Busta n. 1

QUESITO 1

Il candidato illustri la tecnologia di sequenziamento Sanger

QUESITO 2

Il candidato illustri il significato delle mutazioni della proteina spike del virus SARS-CoV-2

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Busta n. 2 - PROVA ESTRATTA

QUESITO 1

Il candidato illustri la tecnologia di sequenziamento Ion Torrent

QUESITO 2

Il candidato illustri la classificazione TIER delle mutazioni somatiche nei tumori

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Busta n. 3

QUESITO 1

Il candidato illustri la tecnologia di sequenziamento WNGS

QUESITO 2

Il candidato illustri il ruolo dei microRNA circolanti

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Materie oggetto del concorso

1. Il concetto di lesione mucositica da trattamento antitumorale
2. Analisi bioinformatica di profili di espressione di micro RNA
3. Ruolo della piattaforma GISAID e piattaforma Icogen nella pandemia da SARS-CoV-2

Informatica

1. Cos'è un sistema operativo?
2. Cos'è un virus informatico?
3. Cos'è un cloud storage?

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Global SARS-CoV-2 genomic surveillance: What we have learned (so far)

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Abstract

The COVID-19 pandemic has brought significant challenges for genomic surveillance strategies in public health systems worldwide. During the past thirty-four months, many countries faced several epidemic waves of SARS-CoV-2 infections, driven mainly by the emergence and spread of novel variants. In that line, genomic surveillance has been a crucial toolkit to study the real-time SARS-CoV-2 evolution, for the assessment and optimization of novel diagnostic assays, and to improve the efficacy of existing vaccines. During the pandemic, the identification of emerging lineages carrying lineage-specific mutations (particularly those in the Receptor Binding domain) showed how these mutations might significantly impact viral transmissibility, protection from reinfection and vaccination. So far, an unprecedented number of SARS-CoV-2 viral genomes has been released in public databases (i.e., GISAID, and NCBI), achieving 14 million genome sequences available as of early-November 2022. In the present review, we summarise the global landscape of SARS-CoV-2 during the first thirty-four months of viral circulation and evolution. It demonstrates the urgency and importance of sustained investment in genomic surveillance strategies to timely identify the emergence of any potential viral pathogen or associated variants, which in turn is key to epidemic and pandemic preparedness.

Keywords: SARS-CoV-2, Viral evolution, Genomic surveillance, Epidemic-pandemic preparedness

1. SARS-CoV-2: an emerging threat of international concern

In late December 2019, The World Health Organization (WHO) office in China was informed about a cluster of novel cases of pneumonia of unknown aetiology detected in the city of Wuhan, Hubei province (Huang et al., 2020; Wu et al., 2020) (Fig. 1). Shortly afterwards, a new type of coronavirus, later named SARS-CoV-2, was isolated and identified by the Chinese authorities and its genetic sequence was shared with the international community on 10 January 2020 (Zhou et al., 2020) (Fig. 1). The coronavirus disease 2019 (COVID-19) caused by SARS-CoV-2 was classified as a pandemic on 11 of March 2020 (Cucinotta and Vanelli,