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Short Communication

Understanding the genetics of COVID-19

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ABSTRACT

The genome of SARS-CoV-2 is composed of a single strand of RNA with a positive strand (ready for translation and consequent synthesis of its proteins). The genome is considered large, with 29,903 base pairs. There are at least 50 different sites where translation can begin (open reading frames – ORFs). These ORFs are each of the RNA sequences understood to include a start codon (AUG), a stop codon (UAG, UAA, or UGA), and the codons between them. This variable origin of transcription sequences allows the SARS-CoV-2 virus to encode for around 50 proteins that have non-structural, structural, and accessory functions.

Keywords: SARS-CoV-2; Genomics; Nucleotide

INTRODUCTION

The initial two-thirds of the RNA sequence encode the two main transcriptional units, ORF1a and ORF1ab; these units encode two polyproteins (PP1a and PP1ab, respectively). The larger unit, PP1ab, contains ORFs for at least 16 non-structural proteins (Nsp1−16) [1]. The non-structural proteins have various functions in biological phenomena that are important for the virus such as replication, correction of replication errors, translation, suppression of host proteins, immune response blockage, and RNA steadying. The final third of the RNA encodes proteins that define the structure of SARS-CoV-2 as well as accessory proteins. Addition genes are distributed among the genes that encode structural proteins and the 3' end of the genome and contain at least nine ORFs for accessory proteins; these proteins are not significant for viral replication but play an important role in interactions between the virus and host, including modulating and blocking the production of pro-inflammatory cytokines. Finally, three proteins that structure the virus, known as the spike (S), membrane (M), and envelope (E), are embedded in the outer membrane and give the virus its distinct shape and structure [2]. Inside the virus particle, the RNA is tightly coiled and coated with a fourth structural protein, nucleocapsid (N), which protects its genetic material. New data shows a high-resolution map of the SARS-CoV-2 coding regions, allowing to accurately quantify the expression of canonical viral ORFs and to identify 23 unannotated viral ORFs. The new ORFs recognized may serve as novel accessory proteins or as regulatory units controlling the balanced production of different viral proteins. SARS-CoV-2 genome in record time and study it in detail could make all the difference in how we deal with this intimidating pandemic. Savings in local industrial installations that can produce reagents for molecular biology and pharmaceuticals, as well as in genetic research and in human and institutional resources for studying genomes have clearly become a strategic objective for every country that wants to be self-sufficient now and during future pandemics [3,4]. Individuality in this field of knowledge is not a matter of status or elitism, but rather is vital for sympathetic the epidemiology and spread of these infectious agents among our population, quickly knowing potential evolutionary changes, diagnosing individuals through the genomic testing of these infectious agents, understanding clinical and therapeutic variability, and emerging safe and effective vaccines with the degree of urgency that is obviously necessary to combat COVID-19.

CONCLUSION

The main limitations of this review come from what is still unidentified concerning the genetics of COVID-19, the unparalleled volume and speed of scientific information about COVID-19 with new data accumulating on a daily basis, and the fact that we are writing it in the middle of the pandemic. For sure there will be valuable new information not comprised in this review by the time it is published. Even so, this narrative

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review should be useful as a basis for sympathetic the genetics of COVID-19.

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