

## Presentation at the Grand Challenges Annual Meeting 2022 in Brussels



From 23 to 26 October 2022 Professor Placide Mbala, Head of the Department of Epidemiology and Global Health at the Institut National de Recherche Biomédicale, took part in the activities of the Grand Challenges Annual Meeting 2022. *(Read the article on Page 2)*

## Various trainings on the diagnosis and genomic surveillance of SARS-CoV-2 and other pathogens



From July to December 2022, the teams of the Pathogen Genomics Laboratory trained several health providers in the genomic surveillance and diagnosis of several pathogens *(Read the article on Page 6-7)*

## Capacity building on whole genome sequencing of Ebola virus Sudan in Uganda



A team from the Pathogen Genomics Laboratory carried out a mission to Kampala (Uganda) from 5 to 9 December 2022 to strengthen the capacities of laboratory technicians and bioinformaticians of the Central of Public Health...*(Read on Page 8-9)*

## Measles Whole Genome Sequencing in Democratic Republic of Congo

***The Institut National de Recherche Biomédicale (INRB) initiated measles virus sequencing activities in the Democratic Republic of Congo (DRC) with the support of The University of Nebraska Medical Center (UNMC), Bio Surv International, Artic Network and Africa CDC.***

One of the measles elimination strategies proposed by the World Health Organization (WHO) is molecular surveillance of circulating strains of the virus. Measles remains a recurrent disease in the Democratic Republic of Congo and responsible for several epidemics and deaths each year, with children under 5 years of age being the most affected.

As part of support for surveillance activities of this disease, the Pathogen Genomics Laboratory team welcomed from 5 to 8 September 2022 scientists from The University of Nebraska Medical Center (UNMC) and Bio Surv International for pilot analyses of samples taken in active epidemic areas. Two sequencing strategies were tested: the whole genome and



*The INRB Pathogen Genomics Laboratory team with the UNMC team at the INRB Sequencing Laboratory*

the N gene. Preliminary results have led to the detection of strain B3. As perspectives, on the one hand more optimizations will make it possible to refine the techniques used. On the other hand, samples from several provinces should be further collected in order to characterize and map the predominant strains.



*Group photo between the INRB Pathogen Genomics Laboratory, Bio Surv International and UNMC.*



# Presentation at the Grand Challenges Annual Meeting 2022 in Brussels

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*Placide Mbala (INRB) and Alex Shaw (Imperial College London) presenting Bill Gates with the poster « **Rapid and Direct Sequencing of Poliovirus from Stool Samples for Routine Surveillance of Acute Flaccid Paralysis (AFP) in the Democratic Republic of Congo**, this study is funded by the Bill and Melinda Gates Foundation.*

Grand Challenges is a family of initiatives encouraging innovation to solve major global health and development problems. Each initiative is an experiment in using challenges to focus innovation on achieving impact.

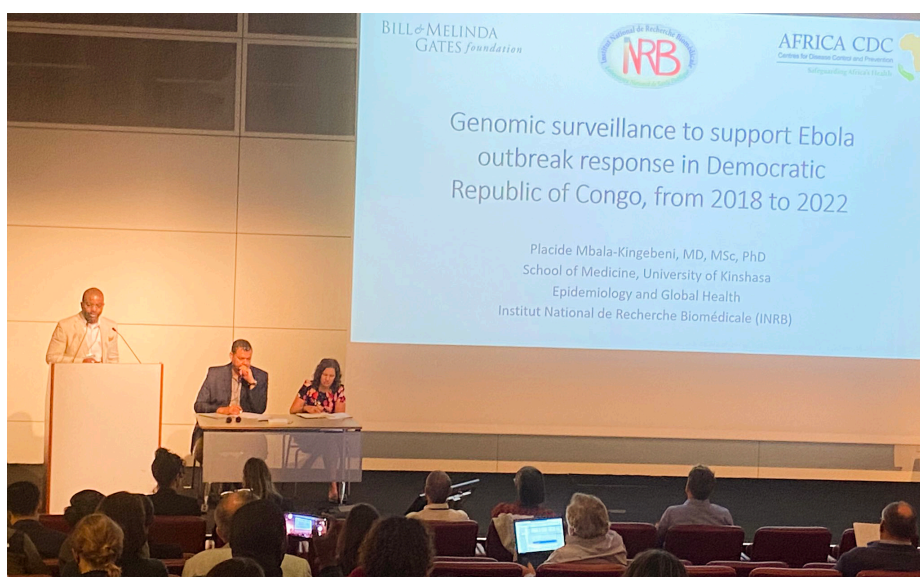
Grand Challenges Annual Meeting brings together funding and research partners across the Grand Challenges network and beyond.

