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Speakers line-up and abstracts

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Elevated SARS-CoV-2 viremia in different ethnic groups: relationship with increased COVID-19 disease severity

Douglas Jay Perkins, *New Mexico University, USA*

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There are limited data describing COVID-19 disease severity in disproportionately affected minority groups, particularly American Indians/Alaska Natives (AIs/ANs). This prospective observational study (15 May-20 October 2020) at the University of New Mexico Hospital determined the relationship between SARS-CoV-2 viral burden and clinical outcomes in patients (n=94) of different ancestries. SARS-CoV-2 viral loads in the upper

respiratory tract (URT) and peripheral blood (viremia) were quantified on days 0, 1, 2, 3, 6, 9, and 14 in hospitalized COVID-19 patients with non-severe and severe disease. The cohort was stratified into AI/AN and all other races/ethnicities combined (non-AI/AN). Among the 94 patients, 45.7% identified as AI/AN. Baseline characteristics (i.e., comorbidities and laboratory values) at admission were similar between the AI/AN and non-AI/AN groups. Individuals of AI/AN descent had more severe disease (odds ratio [OR]=7.46, [95% CI, 2.20-25.29], *P*=0.001, adjusted for age, sex, remdesivir, and steroids). Viral loads in the URT were comparable between ancestral groups with non-severe and severe disease. However, viremia was higher in the AI/AN group with severe disease on days 0, 1, 2, and cumulatively across 14 days (*P*=0.009). AI/AN ancestry was associated with a greater risk of having viremia (OR=4.73, [1.67-13.43, *P*=0.004, adjusted with identical covariates). SARS-CoV-2 viremia during hospitalization was associated severe disease (OR=9.19, [3.33-25.34], *P*=1.84x10-5, adjusted with identical covariates). In summary, individuals of AI/AN descent had more severe disease, characterized by elevated blood viral loads, despite comparable comorbidities. Viremia during hospitalization was associated with severe disease and was more common in the AI/AN group. These findings may explain, at least in part, the disproportionate disease burden of COVID-19 witnessed in this population. It will be important to define the biological/molecular basis of these virological findings in future studies to design interventions for improved clinical outcomes.

The speaker:

Dr. Perkins is a tenured Professor of Medicine and Director and Founder of the Center for Global Health in the Department of Internal Medicine at the University of New Mexico. Dr. Perkins received his Ph.D. in neuroscience from Ohio State University (1997) and then did National Institutes of Health (NIH)-funded (T32) postdoctoral training in hematology and tropical medicine at Duke University (1997-2000) under the direction of Dr. Brice Weinberg. Following postdoctoral training, he joined the Malaria Molecular Vaccine Section at the Centers for Disease Control and Prevention (2000-2001) as a Visiting Scholar. Dr. Perkins then became a faculty member at the University of Pittsburgh in the Department of Infectious Diseases and Microbiology

(2001-2008). He then moved to the University of New Mexico (UNM) in the Department of Internal Medicine where he established the UNM Center for Global Health. He has been continuously funded since becoming a faculty member and has procured extramural research support from the NIH, US Department of Defense, and pharmaceutical companies. He has generated over 140 peer-reviewed manuscripts and has greater than 350 conference presentations at national and international conferences. In addition, Dr. Perkins has the longest running continuously funded Global Infectious Diseases training program sponsored by the NIH, Fogarty Internal Center through which he has trained more than 37 long-term trainees (MSc, PhD, MD, and postdoctoral fellows) in the US, Kenya, Ghana, Thailand, and various countries in South America. Research projects in Dr. Perkins' laboratories are based primarily in the US and Kenya. These projects focus on various molecular aspects of the human host-immune response to parasites and viruses, as well as host-parasite interactions. One primary goal of the laboratories is to how genes and gene pathways influence susceptibility to *Plasmodium falciparum*-induced severe malarial anemia in African children. The laboratories are also actively investigating the molecular basis of enhanced immune dysfunction in individuals co-infected with human immunodeficiency virus (HIV) and malaria. Additional projects are focused on the impact of bacteremia on the morbidity and mortality of pediatric populations residing in holoendemic *P. falciparum* transmission areas. The laboratories are also actively engaged in drug discovery and mathematical modeling of infectious disease dynamics. With emergence of the COVID-19 pandemic, the research team has ongoing activities in the US and Kenya to define the role of SARS-CoV-2 viral load dynamics on COVID-19 pathogenesis. The activities in pediatric and adult populations with infectious diseases utilize transcriptomics to identify novel targets for future therapeutics. The research group has active collaborations with the Los Alamos National Laboratories (USA), Temple University, (USA), University of Applied Sciences (Mittweida, Germany), Kenya Medial Research Institute (Kisumu, Kenya), Ministry of Health, Kenya (MOH, Kenya), Maseno University (Maseno, Kenya), Masinde Muliro University of Science and Technology, (Kakamega, Kenya), and Kirinyaga University (Kerugoya, Kenya).

An integrated strategy for sustainable freedom from malaria

***Akira Kaneko**, Osaka City University, Japan & Karolinska Institute, Sweden*

In 1955 the WHO launched the Global Malaria Eradication Programme (GMEP) to interrupt malaria transmission in all endemic areas except Africa. Heavily reliant on vector control through indoor residual spraying, the campaign achieved limited success and was ultimately abandoned in 1969. Some of the factors contributing to the failure of the campaign included insecticide and antimalarial resistance, the vertical approach that lacked local community input, and the lack of program flexibility to adapt to local epidemiology. Withdrawal of strong support for malaria control in the ensuing decades led to a resurgence of malaria, and many countries were encouraged to pursue control and case management instead of elimination. It was during this time of retrenchment that I initiated the ambitious Aneityum Project in the Republic of Vanuatu, with the explicit goal of achieving sustainable malaria elimination.

To be successful, a malaria control programme needs to be tailored to the local epidemiological characteristics. Vanuatu consists of 80 inhabited islands in the Southwest Pacific. As the southernmost island of the archipelago, Aneityum Island is located at the margin of range of the *Anopheles* vector mosquitoes. In the 1980s malaria was highly endemic on Aneityum; both *Plasmodium falciparum* and *P. vivax* were present. I aimed to assess whether malaria can be eliminated on isolated islands. Launched in 1991, the Aneityum Project used an integrated strategy with a high degree of community engagement to address many of the shortcomings of GMEP. High community involvement as measured by MDA compliance (88·3%) and ITN provision (0·94 nets per villager) has resulted in sustained interruption of malaria transmission in Aneityum. The

surveys showed complete absence of *Plasmodium falciparum* after MDA, and *P vivax* disappeared from 1996 onwards, with the exception of two instances of imported infections (one mixed infection in 1993 and one P vivax infection in 1999). Freedom from malaria was declared in 2000 and reported as "Malaria eradication on islands" in *the Lancet* (Kaneko et al. 2000).

