K **:** COVID$_{19}$; SARS-*C* *V*$_2$; Asymptomatic patient; Physical exercise; Good nutrition

I c

e rst scienti c study describing *C* *a* (HC *V* - human *C* *a*) as a disease promoter human was released in the 1960s, although, the virus was initially founded in *Ga* *a* *d* *e* *c* birds in 1930 [1]. Currently, coronaviruses are classi ed in the order *N d* *a e* , subfamily *O* *c* *a* *ae* and subdivided in four genus: *A* *ac* *a* (-*C* *V*), *Be ac* *a* (-*C* *V*) and some members belonging to *Ga* *ac* *a* (-*C* *V*) are pathogens to mammalian, although some strains belonging to genus -*C* *V* and *De* *ac* *a* (-*C* *V*) have adapted to cause disease in avian. Among the viral strains classi ed as HC *V*, the following stand out: -HC *V*$_{229E}$, -HC *V*$_{NL63}$, -HC *V*$_{OC43}$, -HC *V*$_{HKU1}$, -MERS-*C* *V*, -SARS-*C* *V* and -SARS-*C* *V*$_2$.

e strains -HC *V*$_{229E}$ and -HC *V*$_{OC43}$ rst identi ed in the mid-1960s [1-3], are closely related with the common cold syndrome and pneumonia [4-8], uncommonly causing severe diseases. It was also reported that both strains can cause LRTI (Lower Respiratory Tract Infections) and otitis media [3]. Often this virus is detected in co-infections with other strains of viruses and bacteria resulting respiratory infections [4 ,9-11]. In addition, this virus also is widely distribution worldwide with seasonal outbreaks [12]. HC *V* infections have been described for decades, occurring in 2- to 3-year cycles [13], with seasons of high infections rates caused by strains -HC *V*$_{229E}$ or -HC *V*$_{OC43}$ and sporadic infections caused by strains belonging to the others HC *V* groups [12].

e strain -HC *V*$_{NL63}$ was reported for the rst time in 2004 in a baby from Netherlands suffering from bronchiolitis [11,14]. However, this strain seems to affect mostly immunocompromised children inducing symptoms as cough, fever, and rhinorrhea or severe LRTI,

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may be due to the cytopathic effect mediated by local replication of the SARS-*C V*; or indirectly as a result of systemic responses to respiratory failure or the harmful immune response induced by viral infection.

In 2012, the outbreak of a new *C V* capable of causing Middle East respiratory syndrome (MERS-*C V*) was reported, being the rst case occurred in Kingdom of Saudi Arabia (KSA), recording at least 2468 cases and 851 deaths worldwide [19]. Another well-documented case of MERS-*C V* occurred in May 2015, according to information from Korea Centers for Disease Control and Prevention (2015), an infected individual returning from the Middle East started the outbreak of MERS-*C V* in South Korea, which spread over 16 hospitals and 186 patients. On the next year, were reported 1,728 con rmed new cases of MERS-*C V*, and 624 deaths were noti ed in 27 countries [20]. In 2018 a new outbreak of MERS-*C V* was recorded in the Saudi Arabia [21], with 96 new cases. After these outbreaks of MERS-*C V*, very year's new cases are documented, usually associated with infected travels; often, these imported MERS cases resulted in nosocomial transmission [19]. Symptoms of MERS-*C V* are fever, cough and upper respiratory tract (URT) signs and symptoms usually occur rst, followed within a week by progressive LRT distress and lymphopenia[22].

e current pandemic of COVID$_{19}$ (*CO*rona*VI*rus*D*isease and 19 refers to year 2019, was rst reported at Wuhan, China. e clinical manifestations are very similar to SARS-C *V* infection (for that reason it was described as SARS-*C V*$_2$). Elderly population stands out as the group with the highest risk, especially those that feature previous comorbidities [23]. In addition, Jordan and collaborators (2020), reported that the restrictions imposed as a control measure during SARS-*C V*$_2$ pandemic, may lead elderly people to experience loneliness, isolation and loss of mental and physical stimulation, which could increase the severity of infection.

G c c a ac c *CoV*

*C V*s are featured by a positive single-stranded RNA. At the molecular level, *C V*s usually feature high mutation rate due to the propensity of errors during their replication [23-25]. It has been shown that these viruses naturally present 20% homologous RNAs recombination mixed infections with different viral strains the same group [23].