The annual meeting was co-hosted by the Global Grand Challenges partner network and sponsored by Grand Challenges Canada, the U.S. Agency for International Development, Wellcome and the Bill & Melinda Gates Foundation.

The annual session of the Grand Challenges 2022 was attended by Institut National de Recherche Biomédicale (INRB) represented by the Head of the Department of

Epidemiology and Global Health, Professor Placide Mbala who through his various interventions and presentations, shared with the participants the sequencing capacity of his institution and the results

of different surveillance activities for the different pathogens that are sequenced at the Pathogen Genomics Laboratory of the INRB with the support of its partners.



*Presentation by Professor Placide Mbala on Ebola virus disease surveillance in the DRC*



# Pathogen diagnostics and surveillance activities with Vysnova Partners

***Vysnova Partners works in collaboration with the Institut National de Recherche Biomédicale (INRB) in pathogen surveillance for long-term planning to prevent, detect and respond to public health threats in the Democratic Republic of Congo.***



*Working session between the INRB team and Nohelia Navarette, Project Manager (Vysnova Partners) in the DRC*

After the implementation of the molecular diagnostic laboratory of multi-pathogens and the formation of the team of the Pathogen Genomics Laboratory (PGL) of the Institut National de Recherche Biomédicale at the beginning of this year, the PGL has acquired thermocyclers, Quanta Studio7 and Biorad CFX96 Opus for the Multiplex diagnosis of pathogens, in addition to the BIOFIRE platform already installed, thereby strengthening pathogen surveillance activities.

In addition, Vysnova Partners supported the deployment of laboratory teams in the field for real-time sequencing of positive Ebola samples during two epidemics (14th and 15th) that raged in the provinces of Equateur and Nord Kivu in the Democratic Republic of Congo.



*Pathogen Genomics Laboratory team working on BIOFIRE*



# Acquisition of RADI PLCs for Monkeypox real-time PCR

***The Institut National de Recherche Biomédicale has acquired RADI PLCs including an automatic extractor, an automatic reaction mixing dispenser and a thermocycler for real-time PCR. This acquisition will reduce sample processing time.***

RADI's Monkeypox virus detection kit is an in vitro diagnostic medical device, based on real-time PCR technology to detect Monkeypox virus DNA (West African and Congo Basin strains).

The kit is intended for the presumptive qualitative detection of nucleic acid, extracted from the Monkeypox virus from skin, crust or swab samples obtained from patients with signs and symptoms of Monkeypox.

The team of the Pathogen Genomics Laboratory (PGL) and that of the Monkeypox diagnostic laboratory at the Institut National de Recherche Biomédicale was trained by the team of KH Medical on the use of this Kit. The training consisted of DNA extraction from the samples (Crusts, Oropharyngeal Swab, Blood and Vesicle), the preparation of the

master mix, the configuration of the real-time PCR apparatus, the analysis and interpretation of the results. This equipment allows semi-automation

of Monkeypox detection by PCR with a considerable gain in the time of rendering the results.



*The team of the Laboratory of Genomics of Pathogens and that of the Monkeypox diagnostic laboratory in training on the use of the RADI Kit for the diagnosis of Monkeypox*

## The sequencing of the Plague in the DRC



Plague is a bacterial zoonosis caused by *Yersinia pestis* and remains a real public health problem in the Democratic Republic of Congo.