At the start of the 21st century, interest and commitment to eradicate malaria globally were renewed. The success of the Aneityum Project served as a proof of concept for an integrated malaria elimination strategy with significant community participation in a resource-poor setting. Tropical Africa is considered by many as the last obstacle to global malaria eradication. Despite two decades of intensified effort, malaria remains a major infectious disease prevalent in many parts of tropical Africa. Now my team is conducting studies in the Lake Victoria basin of western Kenya to develop an integrated strategy for malaria elimination in highly endemic areas, which are granted by the Science and Technology Research Partnership for Sustainable Development (SATREPS). In the session our recent approaches there will be discussed.

The speaker:

Dr. Kaneko is a Global Health Professor at the Department of Microbiology, Tumor and Cell Biology at Karolinska Institute (Stockholm, Sweden) since 2011. He was appointed Professor of Parasitology in 2010, at the Graduate School of Medicine, Osaka City University (Osaka, Japan).

He has worked as Adjunct Professor, at the Institute of Tropical Medicine, Nagasaki University (Nagasaki, Japan) in 2006. From 2005 to 2010 he has beenResearcher and Lecturer at the Karolinska Institute (Stockholm, Sweden). From 1995 to 2005 he has been Associate Professor at Tokyo Women's Medical University (Tokyo, Japan). In 1994 and 1995 he has worked as Physician at Toranomon Hospital (Tokyo, Japan). Between 1987 and 1994 he has been a Malariologist for the World Health Organization at Port Vila, Vanuatu. From 1985 to 1987 he has worked as Expert on Malaria Parasitology for the JICA Asahan Health Promotion Project in North Sumatra (Medan, Indonesia). Between 1983 and 1987 he has been an Assistant Professor in Parasitology, at the School of Medicine of Hirosaki University (Hirosaki, Japan). In 1982 and 1983 he has been a Resident Physician, at Tokyo Metropolitan Police Hospital (Tokyo, Japan).

Integration of genetic and transcriptional profiles of innate cells to decipher mechanisms of TB susceptibility

***Sara Suliman**, UCSF at Zuckerberg San Francisco General Hospital, USA*

Most people infected with *Mycobacterium tuberculosis* (*Mtb*) never develop TB disease, suggesting host-specific risk factors for disease progression. Transcriptional profiling of samples from TB patients and *Mtb*-exposed controls identified innate pathways associated with progression to TB disease. However, few published studies integrate genetic variation with transcriptional profiles to decipher mechanisms of TB pathogenesis. We sought to determine how genetic polymorphisms influence expression of key innate response genes between individuals at high and low risk of progression to TB. From a prospective Peruvian cohort of household contacts of TB patients, we re-recruited fully genotyped former progressors (n=68) and non-progressors (n=67) and stored cryopreserved peripheral blood mononuclear cell samples. We generated monocyte-derived dendritic cells and macrophages by differentiating sorted monocytes in granulocyte-macrophage colony stimulating factor (GM-CSF) and interleukin 4 (IL4), or macrophage colony-stimulating factor (M-CSF), respectively. Samples were analyzed by low-input RNA-sequencing and flow cytometry. We analyzed the impact of genetic polymorphisms on expression of key target genes in an expression quantitative trait loci (eQTL) study. We identified 433 and 355 eQTL events in DCs and macrophages, respectively, 76 of which were unique to one cell type. In addition, we identified a novel interaction between a single nucleotide polymorphism rs2562754 and TB status with expression of *FAH*, the gene encoding for Fumaryl Acetoacetate Hydrolase, which mediates tyrosine

catabolism. This eQTL analysis highlights underexplored candidate TB susceptibility pathways, which are now being functionally validated using CRISPR-based gene editing.

The speaker:

Sara Suliman is an immunologist by training with a focus on understanding risk of progression to active TB disease and developing predictive biomarkers. She is currently an assistant professor at the division of experimental medicine at UCSF and the Zuckerberg San Francisco General Hospital. She was an instructor at the Brigham and Women's Hospital and Harvard Medical Schools, where she focused on dissecting host factors associated with TB risk, including genetic associations and T cell responses. She opened her lab at UCSF in October of this year.

Genomics: a resilient approach to climate change, disease epidemiology and conservation of threatened biodiversity

***Josiah Kuja**, Jomo Kenyatta University, Kenya*

Josiah Kuja[1,2], Anne Muigai[2], Celestine Makobe[2], Eddy Odari[3], Jesse Gitaka[1]

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[2]School of Biological Sciences, Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya

[3]Medical Microbiology Department, Jomo Kenyatta University of Agriculture and Technology, Nairobi, Kenya

Climate change continues to be a grand challenge to bio-economy not only in Africa, but also globally. The Sixth Assessment Report of the Intergovernmental Panel on Climate Change (IPCC) on 9th August 2021 estimated chances of crossing the global warming level of 1.5°C in the next decades given the increased emission of greenhouse gases from human activities (Paglia and Parker, 2021). The IPCC report indicated that the rising temperatures may exceed the 1.5 °C or even 2 °C and this will definitely result in sudden rise in land surface temperatures affecting human activities, disease epidemiology, agricultural activities, and the general biodiversity. The situation would, however, be worse for the African continent that is experiencing sporadic disease outbreak and malnutrition due to persistent heat irradiation and poor agricultural practices. High-elevation metagenomic studies using 16S and 18S rRNA have revealed abundance of beneficial bacterial community structures such as *Cyanobacteria, Proteobacteria, Actinobacteria, Bacteroidetes* on both the ice and periglacial soils, and eukaryotic communities such as *Chlorophyta, Rotifera*, *Thecofilosea* on the periglacial soils, and

Stramenopiles on the high mountains of Africa (Kuja et al., 2018; Vimercati et al., 2019; **Fig. 1**). Similarly, low-level metagenomic studies have revealed high abundance of pathogens in the environmental effluents posing public health risks to the public (**Fig. 1**.). At the gitakalab, we are using next generation sequencing techniques and bioinformatics tools for pathogen surveillance in the environmental effluents. The studies have revealed high abundance of human pathogens that are of public health concern in the sewage effluents within Thika District. Currently, we are exploring the community interactions and the co-occurrence patterns of the antimicrobial resistant genes. Genomic studies are essential for the African continent and the current studies will contribute to disease surveillance, monitoring, and evaluation of drag efficiency in the treatment of outbreaks. Consequently, metagenomics has revealed the ability to determine climate change through the indicator species and changes in the microbial community structures. Genomics is resilient for the identification of pathogens, their interactions, and conservation of biodiversity from unique biomes in Africa for a sustainable agri-environment and improved bio-economy through disease control and management for shared prosperity.

