Bishop. PMID:28967693