As part of support for surveillance activities of this disease, the Pathogen Genomics Laboratory team received from September 22 to 28, 2022 a team from The University of Nebraska Medical Center (UNMC) and USAMBRID for pilot analyses of Plague samples using the Nextera Flex for Enrichment protocol.

*Preparation of the library for sequencing of plague samples*



# 15<sup>th</sup> Ebola outbreak in Beni in North Kivu Province: Sequencing activities in Goma

***A new outbreak of Ebola virus disease initiated by transmission of Ebola virus from a persistently infected survivor or a survivor who has experienced a relapse.***



*Preparation of the library for sequencing Ebola samples*

On Monday, August 15, 2022, the mobile laboratory of the Institut National de Recherche Biomédicale (INRB-BENI) received a sample of oropharyngeal secretion taken from a deceased patient who was being treated at the Beni General Reference Hospital (HGR-Beni). The sample tested positive for Ebola virus (EBOV) using the Cepheid Xpert Ebola test.

For quality control and confirmation, the samples were sent to the Rodolphe Mérieux laboratory of INRB-Goma on Tuesday, August 16, 2022, where the analysis confirmed the case of Ebola virus disease.

The swab sample, BEN1-22, was sequenced in triplicate (A/B/C) at the Pathogen Genomics Satellite

Laboratory in Goma using the Oxford Nanopore Technology (ONT) sequencing platform. The sequencing libraries were prepared using an amplicon sequencing approach, generating identical genomes with genome coverage of 99.2%, 97% and 97.8%, respectively.

The genomic sequence generated from the BEN1-22 sample is grouped with other sequences from the Nord Kivu/Ituri Ebola virus disease (EVD) outbreak between 2018 and 2020.

The new sequence is most closely related to a cluster of cases that occurred in Beni around November/December 2018 and had six additional mutations from this cluster. If the new case of Ebola virus disease was the

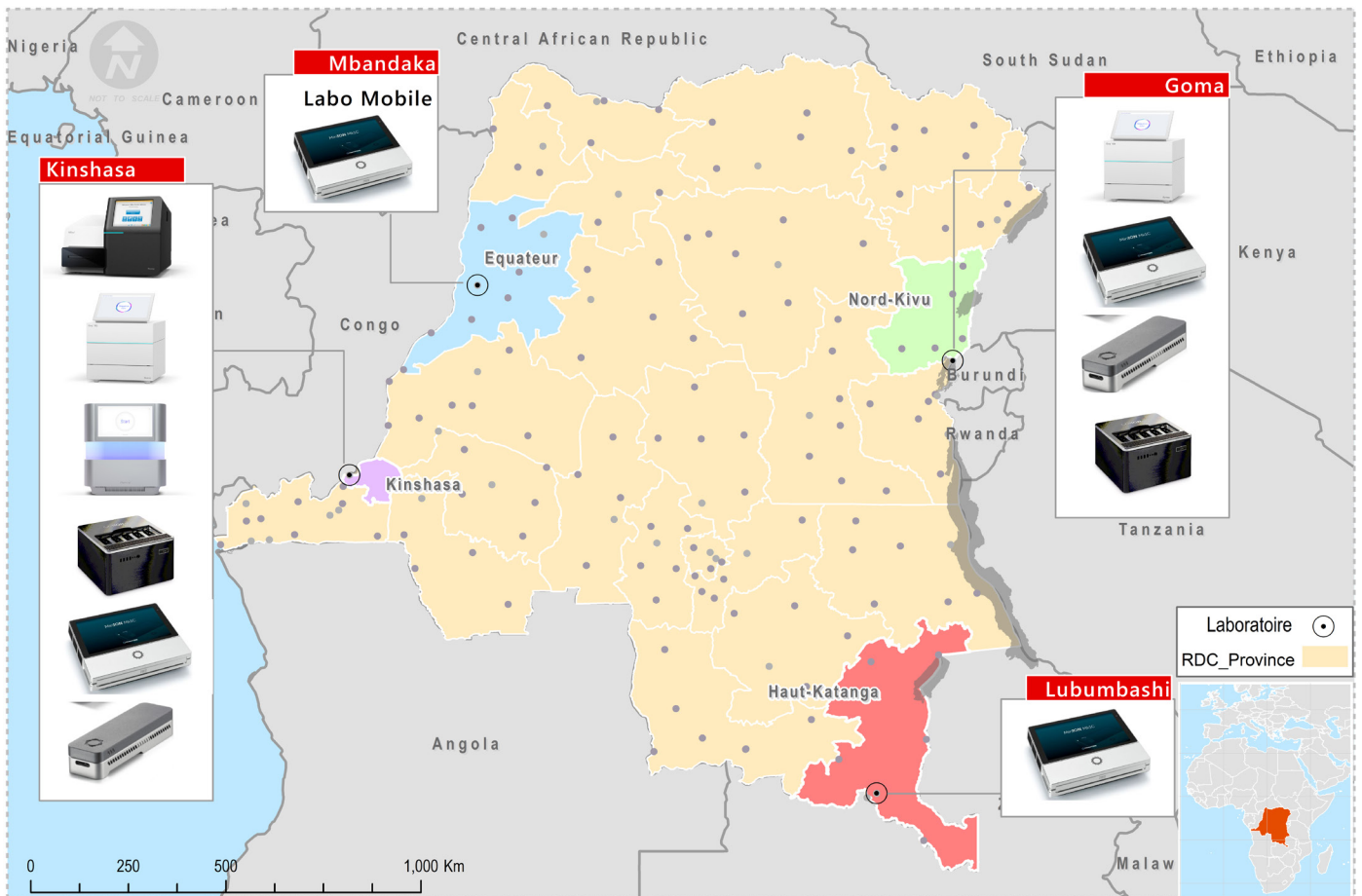
result of continued human-to-human transmission, we would have expected many more mutations to have occurred during this time.

