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High throughput detection and genetic epidemiology of SARS-CoV-2 using COVIDSeq next-generation sequencing

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Abstract

The rapid development of the 2019 Coronavirus Disease (COVID-19), a global pandemic which affects millions of people globally, requires sensitive and high-performance approaches for diagnosing, monitoring and determining the SARS-genetic CoV-2's epidemiology. In this study we used the protocol COVIDSeq involving multiple-plex-PCRs, bar-coding, and the sequencing of high-throughput samples and decided to support SARS-genetic CoV-2's epidemiology. We used 752 clinical samples out of a total of 1536 samples. A thorough analysis revealed a number of six highly confidential COVIDSeq samples that detected SARS-CoV-2 in RT-PCR in 21 and 16 samples classified as inconclusive and pan-sarbon positive respectively suggesting that COVIDSeq could be used as a confirmatory test. Thus, we have analysed COVIDSeq as an additional advanced tool for the development of SARS-CoV-2 gene epidemiology as a potential high sensitivity test.

Introduction

Coronavirus 2019 (COVID-19) is the world pandemic that affects millions of people around the globe, imposing enormous burdens on national health and socio-economic welfare systems. Methods used for testing are mainly subdivided into serological antigen-antbody based tests, nuclear acid-based amplification testing, and sequencing based assays. Some of these approaches have also been adapted to enable higher performances. While serological tests are high-sensitivity and low-specific tests.The Gold Standard for detection and diagnosis has been Nucleic acid-based amplifica refractological treatment, such as quantitative real-time PCR (QRT-PCR), but the negative RT-PCR does not prevent infection in clinical cases which are suspected. The rapid advanced sequence sequencing and analysis techniques of the next generation have enabled us to understand and interpret the genetic makeup of SARS-CoV-2 and its epidemiological evolution. The full SARS-CoV-2 genome sequence was decidibated by viral RNA sequencing from the initial cluster of cases. This study describes application of the recently approved COVIDSeq Protocol for clinical use by the US Food and Drug Authority (US FDA). The protocol provides for the high performance detection and genetic epidemiology of SARS-CoV-2 iso to be used in one sequence with a multiplex amplicon-based PCR enrichment and with barcodes with a performance of 1536 samples using the NovaSeq S4 flow cell. Our analytical assessment suggests that the protocol COVIDSeq may be a sensitive detection approach, with genetic genetic epidemiological insight available. This is the first COVID realistic assessment to our best knowledge.