The speaker:

Josiah Kuja is a Postdoctoral Fellow (College of Graduate Studies and Research, MKU) and a Bioinformatician with a background in Molecular and Microbial Ecology (PhD, MSc, and BSc). His research interest focuses on microbial interactions and their significance in antimicrobial drag resistance, especially in resource-limited settings. He has the knowledge of low (below sea level) and high (above sea level) altitude microbial community structure. He uses bioinformatics tools to uncover the hidden history of microbial interactions and development within their ecosystems. He also uses bioinformatics to justify the significance of genomics in global bio-economy following drastic climate change in the recent decades. Josiah is an enthusiastic research article writer and a reviewer in Current Research in Microbial Sciences (CRMICR), Elsevier. Currently, he is the Project Manager for the African Bio-Genome Project (AfricaBP- https://africanbiogenome.org/steering-committee/), which is an affiliate to Earth Bio-Genome Project (EBP) in which he serves as a member of the scientific committee on sequence data analysis https://www.earthbiogenome.org/data-analysis. AfricaBP and EBP aim at sequencing all non-human living organisms in Africa and the world, respectively for a sustainable development and shared prosperity.

Application of Electrical Impedance Spectroscopy and Tomography to Cell Measurement and Evaluation

Daisuke Kawashima - *Chiba University, Japan*

A non-invasive cell measurement and evaluation method is highly required for tissue engineering and drug discovery. Our research is developing a novel invasive method for cell measurement and evaluation by a combination of electrical impedance spectroscopy (EIS) and tomography (EIT). EIS characterizes the cellular conditions such as viability and extracellular fluid by spectral characteristics in dielectric properties of cells. For instance, the electrical impedance response in low-frequency reflects the ion concentration in extracellular fluid. By applying EIS analysis to EIT, the so-called EIST, images can be provided regarding the spatial distribution of changes in dielectric properties of cells and extracellular fluid. EIST is a powerful imaging tool for cell measurement and evaluation. This talk will discuss an applicability of EIST to cell measurement and evaluation and the prospects for tissue engineering and drug discovery.

The speaker:

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Advanced molecular tools for detection and characterization of exosomes and viruses

Masood Kamali-Moghaddam, *Dept. of Immunology, Genetics and Pathology, Science for Life Laboratory, Uppsala University, Uppsala, Sweden*

DNA-assisted proximity assays are powerful and versatile tools for sensitive, precision high throughput detection of macromolecules such as DNA, RNA and proteins as well as posttranslational modifications in in situ and in liquid biopsies.

Commonly, in these assays the target molecules are recognized by several proximity probes, each equipped with a DNA oligonucleotide. Upon binding of the target molecules, the DNA oligonucleotides are brought in proximity, subjected to enzymatic ligation or polymerization, which results in formation of an amplifiable reporter molecule. The use of multiple recognition events in combination with signal amplification allows highly specific and sensitive detection of the target molecules.

Recently, we have developed a large number of affinity-based proximity assays for single- and multiplex detection of large complexes. Several of these technologies, such as proximity ligation assay (PLA) combined with flow cytometry readout, multiplex proximity extension assays (PEA), proximity barcoding assays (PBA) and padlock technology are used for sensitive detection and characterization of individual exosomes and viruses.

Here, I discuss the application of proximity assays for screening, characterization and sensitive detection of exosomes and viruses in body fluids.

The speaker:

Dr. Masood Kamali-Moghaddam is currently a Professor of Molecular Diagnostics at Dept. of Immunology, Genetics and Pathology at Uppsala University, Sweden. He received his PhD in Pharmaceutical Microbiology at Dept. of Pharmaceutical Biosciences at Uppsala University in 2001. He held then a post-doctoral position at Center for Molecular Genetics at the University of California, San Diego, and a second post-doctoral position at Dept. Of Genetics and Pathology/ Div. of Molecular Tools at Uppsala University. The research in Prof. Kamali's laboratory is currently focused on development of highly sensitive molecular tools for proteome analysis, and detection and characterization of exosomes as biomarkers for early diagnostics.

Biohacking for the global south: toward self-sufficiency in molecular biology research and training in Africa

***Christopher Kariuki**, Katholieke Universiteit Leuven, Belgium*

Christopher Kariuki[1&2] & Jan Paeshuyse[1]

[1]Laboratory of Host-Pathogen Interactions, Animal and Human Health Engineering, Katholieke Universiteit Leuven (KU Leuven), Belgium

[2]Department of Tropical and Infectious Diseases, Institute of Primate Research (IPR), Nairobi, Kenya

Biotechnology is one of the key Science, Technology, Engineering and Mathematics (STEM) technologies expected to leverage the inclusion of Africa in the fourth industrial revolution (4IR). However, biotechnological research and training is expensive due to the commercialization of reagent supply. This keeps it out of reach for most African researchers and students, limiting their exploitation of biotechnology to resolve both local and global challenges. And, as evidenced by the COVID pandemic, globalization has shifted worldwide challenges to a local level, requiring a trained public that can rapidly respond to these challenges. The goal of this project is to disseminate knowledge and capacity for the Global South for the generation of biological reagents using open-source scientific knowledge and materials. These cost-effectively produced reagents can then be utilized in basic research, as well as for the training of students.

In this talk, several concepts for generation of biological reagents will be discussed. In the first instance, we will demonstrate how to build an off-the-shelf bioreactor from scratch, using readily available materials for the recombinant generation of off-patent *Thermus aquaticus* (*Taq*) DNA polymerase, an essential molecular biology reagent. In the second

instance, we will discuss improvements on the bacterial recombinant expression of single domain antibodies, which have great potential for utility in diagnostics. Lastly, the potential of using open science platforms to stimulate the utilization of locally derived biologics for application in research will be explored.

