

Regional workshop on the implementation of pathogen genomics in Africa



A sustainable, cost-effective system for genomic surveillance of pathogens through integrated transcontinental laboratory networks and data infrastructure. (Read the article on Page 4)

New sequencing techniques for direct detection of Poliovirus



Direct detection of poliovirus in stool using high-throughput sequencing with the Nanopore platform (DDNS) offers a real opportunity to reduce the response time to outbreaks. (Read the article on Page 2-3)

14th Ebola outbreak in Equateur: Deployment of the Mobile Laboratory in the field



Deployment of the mobile laboratory with an MK1C for sequencing of Ebola Virus Disease positive cases in Mbandaka with the support of Vysnova/CDC Atlanta, FIND, WHO and Africa PGI - Africa CDC. (Read the article on Page 5)

Visit of the NIAID/NIH delegation at the INRB from March, 16th to 19th, 2022

A delegation of National Institute of Allergy and Infectious Diseases (NIAID) - National Institute of Health (NIH) visited the new infrastructure of the Institut National de Recherche Biomédicale (INRB) on Wednesday 16 March 2022 including the sequencing laboratory.



Delegation from the National Institute of Health and the Institut National de Recherche Biomédicale (INRB) team at the Sequencing Laboratory

During its visit to the Institut National de Recherche Biomédicale (INRB), the NIAID/NIH delegation was received in the INRB conference room by the Director General of INRB, Professor Jean-Jacques Muyembe, and the Head of the Department of Epidemiology and Global Health, Professor Placide Mbala, for an evaluation of this rich partnership. The joint teams evaluated together the evolution of the activities on different studies in progress and made a projection on those to come. At the end of this exchange, the NIAID delegation visited the Pathogen Genomics Laboratory to have an overview on its sequencing capacity.



Working session between Professor Jean-Jacques Muyembe, the INRB team and the NIH team

New sequencing techniques for direct detection of poliovirus

The direct detection of poliovirus in stool by high-throughput sequencing with the Nanopore platform (DDNS) offers a real opportunity to reduce the response time to outbreaks.



Team of the INRB Pathogen Genomics Laboratory in training on the sequencing of the complete genome of Poliovirus

Late detection of poliovirus transmission has been described as one of the greatest obstacles to polio eradication.

Despite the significant progress made by the Global Polio Eradication Initiative (GPEI) since 1988, polio, a paralytic infectious disease caused by poliovirus, remains a public health problem in countries with poor socio-economic conditions, ruined by armed conflict, with low immunization coverage and delays in detecting poliovirus transmission compounded by a series of logistical challenges that extend the response time to outbreaks beyond the window of maximum impact.

In the Democratic Republic of Congo (DRC), despite its large surface area, only one laboratory is accredited by the World Health Organization (WHO) for the biological diagnosis of poliovirus: the Institut National de Recherche Biomédicale (INRB) in Kinshasa. This laboratory uses an algorithm of detection by cell culture according to the WHO protocol followed by the intra-typical differentiation then the sequencing which is carried out in South Africa.

The direct detection of poliovirus in stools by high throughput sequencing on the Nanopore platform (DDNS) offers a real opportunity to improve the turnaround time of results.

This new method will help reduce the analysis time from sample receipt to sequence delivery to one week. The on-site sequencing help also to avoid bottlenecks in the international samples transportation.

Indeed, the team of the Laboratory of Pathogen Genomics (LGP) of INRB in DRC was trained in August 2021 to sequence the VP1 gene with Nanopore by the team of Imperial College London using the polio sequencing consortium platform with the support of the Bill and Melinda Gate Foundation (BMGF).

Only in 4 months, about 2500 stool samples collected from children notified cases of acute flaccid paralysis of limbs were analyzed by the method which provided excellent results.

