

Capacity for genomic sequencing grows in Latin America and Caribbean with training and equipment provided by PAHO



Staff from the Dominican Republic's Ministry of Public Health were trained to use their new genomic sequencing machine by experts from PAHO and Panama's Gorgas Memorial Institute of Health Studies in Panama.

Washington, D.C. 21 September 2022 (PAHO) – Understanding how the SARS-CoV-2 virus is evolving using whole genome sequencing has allowed countries to launch life-saving public health measures such as rapidly increasing oxygen supply to handle surges of COVID-19 patients. However, when the pandemic first emerged in 2020, only two Latin American countries – Brazil and Chile – had public laboratories capable of this essential process. In response, the Pan American Health Organization (PAHO) initiated the COVID-19 Regional Genomic Surveillance Network (COVIGEN), which promotes expansion of genomic sequencing capacity in Latin America and the Caribbean.

This year, with assistance from PAHO, seven more countries in Latin America and the Caribbean are receiving genomic sequencing equipment and/or training in how to use it. With these additions, COVIGEN incorporates 33 laboratories from 30 countries. This major advance, supported by the US Government (USG) through the American Rescue Plan Act 2021, expands the region's diagnostic capacity and prepares it for the next pandemic.

The countries that have received both PAHO-procured genomic sequencing equipment and training are The Bahamas, Barbados, El Salvador, Guatemala, Guyana, and Honduras. The Dominican Republic’s Ministry of Public Health procured its own genomic sequencing machine, while PAHO and Panama’s Gorgas Memorial Institute for Health Studies provided training on equipment use, genomic sequences generation, and bioinformatic analysis.



COVIGEN’s 33 laboratories include (i) “in-house or in-country sequencing” labs that can sequence samples from their own countries (ii) “external sequencing” labs that do not have that capacity and must send samples to regional reference laboratories for sequencing and (iii) “reference” labs that can sequence local samples and samples from other countries.

By October 2022, the labs with next generation sequencing equipment are expected to be able to use genomic sequencing to rapidly detect variants of concern (VOCs), which can significantly alter transmissibility, severity and/or immunity to viruses.

The SARS-CoV-2 VOCs named so far – Alpha, Beta, Gamma, Delta, and Omicron, which transformed the trajectory of the COVID-19 pandemic – were identified and characterized through genomic sequencing. The VOCs include the most recent sublineages of the globally predominant Omicron variant, BA.1 - BA.5. Genomic sequencing also detects variants of interest (VOIs), which may be able to change transmissibility, severity and/or immunity to the virus.

Some genomic sequencing specialists received training in genomic sequencing during the 26th course on Viral Evolution and Molecular Epidemiology (VEME), an annual session sponsored this year by PAHO and held in August in Panama. The session – supported by USG funding and

organized by Brazil's Oswaldo Cruz Foundation (FIOCRUZ) and the Gorgas Institute – included training from about 50 experts from renowned scientific institutions in the Americas.

The course consisted of theoretical and practical sessions divided into four modules ranging from generation of data from genomic sequencing to more complex analysis of the sequences. For the first time, VEME included a module designed for managers, health managers, and decision-makers.



Participants at the 26th Course on Viral Evolution and Molecular Epidemiology in Panama City, which included training on genomic sequencing of the SARS-CoV-2 virus.

“This type of bioinformatics analysis is not something that is commonly done in public health laboratories in the region because it requires specialized training and education,” said Alexander Martinez Caballero, director of the Department of Genomics and Proteomics Research at the Gorgas Institute. “From now on, many laboratories will be able to perform these analyses in their facilities in a timely manner and for various viruses of interest.”

COVIGEN started out as a handful of public health laboratories, including two reference sequencing labs – the Oswaldo Cruz Foundation/FIOCRUZ and the Institute of Public Health of

Chile – which can carry out genomic sequencing for countries that lack their own capacity. At this moment the network has eight¹ reference sequencing laboratories, including the Centers for Disease Control and Prevention/US-CDC. Throughout the pandemic, PAHO has supported COVIGEN by covering the costs of the shipment of samples from one lab in the network to another and by supplying the reagents needed for genomic sequencing.

PAHO encourages labs to send genomic data on SARS-CoV-2 to GISAID, a global open-source platform that promotes exchange of genomic sequencing data of influenza and other respiratory viruses. Sharing genomic information is critical to understanding evolving patterns of a virus, following its geographic distribution and spread, characterizing risk and impact on public health countermeasures, and identifying severity or immune resistance markers as early as possible.

¹ FIOCRUZ, Brazil; ISPCH, Chile; US-CDC, United States; The Gorgas Memorial Institute for Health Studies, ICGES Panama; Institute of Epidemiological Diagnosis and Reference, InDRE, Mexico; University of West Indies, UWI, Trinidad and Tobago; Costa Rican Institute of Research and Teaching in Health and Nutrition, INCIENSA, Costa Rica; National Institute of Health Studies, INS, Colombia.