The speaker:

Christopher K. Kariuki is currently a research scientist at the Animal and Human Health Division in the Department of Biosystems (BIOSYST), KU Leuven, Belgium. With a background in Molecular Biology (MSc) and Bioscience Engineering (PhD) from Vrije Universiteit Brussels (VUB), Brussels, Belgium. His current research interests include molecular biology, nanotechnology, structural biology and biochromatography with specific interests in bacterial recombinant protein expression and biophysical protein characterization.

Exploring the biodiversity of wetland ecology for sustainable African bioeconomy

Evans Chidi Egwim, *Federal University of Technology Minna, Nigeria*

The number of governments worldwide embracing the vision of a sustainable bioeconomy is constantly rising. However, the concept of sustainable bioeconomy has not been adequately examined and integrated into policy making in most African countries. One factor facilitating the transformation of economies to such sustainable bioeconomies will be R&D, institutionalization, exploration of natural potentials and entrepreneurial activity. Africa is known to be endowed with natural resources but lacks systematic and strategic approaches to exploring these abundant bioresources. African countries are largely confronted with unsustainable exploitation of their resources, unprecedented waste generation, food insecurity and lack of access to energy. These challenges and others such as climate change, soil degradation, deforestation, poverty, poor industrial production and continued loss of biodiversity needs to be addressed if African will survive in the future bioeconomic wave. This paper therefore x-rays the abundant natural resources of African wetlands and suggests how these bioresources could be integrated into the drive for sustainable bioeconomy for Africa. Some of the authors products from wetland natural resources are. 1. Biogas, Organic fertilizer and nano cellulosic fibre from water hyacinth. 2. Biodegradable films and food flavour from Typha latifolia, different industrial and pharmaceutical raw materials from mushrooms, 3. Biodiesel, carbon capture and organic fertilizers from different wetland algae.

Cell culture innovation for regenerative medicine

***Hiroko Hanzawa**, Center for Exploratory Research, Hitachi Kobe Laboratory, Research & Development Group, Hitachi Ltd., Kobe, Hyogo, Japan*

Regenerative medicine is known as an innovative strategy, using cells and tissue, for injuries and diseases that are hard to cure by conventional treatments. Cells and tissue for therapeutic usage have long been cultured manually by skilled experimental operators in cell culture clean rooms that comply with good manufacturing practice (GMP) requirements. Issues of manual cell culturing are relatively high labor costs, variable cell quality depending on operator's skill, and the risk of biological contamination caused by human intervention. Facility maintenance costs are also high since the process is done in spaces kept to a high standard of cleanliness. To overcome these issues and make regenerative medicine more widely implemented, we have adopted an open innovation approach by working with partners from academia and pharmaceutical industries and has made it available in the form of automated cell culture technology for therapeutic cell products for the practical application.

Hitachi's automated cell culture technology are closed systems which is based on a fundamentally different concept from open system such as manual culture operating inside a CO_2 incubator or safety cabinet. Single-use cell culturing module is lowering the risk of contamination from external environment and enables therapeutic grade cell production with guaranteeing a high degree of safety. We are now developing on the next generation, intelligent automated cell culturing technology. Conventional automated cell culture system has been operated in accordance with a cell culturing protocol that established on manual cell culture in advance. In contrast, the intelligent automated cell culturing will achieve the reliable

and efficient production of high-quality cells by using systems equipped with AI to assess the cell condition in a non-invasive and real time way of measurements of the cells, also utilizing automatic feedback control to maintain optimal culturing conditions in future.

A part of this study was demonstrated by the Japan Agency for Medical Research and Development (AMED, Grant No. JP21be0404010).

The speaker:

Dr. Hiroko Hanzawa joined Hitachi Ltd.'s Advanced Research Laboratory, 1991. She received Ph. D degree from Tokyo University of Agriculture and Technology, Tokyo 2006, in the field of biotechnology and life science. In parallel to her activity in Hitachi R&D, she also contributed to the national projects for a wide spectrum of research field and has built her skills and knowledge interdisciplinarily. Her current interests are regenerative medicine and cell therapy, and she is working hard to establish an innovative technology such as automated cell culture at Hitachi Kobe Laboratory which is founded at Kobe biomedical cluster in 2017.

Development and evaluation of point of care tests for Rift Valley Fever diagnosis

***Shingo Inoue**, Institute of Tropical Medicine, Nagasaki University, Japan*

Shingo Inoue[1], Fuxun Yu[1], Nicholas Ragot[2], Allan ole Kwallah[2], Benson Mwangi[2], Ferdinard Adungo[1,2], Tetsuya Oda[3], James Kimotho[2], Rosemary Sang[2], Matilu Mwau[2], Kouichi Morita[1]

1. Department of Virology, Institute of Tropical Medicine, Nagasaki University, Japan
2. Kenya Medical Research Institute, Kenya
3. Otsuka Pharmaceutical Company, Japan

Rift Valley fever (RVF) is one of the important zoonotic arbovirus diseases in Kenya and African continent. RVF outbreak occurred in every 5 to 10 years due to heavy rain falls which were related to the Indian Ocean Dipole and followed by the emergence of large number of mosquitoes.

Nagasaki University and the Kenya Medical Research Institute (KEMRI) studied together for the development of point of care (POC) test kits for rapid diagnosis of patients under the JICA-AMED-SATREPS Project during 2012-2017. The project has aimed to set up the facility and entire production system from the preparation of law materials up to the final products and its quality control locally in KEMRI, Nairobi. The project focused on (1) production of viral protein using recombinant DNA technology, (2) development of monoclonal antibodies against RVFV, (3) development of immunochromatographic test kit as POC tests to detect IgM antibody and the virus.

The project has successfully developed the POC test kits using the recombinant RVFV nucleocapsid protein and monoclonal antibodies and these kits can detect IgM against RVFV and the virus. The quality control

results indicated 96% sensitivity and 100% specificity for IgM detection from 2 uL of serum samples even after 2 years from the manufacture.

