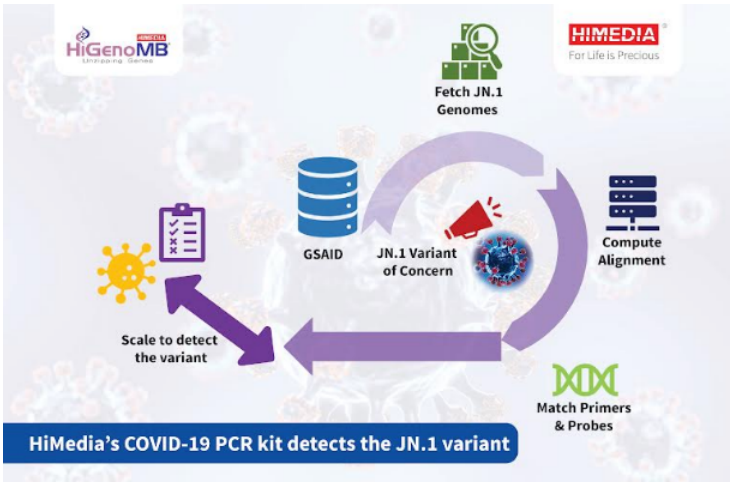
BioSpectrum
the business of Bi
24 years of leveraging the business of Bio
www.biospectrumindia.co

HiMedia launches COVID-19 PCR Kit to detect JN.1 variant

26 December 2023 | News

Bioinformatics experts team at Hi-Gx360Â® analysed the latest genome sequencing data available from GSAID in depth



HiMedia Laboratories has announced that its RT-PCR kits are capable of detecting the recently discovered JN.1, SARS-CoV-2 variant. The portfolio includes:

- MBPCR243 - Hi-PCR® Coronavirus (COVID-19) Multiplex Probe PCR Kit
- MBPCR255 - Hi-PCR® Triplex COVID-19 Detection Kit
- MBPCR262 - Hi-PCR® COVID FLU Multiplex Probe PCR Kit
- MBPCR270 - Hi-PCR® COVID FLU RSV Multiplex Probe PCR Kit

JN.1 (BA.2.86.1.1) is a descendant of the BA.2.86 (Pirola). Pirola is the nickname of the BA.2.86 variant of Omicron, a variant of SARS-CoV-2. The number of cases caused by JN.1 and its close relative Pirola is on the rise all over the world.

The first case of this variant was detected in Denmark in August and later in USA. Cases of JN.1 have been found in some European countries, in Singapore, in China, and recently in Kerala, Maharashtra and in other states across India.

The company has tested the impact of the variant on its Multiplex PCR Kit. Mutations, especially in RNA viruses like SARS-CoV-2 were expected and strain JN.1 is an example of the same. Its immune-escape capabilities have made it a variant of concern.

“Multiplexing has the substantial advantage of increased accuracy of data normalization, more data and higher throughput with limited samples in addition to sensitive and specific detection of multiple targets while eliminating the possibility of false positives, all in just one single run” says Dr Rajas V Warke – Director of HiGenoMB® and Virology, HiMedia Labs.

To determine whether their RT-PCR kits can detect the JN.1 variant of the virus, the bioinformatics experts team at Hi-Gx360® analysed the latest genome sequencing data available from the Global Initiative on Sharing All Influenza Data (GSAID) in depth.

DNA sequences are dynamic; the potential of the sequences to mutate due to errors in DNA replication caused by various genetic or acquired possibilities makes it imperative to keep learning and upgrading kits for attaining accuracy in diagnosis. In summary, based on the company's comprehensive bioinformatics analysis, all of above mentioned kits can detect the JN.1 variant.