From March 19 to April 02, 2022, a large polio sequencing consortium team visited Kinshasa in the Democratic Republic of Congo for a further training on other sequencing protocols of the poliovirus whole genome (whole genome sequencing that offers the possibility of determining mutations beyond the VP1 gene) and PAN-EV capsid sequencing (possibility of detecting even other non-polio enteroviruses that also participate in the genome). beyond the VP1 gene and PAN-EV capsid sequencing (with the possibility to detect even other



Capacity building of the bioinformatics team for analysis

non-polio enteroviruses that also are implicated in the genesis through recombination of VDPV vaccine-derived strains); and during the same period the analyses of wastewater samples from the environmental surveillance of poliovirus were also made.

This great consortium is composed of:

- **Imperial College London:** Alex Shaw, Catherine Troman, Joyce Akello and Nicholas Grassly
- **National Institute for Biological Standards and Control (NIBSC):** Erika Bujaki and Javier Martin
- **University of Nebraska Medical Center:** Bailey White, Catherine Pratt
- **Bill and Melinda Gate Foundation (BMGF):** Kathleen Rankin
- **Institut National de Recherche Biomédicale(INRB)**

The results of the analyses show equivalent sensitivity and specificity to culture. The similarity of DDNS consensus fasta genome and traditional sanger of all culture supernatant was average



Family photo of teams from INRB, the University of Nebraska Medical Center and the Bill & Melinda Gate Foundation.

99.9%). DDNS VP1 sequences were obtained at a mean time of 7 days after sample receipt, compared with 33 days for cell culture, intratypical differentiation (ITD), and Sanger sequencing. This helped for early detection of a new emergence of

cVDPV2 in Maniema.

DDNS results are shown to be sensitive, specific and accurate for an early identification of Poliovirus, an important resolution of one of the goals of the IMEP strategic plan for 2022 - 2026.

PCR screening and sequencing techniques

The AFROSCREEN project structures a network of 25 laboratories, reference centers and partners in 13 African countries. It is currently focused on the genomic surveillance of SARS-CoV-2 and the evolution of variants through high-throughput screening PCR and sequencing techniques on the Illumina platform, using the Covidseq kit.



Regional Workshop on Pathogen Genomics Implementation

A sustainable and cost-effective system for genomic surveillance of pathogens through integrated transcontinental laboratory networks and data infrastructure.



Family photo of workshop participants

From February 28 to March 2, 2022, a regional workshop on the implementation of pathogen genomics in public health in the Central African region was organized in Libreville, Gabon by the Africa Centers for Disease Control and Prevention (CDC) Pathogen Genomics Institute.

This workshop is part of activities to improve a sustainable and cost-effective system of pathogen genomic surveillance through integrated cross-continental laboratory networks and data infrastructure.

The Pathogen Genomics Laboratory of the Institut National de Recherche Biomédicale was represented by biologist Amuri Aziza, who gave an overview of Pathogen Genomics in the Democratic Republic of the Congo and the progress made to date in the DRC genomic surveillance. She concluded by presenting the evolution of activities

at the Pathogen Genomics Laboratory on sequencing in the management of Ebola Virus Disease (EVD) outbreaks,

rapid detection and sequencing of Poliovirus from stool samples using nanopore technology.



Biologist Amuri Aziza, Head of the Pathogen Genomics Laboratory of the Institut National de Recherche Biomédicale (INRB)

14th Ebola outbreak in Equateur: Deployment of the mobile laboratory in the field

Deployment of a mobile laboratory with an MK1C for sequencing positive Ebola virus disease cases in Mbandaka with the support of Vysnova/CDC Atlanta, FIND, WHO and Africa PGI - Africa CDC



Mobile laboratory

A new Ebola outbreak was declared by health authorities in the Democratic Republic of Congo (DRC) on Saturday, April 23, 2022, after the confirmation of a case in Mbandaka in Equateur Province, NorthWestern DRC. This was the third emergence in this province since 2018. This new confirmed case of Ebola occurred in the Wangata Health Zone, city of Mbandaka.

A team from the Pathogen Genomics Laboratory of the Institut National de Recherche Biomédicale (INRB) was deployed to Mbandaka from April 23 to June 27, 2022 with a mobile laboratory and a MinION Mk1C sequencer.

