

Related Work

- The COVIDSeq approach also offered insight into SARS-CoV-2 isolates' genetic epidemiology and evolution. A sig- to-a large number of genomes that had an insight into the prevalent lineage/clades of the virus could be carried out for this phylogenetic examination [23–25]. The analysis also reports for the first time in two lines B.1.112 and B.1.99.India. Indian. In previous reports, B.1.112 and B.1.99 were reported respectively from the USA and UK. Implies their origin, distribution and possible introductions to India beyond India. Travellers from those countries would need more information to confirm this the asumption.
 - Our analysis shows that the technical duplicates and the high concurrence of SARS-CoV-2 detection between COVIDSeq approaches and RT-PCR approaches are highly consistent. Our comparative analysis of the RT-PCR and COVIDSeq SARS-CoV-2 Detecting test has shown that the COVIDseq test is comparable to that of RT-PCR in terms of sensitivity, precision and accuracy. COVIDSeq protocol, deleted from RT-PCR assays, suggest a comparable sensitivity of a sequence-based test compared to RT-pCR in samples precluded as non-conclusive (21/35) and pan- sardine (16/ 43) and negative (6/19).. This was spilled into 43/97 additional samples and a potential 5.71 percent gain in all the samples.
 - Finally, our analysis suggests that COVIDSeq is a high performance, high-performance, SARS-Co V-2, based approach. COVIDSeq also has an additional benefit to enable SARS-CoV-2 genetic epidemiology.
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 - ❑ Langat P, Raghwani J, Dudas G, Bowden TA, Edwards S, Gall A, et al. Genome-wide evolutionary dynamics of influenza B viruses on a global scale. PLoS Pathog. 2017; 13: e1006749. <https://doi.org/10.1371/journal.ppat.1006749> PMID: 29284042