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Multi-institutional team identifies COVID-19 RNA variations and implications

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Using genomic sequencing methods, scientists from top institutes, including IIT Jodhpur, identify variations in COVID-19 RNA and their implications



A multi-institutional team, co-led by Dr Mitali Mukerji of the Indian Institute of Technology (IIT) Jodhpur, has used state-of-the-art genomic sequencing methods to identify variations in the RNA of the COVID-19 virus.

The scientists have also studied the fixation of these intra-host variations into extra-host variations and mutations that lead to variants.

The research team studied intra-host Single Nucleotide Variations (iSNV) using a sequencing platform called Illumina. The identification of iSNVs can help in the identification of key sites in the viral RNA that are important for its survival and spread. It also helps in the design of therapeutic protocols to treat COVID-19 infections, and to know the differences in individual and population responses to the infection.

An important distinction of this research study is that it was conducted primarily by a team of computational graduates from across distant locations, proving that the pandemic has generated novel cooperation, sharing, and resource-sharing modes for innovative research.

The research was initiated at the Council of Scientific and Industrial Research-Institute of Genomics and Integrative Biology (CSIR – IGIB, (Delhi), and was led by IIT Jodhpur and Institute of Life Sciences (Bhubaneswar). Other collaborating institutes are the Academy of Scientific and Innovative Research (Ghaziabad), Council of Scientific and Industrial Research – Center for Cellular and Molecular Biology (CSIR-CCMB), (Hyderabad), and National Center for Disease Control (NCDC), (New Delhi).