This mobile laboratory has been tested for its capacity to be deployed in the

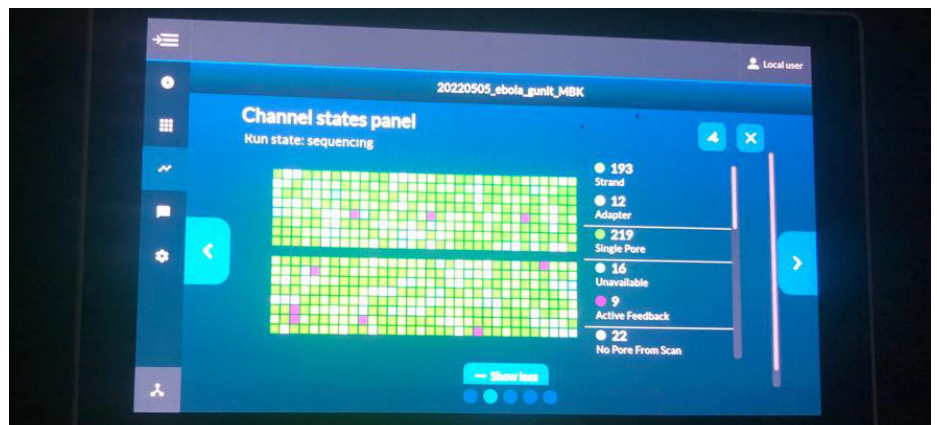
field during an epidemic. In Goma and Kongo Central, respectively in 2021 and 2022.

The activities of sequencing during epidemics had as objectives to determine the origin of the epidemic, to

establish transmission links between confirmed cases.

A total of 1000 samples were tested during this 14th Ebola outbreak in Mbandaka, of which 4 were confirmed and 1 probable. The first positive sample was sequenced in Kinshasa at the INRB Pathogen Genomics Laboratory and other positive samples were sequenced at the mobile laboratory deployed in the field. We were able to generate the complete genome of the Ebola virus, to establish the links between positive cases. Finally, this deployment provided an opportunity for training on SARS-CoV-2 genomic surveillance in Equateur and capacity building of local teams.

Sequencing results suggested zoonotic transmission as a likely hypothesis in the re-emergence of Ebola Virus Disease (EVD).



Monkeypox sequencing

As a result, the National Institute of Biomedical Research (NIBR) has focused its sequencing efforts to intensify epidemiogenomic surveillance of the disease.

The metagenomic approach has allowed the detection of the Monkeypox virus in different contexts since 2018. It is also worth noting that we have observed over time, the notification of cases in new provinces with no history or documented history of Monkeypox. In 2022, a total of 23 samples were sequenced, 17 of which had more than 90% coverage. Submission of sequences on Gisaïd, exploration of protocols and improvement of yields for MPX sequencing with Nanopore.



Various trainings on SARS-CoV-2 genomic surveillance and field trips

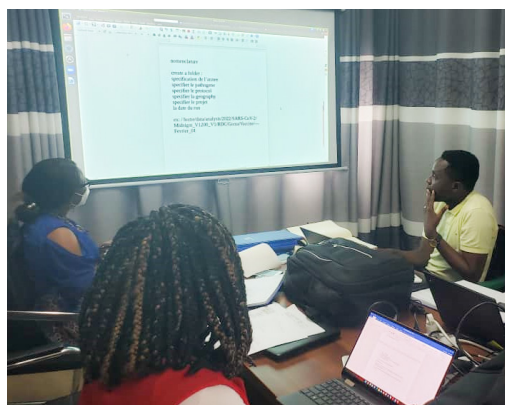
From January to June 2022, teams from the Pathogen Genomics Laboratory, members of the Department of Epidemiology led by Professor Placide Mbala, conducted several field activities and trained several health providers (Laboratory Technicians and Biologists) inside and outside the country in the genomic surveillance of SARS-CoV-2



From January 30 to February 13, 2022, the Pathogen Genomics Laboratory team visited Kongo Central Province to test the deployment of the mobile laboratory, and train local staff in genomic surveillance and sequencing of SARS-CoV-2 samples, and review good storage and shipment practices.