The speaker:

Prof. Shingo Inoue is currently a professor, NUITM-KEMRI Project, Institute of Tropical Medicine, Nagasaki University, Nairobi, Kenya. He graduated with a Ph.D. in a Veterinary Medicine from the Gifu University (studied in the Obihiro University, Obihiro, Japan) in 1997. He then joined to the Institute of Tropical Medicine, Nagasaki University as a post-doc fellow. Since then, he is studying on arboviruses such as dengue virus, chikungunya virus, West Nile virus and Rift Valley fever viruses. Serology and vaccine development are his major research interests.

Development of a new therapy for P. falciparum malaria

***Philip Low**, Purdue University, West Lafayette IN 47907, USA*

Despite malaria's designation by the World Health Organization (WHO) as one of six consensus global health priorities, malaria still remains a major health problem, with nearly half of the world's population at risk of contracting the disease, 200 million new infections/year, and nearly 410,000 deaths/year. According to WHO, one child dies of malaria every minute, and the absence of an effective vaccine together with the emergence of drug resistant strains foreshadow a possible crisis that can only be prevented by discovery of a mutation-resistant therapy for the disease. In studying the biology of the malaria parasite within its human erythrocyte host, we discovered that the parasite must activate an erythrocyte tyrosine kinase in order to escape from its red cell host at the end of its normal life cycle. We also observed that several inhibitors of this erythrocyte tyrosine kinase could prevent propagation of the parasitemia both in vitro and in vivo. Encouraged by these observations, we initiated phase 2 human clinical trials of the therapy in a region of Vietnam and Laos where 1/3 of patients with *P. falciparum* malaria experienced significantly delayed parasite clearance (DPC; continued parasitemia following 3 or more days of standard therapy). In contrast to patients treated with the usual therapy, patients treated with our new therapy experienced a significantly accelerated decline in both parasite density and pyrexia (fever), with no DPC and no drug related toxicities. Moreover, these significant improvements were surprisingly most pronounced in patients with the highest parasite densities, where serious complications and death are most frequent. Most importantly, because our therapy's mechanism involves inhibition of a red blood cell enzyme, it should be

impossible for the parasite to mutate resistance, since the parasite cannot mutate a human enzyme. Taken together, these data argue that this new malaria therapy can afford faster clearance of the parasite with little or no accompanying toxicity and very low probability of development of resistance mutations. With widespread use of this tyrosine kinase inhibitor, it is hoped that the plague of *P. falciparum* malaria can soon be eliminated.

The speaker:

Dr. Philip S. Low is the Presidential Scholar for Drug Discovery and the Ralph C. Corley Distinguished Professor of Chemistry at Purdue University. Dr. Low has spent over >45 years designing targeted imaging and therapeutic agents for the diagnosis and treatment of many human diseases. He has published >475 scientific articles that have earned an H-index of >110 and has >500 US patents/patents pending. Eight drugs stemming from his research are currently undergoing human clinical trials and seven companies (Endocyte Inc., OnTarget Laboratories Inc., Umoja Biopharma, Morphimmune Inc., Novosteo Inc., Eradivir Inc. and ErythroCure Inc.) have been founded to commercialize these discoveries. One of Low's drugs (^{177}Lu-PSMA-617) recently received "Breakthrough Therapy Status" from the FDA and a second (OTL38) received "Expedited Review" by the FDA, both leading to their accelerated approval in 2021. Based on these contributions, Low has been recognized with many national and international awards, including the AACR Award for Chemistry in Cancer Research, the ACS Award for Cancer Research (Sosnovsky Award) and an NIH MERIT Award among many others. Dr. Low received his B.S. in Chemistry from BYU (1971) and his Ph.D. in Biochemistry from UCSD (1975).

Recent advances in microfluidic paper-based analytical devices

***Charles Henry**, Department of Chemistry, Colorado State University, USA*

There is a continuing interest in the development of low-cost sensor systems to detect infectious diseases. Paper-based analytic devices have been used for centuries but a renewed interest in the substrate as a material for microfluidics started a decade ago when patterned paper was used to carry out multiplexed chemical analysis of urine samples. Since that time, the field has exploded in methods for fabrication, methods for detection, and applications. Devices made purely from paper, however, suffer from several significant problems mainly surrounding the slow capillary flow obtained in most paper and the challenges associated with physical manipulations such as rinsing in paper-based devices. To address these problems, we have recently investigated the combination of paper and plastic to achieve higher flow rates and/or provide straightforward methods that enable multistep assays to be performed. We have developed a variety of colorimetric and electrochemical methods that target DNA/RNA, proteins, and intact particles using this platform that provide sensitive and selective results in different sample matrices. To this end, recent results focused on detecting bacteria, including anti-microbial resistant bacteria, and viruses, including SARS-CoV-2 will be presented.

The speaker:

Charles S. Henry received his PhD from the University of Arkansas followed by postdoctoral studies at the University of Kansas. He started his academic career at Mississippi State University before moving to Colorado State University in 2002, where he is currently Professor of Chemistry. His research interests lie broadly in the areas of microfluidics and electrochemistry with application to questions in bioanalytical and environmental chemistry. He has made key contributions in paper-based microfluidic

devices, electrochemical sensors, and organ-on-a-chip devices. He is also an associate editor for *Analytica Chimica Acta*.

Preliminary findings on virucidal activities of extracts of selected Nigerian vegetables with potentials for use as Covid-19 therapy

***Dickson A. Musa**, Trans-Saharan Disease Research Centre, IBB University, Nigeria*

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Several factors have been adduced for the low mortality COVID-19 in Africa. In this study we explored the potentials of diets as conferring protective effect against COVID-19 in Africa. Five vegetables eaten in Nigeria were evaluated for their virucidal properties as a prototype for developing COVID-19 therapy. Two of the samples exhibited potentials for physiological and environmental viral control.

The COVID-19 pandemic is one of the most serious public health emergencies that the world has faced recently. While the pandemic has dramatically impacted most continents, the impact on Africa has been comparatively substantially low (Adams *et al.,* 2021). Several factors have been adduced for the low mortality due to COVID-19 recorded in Africa. The factors proposed include lower population mean age, lower life expectancy, lower pre-COVID-19 era '65yr+ mortality rate', and smaller pool of people surviving and living with cardiovascular diseases (Lawal, 2021), prior exposure to coronavirus infection (Adams *et al.,* 2021) and trained immunity (Gosh *et al.,* 2020). Another factor that has not been properly investigated in the diet. This research was therefore aimed at evaluating the potentials of some common Nigerian vegetables for their antiviral and immune modulating properties as a prototype for COVID-19 therapy.

