Introduction

In late December 2019, pneumonia of unidentified cause was first reported in Wuhan, China .Clinical diagnosis using various commercialized assays targeting multiple common respiratory pathogens failed to identify the causative agent. However, the next-generation sequencing (NGS) of clinical samples, particularly bronchoalveolar lavage fluid from the first group of patients, soon identified a novel coronavirus. later named severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2).In this article we summarize (NGS) approaches for SARS-CoV-2 discovery and surveillance. **NGS is also known as “**high-throughput sequencing**”** which has become one of the most used approaches in the virusresearches. as themetagenomics has proven **to be** highly efficient approachin the discover of virus**.** And in the case of theabundance of the target virus ‘SARS-CoV-2’**, t**he metagenomic approach worksbetter **.**The efficiency of the discover of the virus is depend on the bioinformatics tools used in the downstream and this because of the ‘NGS’, which usually generate a lot of sequencing reads with or without a priori knowledge of SARS-CoV-2. There are an important steps to make the typical NGS workflow and there are a lot of applications available for every step . And the resources for ‘SARS-CoV-2’ discovery and genomic surveillance are exist.Quality control of NGS data w**h**ich is known as ‘ Quality profiling ‘, in this step the NGS raw data is preprocessed for the subsequent analysis **,** Removal of the host\rRNA data : the next challengeafter the Quality controlis to process a huge amounts of the data efficiently **,**Reads assembly: there is approach called ‘De novo assembly’ and this is the best in the context of emerging infectious diseases where no reference genomes are av**ailable,**Taxonomic classification : this is the next step after the reads are assembled into contigs, to assign contigs to a specific taxon **and** Virus genome classification : after the contigs are extracted**.**challenges remain when employing NGS data for virus discovery, especially when proportion of virus reads is very low. As a consequence, we should understand better virosphere and this requires more adequately validated methods and advances in computational .Abstract

In early January 2020, the novel coronavirus (SARS-CoV-2) responsible for a pneumonia outbreak in Wuhan, China, and we identify it using the next-generation sequencing (NGS) and readily available bioinformatics pipelines. In addition to the discover of the virus, and these NGS technologies and the resources of bioinformatics are currently used for ongoing genomic surveillance of SARS-CoV-2 worldwide, tracking its evolution and patterns of variation on the global scale. In this review, we summarize the resources of bioinformatics that used for the discovery and surveillance of SARS-CoV-2 and the Bioinformatics resources for genomic and evolutionary analyses like :‘ Multiple sequence alignment’ ,the Accurate multiple sequence alignment (MSA) is the foundation of all the sequence analyses of the comparative genome. also there are the Phylogenetic and evolutionary analyses which is the central to understand the evolution and the emergence of SARS-CoV-2 and also can be estimated by a variety of approaches or methods .Also we dedect coronavirus recombination as we know that the Coronaviruses have undergone frequent recombination so the occurrence of this process should be considered carefully and by using the homology modeling.And finally , we can say that the generation of such a huge amount of the data represents both a challenge and an achievement. And we can say that the technical advances in NGS and bioinformatics enabled us to identify the causative agent of COVID-19 rapidly.