Therefore, our initial results indicate that this case likely represents a new surge in the 2018-2020 EVD outbreak in North Kivu/Ituri, initiated by transmission of Ebola virus from a persistently infected survivor or a survivor who experienced a relapse. This case may be the index case, or there may be previous cases that have not been detected. Epidemiological investigations are ongoing to determine the source.

<https://virological.org/t/august-2022-evd-case-in-drc-linked-to-2018-2020-nord-kivu-evd-outbreak/889>



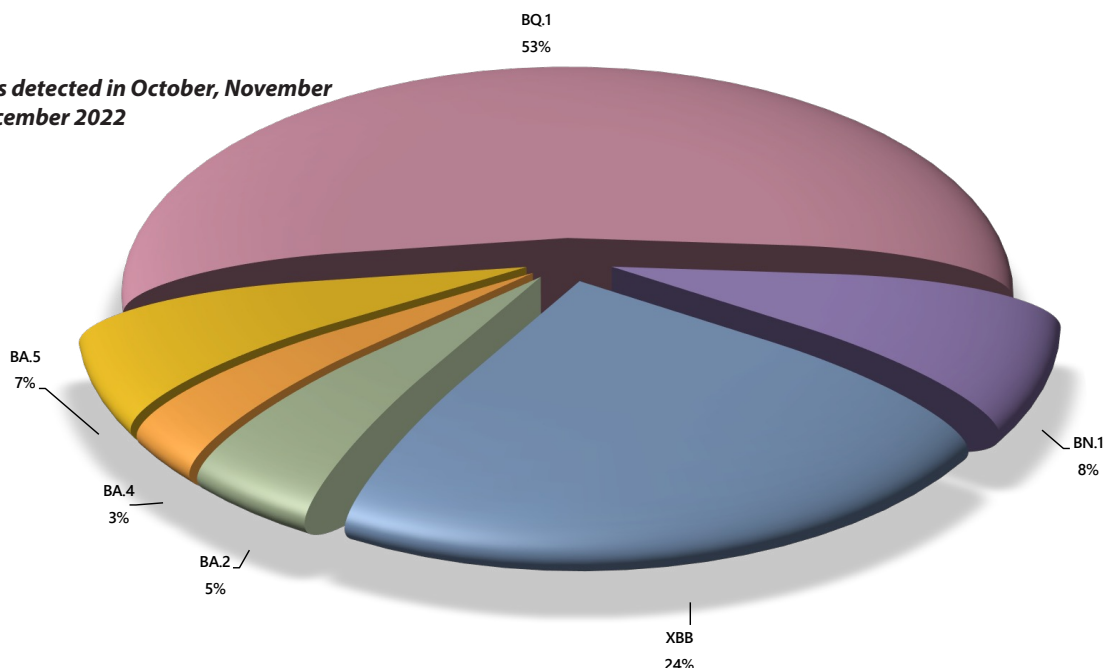
# Our capabilities in terms of sequencers in the DRC