Crude extracts of five vegetables, labeled as A, B, C, D and E, were obtained by maceration in 4 different solvents each; cyclohexane, dichloromethane, methanol and distilled water. Treatment of the extract obtained were carried out in Phosphate Buffer Solution (PBS) and in water. Bacteriophage MS2 was used as a model organism. The double layer agar plaque assay was used to determine the infectivity and titre of bacteriophage MS2 after purification and before and after treatment with extracts of the vegetables to know the rate and extent of inactivation. Treatment in PBS produced better results than treatment in water. Cyclohexane extracts of D ($PD1_{10}$) and A ($PA1_{10}$) had the highest pfu log reduction of 4.11 and 3.99 receptively at 10mg/ml concentrations in PBS. $WD1_{10}$ and $WA1_{10}$ also had the highest pfu log reduction of 2.80 and 1.37 in water. This suggest that the extracts have potentials for both physiological and environmental applications.

Some vegetables used as food in Nigeria possess bioactive substances with virucidal properties that can be investigated further as a prototype for COVID-19 therapy.

ENMED: shifting the paradigm in medical education through blending of engineering and medicine

***Michael R. Moreno**, Innovation for Engineering Medicine, Department of Mechanical Engineering, Texas A&M University*

The new Intercollegiate School of Engineering Medicine (ENMED) offers a revolutionary Medical Education Program wherein students receive a Medical Doctorate (MD) and a Master of Engineering (ME) degree focused on the design and implementation of medical technologies in the same four years. The ENMED Medical Education Program was developed as a tripartite collaboration between Texas A&M University's College of Engineering, College of Medicine, and Houston Methodist Hospital. The goal of the program is to make a significant contribution to the positive transformation of health care for all through training a new kind of inventive, problem-solving doctor called a "physicianeer". Physicianeers will be uniquely qualified to address some of health care's greatest challenges. An innovative blended curriculum has been developed to integrate engineering and medicine in their training. The program is located at the in the famed Texas Medical Center (TMC), arguably the largest medical center in the world. The TMC is home to numerous hospitals, medical technology start-ups, and incubators. It is a hotbed of innovation and the perfect location for the deployment of the ENMED Medical Education Program. Graduates from the program will be inventors and early adopters of transformational technologies, maintain a unique vigilance for opportunities to innovate during their clinical practice, and possess real-world experience developing innovative medical technologies acquired through "innovation rotations" with EnMed researchers, collaborators,

industry partners, and government agencies. The program also incorporates a Global Health component and has provided students unique opportunities in Rwanda. Partnership formation is an ongoing process and is considered one of the primary ways in which ENMED can continue to accelerate progress. The use of CAD/CAM technologies enables intercontinental collaboration at a distance and is currently being explored as a way to expand international student and faculty interaction.

The speaker:

Dr. Moreno is an Associate Professor and J. Mike Walker '66 Faculty Fellow in the Department of Mechanical Engineering with joint appointments in the Departments of Biomedical Engineering, Medical Education, Health and Kinesiology, and Small Animal Clinical Sciences here at Texas A&M University (TAMU). He currently serves as Director of Innovation for Engineering Medicine (ENMED), a collaborative initiative between the TAMU College of Engineering and College of Medicine, and Houston Methodist Hospital (HMH) in the Texas Medical Center. ENMED recently implemented an innovative medical education program wherein medical students simultaneously earn a medical doctorate and master of engineering degree focused on the design and implementation of medical technologies in just four years. Dr. Moreno has been a key developer of the curriculum which blends the engineering and medicine content. He recently began collaborating with the HMH Center for Patient Outcomes on the development of a related certificate program focused on Healthcare Data Science. Dr. Moreno has leveraged his graduate training in Science Education in designing and developing courses such as Engineering Innovation in Medicine, Medical Device Design, Bio-Inspired Engineering Design, Biofluid Mechanics, Biosolid Mechanics, Orthopedic Biomechanics, and Comparative Biomechanics. He also leads the Engineering World Health (EWH) Summer Institute in Rwanda which is focused on improving healthcare in resource limited settings. Prior to COVID, he coupled ENMED with EWH and mentored an ENMED student in Rwanda that worked on a Digital Health project in collaboration with the Rwanda Centre of Excellence in Biomedical Engineering. As a Hispanic, United States Air Force military veteran that grew up in a low socioeconomic setting, Dr. Moreno has made a personal commitment to recruiting and mentoring students from under-represented groups. He leads a very popular and competitive undergraduate research program in his laboratories and has offered summer research opportunities for secondary school students from under-represented groups. He has over 20 years of experience developing technologies in the fields of experimental biomechanics and medical research across multiple scales and has been awarded 8 patents. His Biomechanical Environments Laboratory operates in accordance with the Food and Drug Administration (FDA) Quality System Regulation

(QSR) and has designed custom mechanical testing systems and protocols for FDA Good Laboratory Practices (GLP) preclinical mechanical testing and animal safety studies. In addition to his academic research, Dr. Moreno is a co-founder of Biomechanics Innovation Group (BIG) LLC and has worked as a consultant in developing experimental flow and mechanical testing systems and protocols for several major medical device companies (e.g. Boston Scientific, Medtronic, Cordis, Flowmedica, etc.). He is coauthor of 38 peer-reviewed publications including seven book chapters and has 8 patents awarded. His research has been supported by federal funding from NIH, NSF, and DARPA, as well as, hospital and corporate sponsors.

Point of care Isothermal Nucleic Acid amplification Platform for Covid-19 Diagnostics designed to meet the needs at resource limited settings

Aman Russom, *KTH Royal Institute of Technology, Division of Nanobiotechnology, Department of Protein Science, Science for Life Laboratory, Solna, Sweden*

The demand for scalable, rapid and sensitive COVID-19 diagnostics is particularly pressing at present to help contain the spread of infection and prevent overwhelming the capacity of health systems. While high-income countries have managed to rapidly expand diagnostic capacities, such is not the case in resource-limited settings of low- to medium-income countries. We report the development of an integrated modular centrifugal microfluidic platform costing less than 250 USD to perform loop-mediated isothermal amplification (LAMP) of viral RNA directly from heat-inactivated nasopharyngeal swab samples. Here, LAMP, centrifugal microfluidics, smartphone-based detection and recent developments in RT-LAMP applied to the detection of SARS-CoV-2 RNA are combined to develop a novel cost-effective and fully integrated platform for COVID-19 diagnostics directly from heat-inactivated nasopharyngeal samples. The direct detection from heat-inactivated samples was achieved using (1) a one-pot combination of reverse transcriptase and polymerase enzymes for robust isothermal amplification and (2) a novel agarose bead-based signal enhancement strategy for improved fluorometric detection. The platform was validated with a panel of 131 nasopharyngeal swab samples collected from symptomatic COVID-19 patients.