After an introduction to genomic surveillance training in Kinshasa (DRC) for Chadian laboratory technicians and biologists, a team of two members of the INRB Pathogen Genomics Laboratory traveled to Chad to organize a training workshop on SARS-CoV-2 whole genome sequencing using Midnight protocol and implementation of NGS lab from February 22 to March 10, 2022, at the Mobile Laboratory in N'djamena.



To follow up on the sustainability and autonomy of the sequencing activities of all Covid-19 positive samples and to strengthen the capacity of the team in charge of bioinformatics analysis at INRB Goma, a team from the Pathogen Genomics Laboratory went to Goma from January 28 to February 10, 2022, to continue the training initiated in Kinshasa.



To strengthen the capacities of our different partner laboratories at the provincial level, the INRB Pathogen Genomics Laboratory sent two members of its team to the province of Equateur from February 26 to March 2, 2022, to initiate the technicians and biologists of the provincial laboratory of Mbandaka in genomic surveillance.



Introduction to SARS-CoV-2 genomic surveillance and bioinformatics analysis for 2 members of the Republic of Congo team. This training was organized at the Institut National de Recherche Biomédicale, from April 27 to May 7, 2022.

We received a delegation of 4 laboratory technicians from the provinces of Lualaba and Haut Katanga for training on the sequencing of SARS-CoV-2 from 16 to 26 May 2022. The team arrived with 52 samples of which 35 were from Lualaba and 17 from Haut Katanga in ambient temperatures. They proceeded to the inventory, extraction and sequencing of SARS-CoV-2 samples under the supervision of the laboratory team.

Sequencing and storage infrastructures



The Pathogen Genomics Laboratory has a range of sequencing facilities to carry out its activities. It is equipped with the following sequencers: GridION, Nextseq, Miseq, Iseq and MK1C. In addition, the team in charge of bioinformatics tasks has at its disposal storage (servers) and analysis tools.



Visit of the Vysnova Partners team and George Washington University in the Democratic Republic of Congo (Kinshasa and Goma)

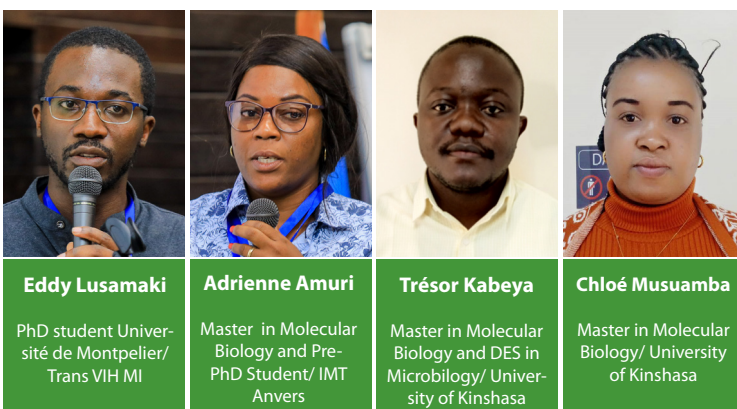


From March 24 to April 2, 2022, a delegation from Vysnova Partners and George Washington University visited the sequencing laboratory of the National Institute for Biomedical Research (INRB). This visit was followed by the implementation of the multi-pathogen molecular diagnostic laboratory. The team of the Pathogen Genomics Laboratory was trained on the use of the BIOFIRE platform. A total of 41 negative samples collected during the different outbreaks (Ebola, Chikungunya, Monkeypox, influenza viruses) that occurred in DRC were analyzed. The results obtained led to the submission of an abstract to the 71st Meeting of the American Society of Tropical Medicine and Hygiene.

All those activities of the first semester of 2022 couldn't be realized without your rich collaboration and precious support



Master and PhD team members



A total of **1741** sequences have been shared on GISAID since the beginning of the Covid-19 pandemic in the Democratic Republic of Congo

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