# Genomic surveillance of SARS-CoV-2 in the DRC

Since the beginning of the pandemic a total of 4168 samples have been analyzed and 1685 sequences shared on Glsaid

*Variants detected in October, November and December 2022*





# Symposium with Africa CDC in Addis Ababa, Ethiopia on «Beyond COVID-19»

*Pathogen genomics and bioinformatics for health security in Africa, a symposium held from Tuesday 29 November 2022 to Thursday 01 December 2022. The Pathogen Genomics Laboratory of the Institut National de Recherche Biomédicale was represented by one of its members at this event.*



Organized by Africa CDC with the support of its partners, the symposium brought together from 29 November to 1 December 2022, 144 participants from 50 Member States and 31 partners and stakeholders around the theme «Beyond COVID-19: Genomics and Bioinformatics of Pathogens for Health Security in Africa».

The symposium focused in particular on existing capabilities along the genomics and pathogen bioinformatics value chain. This ranges from pathogen sequencing and analysis, to supply chain issues, to data generation and sharing, and the international policies and agreements that govern these processes.

The Pathogen Genomics Laboratory of the Institut National de Recherche Biomédicale (INRB) was represented by Biologist Amuri Adrienne, who through her intervention shared the experience of the INRB on the progress made, lessons learned and next steps in the sequencing of SARS-COV-2 in the Democratic Republic of Congo.



*Amuri Aziza Adrienne  
Medical Biologist, National Institute for Biomedical Research (INRB), DRC*



# Capacity building on whole genome sequencing of Ebola virus Sudan in Uganda

***A team from the Pathogen Genomics Laboratory of the Institut National de Recherche Biomédicale carried out a mission to Kampala (Uganda) from 5 to 9 December 2022 to strengthen the capacity of laboratory technicians and bioinformaticians of the Central of Public Health Laboratories (CPHL) on the sequencing of the whole genome of Ebola virus Sudan using the Nanopore platform. This training was funded by the Africa CDC-Pathogen Genomics Initiative (PGI) and African Society for Laboratory Medicine (ASLM).***



*The team from the Institut National de Recherche Biomédicale (INRB), the Central of Public Health Laboratories (CPHL) and Africa CDC at the end of the first day of the training.*

Viral haemorrhagic fevers pose a threat to public health worldwide, they include a number of serious, and potentially fatal, diseases caused by viruses such as Ebola and others.

Since 20 September 2022, Uganda has declared an Ebola outbreak after a case of Ebola virus was confirmed in the central part of the country. By the end of November, the country had confirmed 142 cases, including 86 recovered and 56 deaths, a case fatality rate of about 40%. As the country strives to fully control the epidemic, genomic surveillance is part of the planned interventions to support and monitor the evolution of the virus, identify chains of transmission and trace the origin of the epidemic.

It is in this context that the Central of Public Health Laboratories (CPHL), with

the support of Africa CDC through the Pathogen Genomics Initiative (PGI), requested technical support from the Institut National de Recherche Biomédicale (INRB) through its

Pathogen Genomics Laboratory (LGP) to strengthen the genomic capacity of CPHL staff to sequence the Ebola virus Sudan and support outbreak response activities in Uganda.