CYP2D6 genotyping analysis and functional characterization of novel allelic variants in a Kenyan and Ni-Vanuatu population

***Masahiro Hiratsuka**, Tohoku University, Japan*

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Cytochrome P450 2D6 (CYP2D6) is responsible for the metabolic activation of primaquine, an antimalarial drug. CYP2D6 is genetically polymorphic, and these polymorphisms are associated with interindividual variations observed in the therapeutic efficacy of primaquine. While CYP2D6 allele and phenotype frequencies have been extensively studied, currently, very little ethnically specific data is available regarding the East African and South Pacific region, including Kenya and Vanuatu. The absence of information regarding gene polymorphisms and their resulting clinical effects in these populations may hinder treatment strategies and patient outcome. Given the scarceness of CYP2D6 related data in these populations, the purpose of this study was to perform a pharmacogenomic analysis of the Kenyan and Ni-Vanuatu population and ultimately characterize the enzymatic properties of eight novel CYP2D6 variant proteins expressed in 293FT cells *in vitro*. Our study revealed a prevalence of functional alleles in both populations a low frequency for decreased function defining genotypes in the Ni-Vanuatu population, with

approximately 36% of our Kenyan subjects presenting substrate-dependent decreased function alleles. Additionally, 6 variants (P171L, G306R, V402L, K1, K2, and K3) showed significantly reduced intrinsic clearance compared to wild-type CYP2D6.1. Our findings provide insights into the allele-specific activity of CYP2D6, which could be clinically useful for malaria treatment and eradication efforts.

The speaker:

Dr. Masahiro Hiratsuka is currently an associate professor at Graduate School of Pharmaceutical Sciences, Tohoku University in Japan. He graduated with a PhD in Pharmaceutical Sciences from Tohoku University, Japan in 1996. He moved to the Department of Pharmaceutical Sciences at Tohoku University Hospital, where he started research regarding pharmacogenomics in 1998. In 2006, he attended Section of Pharmacogenetics, Department of Physiology and Pharmacology at Karolinska Institutet as a guest researcher in the laboratory of Professor Magnus Ingelman-Sundberg. His current research interests include pharmacogenomics, drug metabolism, and clinical pharmacology.

Impact of IRS on malaria prevalence in the Lake Victoria basin, Homa Bay, Kenya

***Wataru Kagaya**, Osaka City University, Japan*

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Indoor residual insecticide spraying (IRS) is one of the key pillars of malaria control, and there is a need to monitor and evaluate its long-term effectiveness in establishing malaria elimination strategies using IRS. Homa Bay County, located along Lake Victoria in Kenya, has been experiencing high malaria prevalence and has been implementing an annual IRS program under the county government since 2018. We assessed its effectiveness through a cross-sectional malaria survey conducted periodically.

IRS was conducted in February and March in 2018 using Actellic® 300CS throughout Homa Bay County except for small islands in the lake. However, from 2019 onwards, the IRS is being conducted at the same time of the year with the exclusion of the large island, Mfangano. The cross-sectional malaria survey was conducted in January and February of each year starting in 2018, targeting approximately 200 school children in each area. The survey sites were Ungoye in the mainland where IRS is regularly conducted, Wakula on Mfangano Island where IRS was conducted only in

2018, and a small island, Ngodhe where IRS is not conducted. Plasmodium infections were detected by PCR.

Between 2018 and 2019, both Ungoye and Wakula showed a significant decrease in malaria prevalence (62.9% to 24.5%, 52.1% to 28.0%, all $p<0.001$). In 2020, however, Ungoye showed a further significant decrease (11.5%, $p<0.001$), while Wakula, where IRS was suspended, showed a resurgence of transmission, and the prevalence was almost same level as the time before IRS (46.7%). There was no significant change in Ngodhe Island throughout the period.

The significant suppression of transmission in Ungoye and Wakula in 2018 indicates the effectiveness of IRS, while the resurgence of transmission in Wakula after 2019 suggests that its effectiveness of IRS may be short-lived. Since repetitive IRS is a costly and labor-intensive intervention, combining with tools to sustain the effect in a long term will be key toward malaria elimination.

The speaker:

Dr. Wataru Kagaya is a clinical lecturer at Osaka City University, Japan. He graduated with a PhD in Parasitology from Tokyo Medical and Dental University, Japan in 2016. Since 2020, he bases in Mbita, Homa Bay, Kenya and leads cluster randomized control trial of novel vector control tool and cohort study on malaria transmission as a field research coordinator in SATREPS project.

Development of point of care end game diagnostics for Africa

***Jesse Gitaka**, Mount Kenya University, Kenya*

Communicable diseases continue to be major health burden in Africa. Malaria, HIV, TB and neglected tropical diseases have ravaged most health systems in Africa, and the situation is made worse by the ongoing COVID 19 pandemic. Highly reliable, field deployable point of care diagnostics are needed to enable detection of infectious reservoirs to effectively break transmission towards elimination and eventual eradication of these communicable diseases. However, Africa, has been lagging behind in designing and developing home grown solutions.

Gitakalab, at Mount Kenya University is working on several communicable diseases including SARSCoV2, malaria, TB, and Curable Sexually Transmitted infections to develop highly sensitive and specific tools based on deep genome mining, CRISPR Cas 12 and immuno-magnetic separation assay technologies. The group is levering on local and international collaborations with sustainable models of post-doctoral training and community engagement to stimulate academic innovation and vibrant biotechnology value chain in Kenya and Africa.

We shall share our experiences, opportunities and challenges and seek strategies to more efficiently achieve impact, in developing assays and diagnostics that will contribute to eliminating communicable diseases in Africa and being better prepared for emerging and re-emerging infectious diseases threats.

