



# UNIVERSITY OF GHANA

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### NEWS RELEASE

#### UNIVERSITY OF GHANA SCIENTISTS SEQUENCE GENOMES OF NOVEL CORONAVIRUS

Scientists at the University of Ghana have successfully sequenced genomes of SARS-CoV-2, the virus responsible for the global COVID-19 pandemic, obtaining important information about the genetic composition of viral strains in 15 of the confirmed cases in Ghana.

The scientists, who work at the Noguchi Memorial Institute for Medical Research (NMIMR – College of Health Sciences) and the West African Centre for Cell Biology of Infectious Pathogens (WACCBIP – College of Basic and Applied Sciences) at the University, analyzed samples from selected cases to gain a comprehensive understanding of the variations of the virus that are present in the country.

Genome sequencing allows for the compilation of the most comprehensive information about an organism’s genetic makeup. Using advanced next-generation sequencing methods, scientists are able to track and compare viral mutations to understand the origins of imported strains and to discover if any novel strains are emerging locally.

“The successful establishment of this sequencing capability at University of Ghana is a significant milestone in Ghana’s response to the pandemic, as it will strengthen surveillance for tracking mutations of the virus and aid in the tracing of the sources of community infections in people with no known contact with confirmed cases,” said Prof. Abraham Anang, Director of NMIMR.

Samples analyzed were taken from two travelers who arrived in Ghana from the UK, one from Norway, one from Hungary, one from India, and one traveler who arrived from the United States through the United Arab Emirates. Nine samples were taken from individuals who had no travel history, who are believed to have acquired the infection locally.

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“The data tells us that, while there were some differences between the strains from the various countries, all the 15 genomes generally resembled (with >92% similarity) the reference strain that was isolated in the Wuhan Province of China, where the outbreak began,” said Prof. Gordon Awandare, Director of WACCBIP. “This confirms that we are dealing with the same pathogen, and that it has not yet changed its genetic make-up significantly. It is natural that pathogens will evolve as they encounter different environmental challenges, so we will need to continue monitoring to keep track with these changes and determine how they impact on the efficacy of potential drugs or vaccines that are being developed”, he added.

The information from the sequence data has been shared with scientists around the world through an open access platform known as the Global Initiative on Sharing All Influenza Data (GISAID) database, where other sequences from various countries are stored (<https://www.gisaid.org/>).

“The University of Ghana is proud to note that this feat was achieved entirely by local scientists using established local capacity including our Next Generation Sequencing Core and ‘Zuputo’, our High Performance Computing system, which are jointly managed by NMIMR and WACCBIP, with support from University of Ghana Computing Systems,” said Prof. Ebenezer Oduru Owusu, Vice Chancellor of the University.

“We would like to express our gratitude to the Government of Ghana, and all the funding agencies that have provided grants to support the operations of our two flagship centres of excellence for biomedical research,” the Vice-Chancellor added.

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