Ministry of Science & Technology

Department of Biotechnology organizes Public Webinar on the “Genome Sequencing of SARS-CoV-19”

Need for viral genome sequencing, the process through which viral variants emerge naturally and their relevance in terms of various aspects of public health: Dr Renu Swarup

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In the backdrop of reports of emergence of variants of the SARS-CoV-2, in the UK and some other parts of the world, the Government of India had established a national multi-agency consortium, Indian SARS-CoV-2 Genomic Consortium (INSACOG) in December 2020, consisting of ten laboratories of the **Department of Biotechnology**, **Council of Scientific and Industrial Research** (CSIR), **Indian Council of Medical Research** (ICMR) and Ministry of Health & Family Welfare (MoHF&W) with the overall aim of monitoring the genomic variations in the SARS-CoV-2 on a regular basis. The responsibility to correlate the clinical aspects and coordinate the collection of samples from states, for this purpose, was provided to **National Centre for Disease Control** (NCDC), MoHFW. **INSACOG** has a data repository at **IGIB**, New Delhi and **NIBMG**, Kalyani.

For improving the understanding of the nuances of SARS-CoV-2 genome sequencing and its public health relevance in the context of the current pandemic, the **Department of Biotechnology** yesterday conducted a public webinar on the “***Genome Sequencing of SARS-CoV-19***". The webinar aimed at demystifying the science behind mutations in the viral genome, viral genome sequencing, and public health implications of the mutations in the viral genome. A panel of experts from various reputed institutes & organisations discussed different aspects of genome sequencing and highlighted the importance of sequencing the Genome of SARS-CoV-19, and the work done by the Indian SARS-CoV-2 Genomics Consortium in ascertaining the presence of variants of SARS-CoV-2, establishing sentinel surveillance for early detection, and determining the genomic variants in the unusual events/trends.

Dr Suchita Ninawe, Adviser/ Scientist -G, **DBT** welcomed all the experts and the participants to the public webinar. She also given an overview about the Genome Sequencing of SARS-CoV-19 and highlighted that this webinar aims at simplifying the science behind mutations and genome sequencing of SARS-CoV-19 for easier understanding of common man.

Dr Renu Swarup, Secretary, **Department of Biotechnology** in her address said that the main purpose of this webinar was to make it easier for the public to understand the need for viral genome sequencing, the process through which viral variants emerge naturally and their relevance in terms of various aspects of public health.

Dr Shekhar C. Mande, Secretary- **DSIR & DG-CSIR** in his opening remarks explained different mutations and virus strains. He further said that mutations arise through spontaneous errors during the replication of the virus. Some mutations may allow the virus to survive better and evade antibody response and therefore can provide selective advantage to the virus.

Following the opening session, a technical session was held which was chaired by Dr Shahid Jameel, Chairperson of the **Scientific Advisory Group** of the **INSACOG**. In this session, eminent panellists discussed a range of themes, from virus structures to simplifying mutants, different aspects of mutation, understanding of the so-called double and triple mutations, and the public health relevance of all this.

Dr Saumitra Das, Director, **NIBMG**, Kalyani underscored the need for viral sequencing and gave a brief overview of the INSACOG activities. He talked about the different SARS-CoV-2 variants circulating globally and the reported spike gene mutations.

Dr Sujeet Singh, Director **NCDC**, in his presentation talked about monitoring the genomic variations in the SARS-CoV-2 for understanding the mutations, the variants and their potential public health significance.

Dr. Anurag Agrawal, Director, **CSIR-IGIB** explained the process of selection of virus mutants and described the major variants which have been identified from different parts of the country. He also mentioned that the information generated by the **INSACOG** is being shared globally using the global databases like **GISAID**.

Dr Sudhanshu Vrati, Director-**RCB** explained the different between the commonly used terms: mutant, variant, variant of interest and Variant of Concern (VoC). He said that a VoC may have higher transmissibility or can cause a more severe disease; or can show reduced neutralization by antibodies.

Dr. Priya Abraham, Director, **ICMR-NIV** spoke about how RT-PCR has been the corner stone of diagnostic ever since the pandemic started. She mentioned that RT-PCR system being used in the country is able to detect all the variants which have so far been reported from the country. She further pointed out some of the reasons behind the false-negative RT-PCR test reports, which could be sampling error, delays in the screening of individuals and non-adherence of Standard Operating Procedures during transportation of the kits. .

The session was later opened to the media persons and general public for the questions which were responded to by the Experts. During the Q&A session '***Virus mutation' and interlinked issues*** have been further clarified. It was well emphasized that there is no scientific term such as "double" or "triple" mutation of virus. The terms double or triple mutants are colloquial and these are used to emphasize features of a variant. Double or triple mutations as used recently in various media reports, were to signify the number of mutations which escape immunity (immune escape mutant). These variants otherwise harbour 15 lineage defining mutations. However, clinical correlations and epidemiological correlation data determines if the mutation of the virus is a Variant of Interest (VoI) or Variant of Concern (VoC). Current data does not suggest that the surge is solely due to any one variant or any one factor.

The reasons for surge are primarily due to:

1. **Non-adherence to COVID Appropriate Behaviours**
2. **Rising immune escape mutations and some that also increase infectivity.**
3. **Declining immunity**

It is advisable while reporting on mutants, standard WHOs Uniform variant nomenclature be used (for example- B.1.617) when referring to such variants.

The webinar ended with formal vote of thanks by Dr. Onkar Tiwari, Scientist, DBT to all the expert panellists for this informative session that simplifying the science behind mutations and genome sequencing of SARS-CoV-19.

The webinar was seen by more than 1800 viewers through Gotwebinar and YouTube. It also has considerable number of participants from media.

For Further Information: Contact Communication Cell of **DBT**

About DBT: *The Department of Biotechnology (DBT), under the Ministry of Science & Technology, promotes and accelerates the development of biotechnology in India, including growth and application of biotechnology in the areas of agriculture, healthcare, animal sciences, environment and industry.* **For more information, visit**, http://dbtindia.gov.in/

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