The speaker:

Dr Jesse Gitaka is a physician-scientist trained at University of Nairobi, a holder of Masters of Tropical Medicine and PhD in Medical Science from Nagasaki University, Japan. He leads Gitakalab (https://gitakalab.com/) and is the founding Director of the Centre for Malaria Elimination and the Centre for Research in Infectious Diseases at

Mount Kenya University, Thika. His experience spans clinical trials, molecular biology and epidemiology of infectious diseases, field based research and implementation science. Currently, he is a Principal Investigator in several studies in the areas of maternal and newborn health (MNH) and infectious diseases point of care diagnostics development and antimicrobial resistance surveillance. He is an affiliate of the African Academy of Sciences, a Future Leaders-African Independent Researchers (FLAIR) fellow and a Next Einstein Fellow.

Nucleoside-modified mRNA-LNP therapeutic

Drew Weissman, *University of Pennsylvania, USA*

Vaccines prevent 4-5 million deaths a year making them the principal tool of medical intervention worldwide. Nucleoside-modified mRNA was developed over 15 years ago and has become the darling of the COVID-19 pandemic with the first 2 FDA approved vaccines based on it. These vaccines show greater than 90% efficacy and outstanding safety in clinical use. The mechanism for the outstanding immune response induction are the prolonged production of antigen leading to continuous loading of germinal centers and the adjuvant effect of the LNPs, which selectively stimulate T follicular helper cells that drive germinal center responses. Vaccine against many pathogens, including HIV, HCV, HSV2, CMV, universal influenza, coronavirus variants, pancoronavirus, nipah, norovirus, malaria, TB, and many others are currently in development. Nucleoside-modified mRNA is also being developed for therapeutic protein delivery. Clinical trials with mRNA encoded monoclonal antibodies are underway and many other therapeutic or genetic deficient proteins are being developed. Finally, nucleoside-modified mRNA-LNPs are being developed and used for gene therapy. Cas9 knockout to treat transthyretin amyloidosis has shown success in phase 1 trials. We have developed the ability to target specific cells and organs, including lung, brain, heart, CD4+ cells, all T cells, and bone marrow stem cells, with LNPs allowing specific delivery of gene editing and insertion systems to treat diseases such as sickle cell anemia, Nucleoside-modified mRNA will have an enormous potential in the development of new medical therapies.

Microfluidic devices for analysis in resource-limited settings

***Nicole Pamme**, Stockholm University, Sweden*

Nicole Pamme[1,2], Jesse Gitaka[3], Bongkot Ngamsom[1], Pablo Rodriguez-Mateos[1], Samantha Richardson[4]

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[4]Department of Biological and Marine Sciences, University of Hull, Hull, UK

Analytical measurement in resource-limited settings requires portable devices that are accurate and robust, cost effective and, as much as possible, equipment-free.

Our research involves the design and development of analytical workflows with miniaturized analysis systems, so called 'lab-on-a-chip' devices. We have worked on a range of projects with partners in lower- and middle-income countries as well as Citizen Science based approaches. These include pathogen analysis of *E. coli* in drinking water, Group B *streptococcus* in maternal health monitoring and antimicrobial resistant pathogen strains in dairy milk at the point of need. Furthermore, we have studied the development of on-site nutrient levels and contaminant levels in water streams with members of the general public, and, more recently, the study of nutrient levels in soil carried out by farmers on-site.

For this, we are applying a range of technical approaches out of the microfluidics toolbox, carefully considering the context in which the devices are to operate. Stakeholder input right from the start of the project and throughout is vital to success.

The presentation will comprise an overview of these techniques, challenges encountered and lessons learned.

Nanoparticle-based point-of-care molecular diagnostics

***Jacqueline C. Linnes**, Purdue University, USA*

Over 90% of current point-of-care diagnostic health tests still reside within hospital settings. How can we unlock these capabilities and make molecular diagnostics accessible to the patients around the world who need them most? I will discuss advances in nanoparticle-based molecular tests that will put point-of-care tests into the hands of primary care physicians and concerned citizens themselves in order to rapidly detect and monitor a wide range of diseases. These distributed sample-to-answer devices will require highly accurate, portable sensors with near foolproof operation and interpretation. Critically, test developers require an understanding of the stakeholders and end-users of their technologies and the barriers to adoption and use.

The speaker:

Dr. Jacqueline Linnes is the Marta E. Gross Associate Professor in the Weldon School of Biomedical Engineering at Purdue University and is the Director of Diversity, Equity, and Inclusion in the Weldon School of Biomedical Engineering at Purdue University. Her lab develops point-of-care diagnostics, wearable devices, and global health technologies for underserved populations in the US and abroad. Dr. Linnes teaches undergraduate design, graduate diagnostics and instrumentation, and international workshops on human-centered design worldwide. This work emphasizes the translation of fundamental microfluidics and biological assays into point-of-care diagnostics using human-centered design principles. Her extensive experience in translational research includes co-founding and managing early-stage field-testing and user feedback for multiple startup companies.

Cytometry for Life: engaging and enabling science

***J. Paul Robinson**, The SVM Professor of Cytomics and Professor of Biomedical Engineering, Purdue University*

For almost six decades the measurement of cells (cytometry) has been evolving in concert with medicine and engineering enabling discovery in this multidisciplinary environment. The intermingling of basic biology with complex technology has been a driving force as new technologies appear and entire fields of science are born. Such was the case with, blood cell counting, flow cytometry, PCR, sequencing and more recently point-of-care (POC) fields. In every case, there was a three fundamental requirements: A biological problem, an innovative discovery, and a technical solution.

This presentation will outline the evolution of several of these core technologies from conception to implementation and their impact on science and engineering today. As each technology developed, it is important to understand the interaction of basic science, engineering. It is interesting to observe, that in most cases, as technologies become more complex and widespread, an additional component has emerged as being both complementary and necessary – Informatics. This brings computer scientists into the fields of biology and engineering to build collaborative teams that addresses the issues of transforming complex data into useful and applicable results.

More recently, reducing technology complexity has been driven by a need to create rapid and easily understood test results. This has resulted in an expansion of POC approaches across the entire field of biology and medicine. There is a related approach to POC and this is Point-of-Detection (POD) which relates to the ability to rapidly detect the presence

of molecules that may not be directly medical in nature such as detection of pathogens, toxins or pesticides in the food supply, and authentication of foods or reagents for example. While currently moderately high cost, such approaches will eventually be impacted by technology expansion to reduce costs and make such technologies widely available.