*Briefing on the Gunit protocol to use*



The Pathogen Genomics Laboratory conducts genomic surveillance of emerging and re-emerging pathogens with a strong impact on public health. This laboratory plays a central role in the response to various public health emergencies in the Democratic Republic of Congo and the Central African region as well as in other African countries.

The training lasted 5 days and consisted of training laboratory technicians in the wet laboratory application of genomics techniques to sequence Ebola virus on available platforms in the country, training laboratory bioinformaticians in the analysis, interpretation and sharing of sequencing data, interpretation and sharing of sequencing data and finally demonstrating the establishment of a mobile sequencing laboratory mobile in the field.

The Oxford Nanopore Technology (ONT) platform was selected for sequencing activities as part of this technical support to the Central Public Health Laboratories (CPHL) team.

In addition, sequencing activities were also carried out with the Illumina platform to allow not only to compare the results obtained but also to offer the local team the possibility of using the two platforms (Nanopore and



*The team from the Institut National de Recherche Biomédicale (INRB), the Central of Public Health Laboratories (CPHL) and Africa CDC after the first session of the training*

Illumina) for the sequencing of Ebola as for other pathogens for which the CPHL focuses its efforts.

For samples sequenced on ONT, the GUNIT protocol was used with SUDV-1000 primers and DNA Prep. The same samples were used for both platforms.

Bioinformatics analyses for the ONT platform were performed with the artic-wrapper pipeline and Ivar for the Illumina platform. In total, 39 of the 58 samples sequenced with the Nanopore platform had coverage greater than 80%. These results led to the conclusion that the teams had detected the complete genome of Ebola Sudan.



*Visit of the Ebola Treatment Unit at the Regional Referral Hospital in Mubende*

After 4 days of laboratory training, the team of Pathogen Genomics Laboratory (LGP) of Institut National de Recherche Biomédicale (INRB) from Kinshasa, that of the Central of Public Health Laboratories (CPHL) of Uganda and that of Africa CDC made a descent 148.8 kilometers from Kampala, to the regional referral hospital of Mubende (MRRH) which is the Ebola treatment unit (ETU) to test the deployment of the mobile laboratory brought from Kinshasa in the Democratic Republic of Congo with some consumables by the team of the INRB. This exercise provided the local laboratory with insight into the importance of field sequencing activities and how to proceed with deployment.

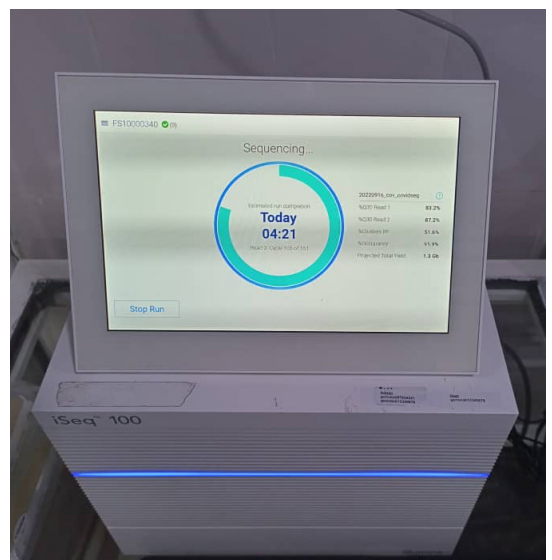


# Various trainings on genomic surveillance of SARS-CoV-2 and other pathogens

*From July to december 2022, the teams of the Pathogen Genomics Laboratory, members of the Department of Epidemiology led by Professor Placide Mbala, carried out several field work and trained several health providers (Laboratory Technicians and Biologists) in genomic surveillance and diagnosis of several pathogens.*



From 1 to 06 August 2022, we organized working sessions with the heads of two laboratories in the Republic of Congo. The support focused on the sequencing of SARS-CoV-2 using the Midnight protocol on the Nanopore platform.



Training organized in Goma from 12 to 23 September 2022 with the support of WHO and consisting in the implementation of the Illumina platform with installation of an Iseq at INRB Goma. This was followed by a retrospective investigation of positive Covid samples taken from an area that reported high case fatality. The reagents for these analyses were acquired thanks to the support of the Afroscreen network (Coviseq kit and Iseq cartridges), Africa CDC (Midnight Kit and Flowcell) and Find (Consumables and Mk1c).





