GENOMIC STUDY OF COVID-19 CORONA VIRUS EXCLUDES ITS ORIGIN FROM RECOMBINATION OR CHARACTERIZED BIOLOGICAL SOURCES AND SUGGESTS A ROLE FOR HERVS IN ITS WIDE RANGE SYMPTOMS

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The COVID-19 corona virus has become a world pandemic which started in December 2019 in Wuhan, China with no confirmed biological source. Various countries reported the genomic sequence of different isolates obtained from infected patients. This allowed us to obtain a number of 38 isolates of full genomic sequences. Alignment of nucleotide (nt) sequence was carried out using Clustal Omega multiple alignment service at the EBI website. Alignment of nt sequence and phylogenetic relationship revealed that the COVID-19 is a new viral strain and its biological source has not been yet detected. The expected orf pattern was different among isolates obtained from the same country or different countries as well as from SARS-CoV isolates or bats CoV suggesting different virus human interaction possibilities during infection and severity. All isolates had the main five orfs (1ab, S, M, N, E), whereas they differed in the expected accessory orfs. Being with the biological source of COVID-19 undetected, the role of human endogenous retrovirus (HERVs) in the regulation of the host cell gene expression or the encoding for products that could modulate COVID-19 infection and the spectrum of its symptoms is discussed.

Key words: *COVID-19, genome, nucleotide sequence alignment, Human endogenous retroviruses (HERVs).*

ГЕНОМНЕ ДОСЛІДЖЕННЯ КОРОНАВІРУСА COVID-19 ВИКЛЮЧАЄ ЙОГО ПОХОДЖЕННЯ ВІД РЕКОМБІНАЦІЇ ЧИ З ОПИСАНИХ БІОЛОГІЧНИХ ДЖЕРЕЛ І ПРИПУСКАЄ РОЛЬ HERV У ШИРОКОМУ ДІАПАЗОНІ ЙОГО СИМПТОМІВ

COVID-19 – це викликане коронавірусом захворювання, яке переросло у всесвітню пандемію, початок якої було зафіксовано у грудні 2019 р. у місті Ухань, Китай, але біологічне джерело якого не було підтверджено. У різних країнах повідомляли про геномну послідовність різних ізолятів, отриманих від інфікованих пацієнтів. Це дозволило нам загалом отримати 38 ізолятів повних геномних послідовностей. Вирівнювання нуклеотидної (nt) послідовності проводили за допомогою множинного вирівнювання Clustal Omega на веб-сайті Європейського інституту біоінформатики (EBI). Вирівнювання нуклеотидної послідовності і філогенетичний зв'язок показали, що COVID-19 – це новий штам віруса, біологічне походження якого ще не було встановлено. Очікувана структура orf була різною серед ізолятів, отриманих з однієї країни або різних країн, а також ізолятів SARS-CoV чи CoV кажанів, що дозволяє припустити різні можливості взаємодії віруса та людини під час інфікування та складності захворювання. Всі ізоляти мали п'ять основних orfs (1ab, S, M, N, E), однак, відрізнялися очікуваними допоміжними orfs. Оскільки біологічне джерело COVID-19 залишається невстановленим, було обговорено роль ендогенних ретровірусів людини (HERV) у регуляції експресії генів клітин господаря чи кодування продуктів, які можуть модулювати інфекцію COVID-19 і спектр її симптомів.

Ключові слова: COVID-19, геном, вирівнювання нуклеотидної послідовності, ендогенні ретровіруси людини (HERV).

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