The whole genome sequencing of SARS-CoV-2 was implemented in the large lab following WHO-supported training for laboratory technicians and biologists from the Haut Katanga and Lualaba laboratory. The provincial laboratory was equipped with a sequencer and a computer. It should be noted that a prospecting visit to these two provinces had been carried out prior to the organization of the training.



In collaboration with Africa CDC, the Institut National de Biomédicale (INRB) through its INRB Regional Training Center of Excellence (CEFRI), the Virology Directorate and the Pathogen Genomics Laboratory, welcomed 17 participants from 11 French-speaking African countries for a 3-day training on epidemiological surveillance and diagnosis of Monkeypox from 27 to 29 September. This training was funded by Africa CDC.



Regional training on Ebola diagnosis organized by the National Institute for Biomedical Research (INRB) in collaboration with Africa CDC: this training was aimed at scientists and laboratory technicians experienced in molecular techniques. The training was attended by 16 participants from 7 English-speaking African countries (Uganda, Ethiopia, Tanzania, Burundi, Rwanda, Southern Sudan and Kenya).



# ASTMH 2022 Annual Meeting

The Pathogen Genomics Laboratory of the Institut National de Recherche Biomédicale took part in the 2022 annual meeting of the American Society of Tropical Medicine and Hygiene (ASTMH)



**Placide Mbala**

**Topic :** Pathogen genomics in the management of emerging and re-emerging diseases in the Democratic Republic of Congo



**Adrienne Amuri**

**Topic :** Detection and sequencing of a Monkeypox virus outbreak in Maniema Province, Democratic Republic of Congo



**Eddy Lusamaki**

**Topic:** Added value of multiplex serology in the investigation of the Monkeypox epidemic in DRC



**Trésor Kabeya**

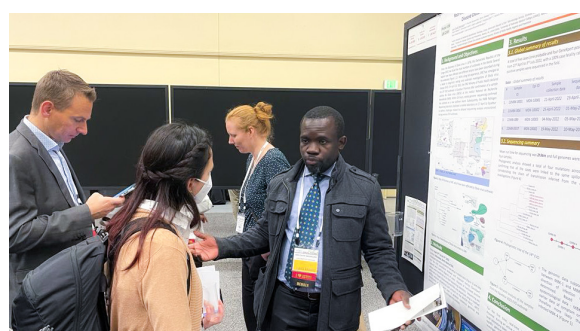
**Topic:** Implementation of direct detection by Nanopore Sequencing of poliovirus in the Democratic Republic of Congo



**Jean-Claude Makangara**

**Topic:** Real-time sequencing in support of the 14th Ebola virus disease outbreak of 2022 in Mbandaka, DR. Congo.

The annual meeting of the American Society of Tropical Medicine and Hygiene (ASTMH) is an international forum for the exchange of scientific advances in tropical medicine, hygiene and global health. This year's session took place from October 30 to November 3, 2022 in Seattle Convention Center/ Seattle, WA, USA. The Pathogen Genomics Laboratory of the Institut National de Recherche Biomédicale in the Democratic Republic of Congo, took part in this event through 4 of its members who presented their work during the online and face-to-face sessions.



Dr. Jean-Claude Makangara in exchange with the participants of the ASTMH 2022 Annual Meeting during the poster presentation session

*The activities of this third quarter of 2022 were made possible thanks to your rich collaboration and valuable support*



## Editorial Board

**Director of Publication**  
Professeur Placide Mbala

### Writing

Eddy Lusamaki  
Adrienne Amuri  
Jean-Claude Makangara  
Gradi Luakanda

### Layout and Design

Gradi Luakanda

### E-mail

labgenpath@inrb.cd

### Phone

+243 896 729 720

+243 813 614 010

### Adress

Avenue de la Démocratie (ex-Huilleries), BP 1197 Kinshasa/Gombe, République Démocratique du Congo