Genetic recombination and point mutations in the genome of *C V*s can be considered as mechanisms of adaptation between strains, since it is speculated that HC *V*$_{NL63}$ has arisen from the evolution of HC *V*$_{229E}$[26]. In 2018, Chinese scientists reported a new genotype of strain HC *V*$_{OC43}$, named H by Zhu and collaborators (2018). It is possible that the H strain emerged as a result after genetic recombination involving seven other stains of HC *V*$_{OC43}$[27], previously identi ed as HC *V*$_{OC43}^{a}$ - HC *V*$_{OC43}^{g}$. In 2006 was described the circulation of HC *V*$_{HKU1}$ strain throughout the United States, however, with genetic differences from the stain originally identi ed in Hong Kong, revealing the easy adaptation of *C V* strains to different environmental and climatic conditions [28].

Scienti c approaches involving *c* simulation have been useful to address may hypotheses. In 2006, a prospective study developed by [29], using *c* predictions, analyzed 25 variants of HC *V*$_{229E}$ disseminated in Australia, described during the years of 1979 to 2004. In the study, gene product S and N (spike protein and nucleoprotein) were selected, considering them primary role of facilitates the virus binding to the host cell. In this research the authors concluded that S protein has not mutated over the years, therefore, a type of positive selection mechanism exists, and probably are one of the mechanisms responsible for the emergence of new viral strains [29]. ese results were corroborated by Li and collaborators (201.lqn considering them

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Test	Results	Method	Reference value
Triglycerides	263 mg/dL	Enzymatic	< 150 mg/dL
Total cholesterol	218 mg/dL	Direct enzymatic	< 200 mg/dL
HDL	48.5 mg/dl	Colorimetric without precipitation	23-92 mg/dl
LDL	106.0 mg/dL	Direct enzymatic	< 130 mg/dL
VLDL	52.6 mg/dL	Calculation	< 40 mg/dL
Glucose	88 mg/dL	Enzymatic	70 – 99 mg/dL
Vitamin D	27.7 ng/mL	Chemiluminescence – LIAISON DiaSorin	
Vitamin B12	566 pg/mL	immunoassay – Immulite 2000 XPI – Siemens	193 – 982 pg/mL
Calcium	7.8 mg/dL	Colorimetric	8.6 – 10.3 mg/dL
Magnesium	2.2 mg/dL	Colorimetric	1.9 – 2.7 mg/dL
Urea	31 mg/dL	Kinetics	15 – 43 mg/dL
Creatinine	0.9 mg/dL	Colorimetric	0.6 – 1.3 mg/dL
Alkaline phosphatase	59 U/L	Enzymatic	34 – 104 U/L
GGT	62 U/L	Colorimetric	9 – 64 U/L
TGO	22 U/L	Enzymatic	13 – 39 U/L
TGP	30 U/L	Enzymatic	7 – 52 U/L
Serum phosphorus	3.5 mg/dL	Colorimetric	2.5 – 5 mg/dL
Chlorine	106 mEq/L	Colorimetric	98 – 107 mEq/L
Sodium	139 mEq/L	Colorimetric	136 – 145 mEq/L
Potassium	4.4 mEq/L	Colorimetric	3.5 – 5.1 mEq/L
TSH	1.030 µlU/mL	Microparticle chemiluminescent immunoassay – Immulite – Siemens	1.01 ng/dL
Free thyroxine (T4)	1.01 ng/dL	Microparticle chemiluminescent immunoassay – Immulite – Siemens	2000 XPI 0.89 – 1.79 ng/dL

Table 1: Laboratory tests requested for Biochemical analysis, method used for diagnosis and reference values adopted at the Hospital Geral Dr. César Cals, Fortaleza-CE.

5. Pene F, Merlat A, Vabret A, Rozenberg F, Buzyn A (2003) Coronavirus 229E-related pneumonia in immunocompromised patients. Clin Infec Dis 37:929-932.

6. Vabret A, Mourez T, Gouarin S, Petitjean J, Freymuth F (2003) An outbreak of Coronavirus OC43 respiratory infection in Normandy, France. Clini Infect Dis 36:985-989.

7. Pfefferle S, Oppong S, Drexler JF, Gloza-Rausch F, Ipsen A, et al. (2009) Distant relatives of severe acute respiratory syndrome Coronavirus and close relatives of human Coronavirus 229E in bats, Ghana. Emerg Infec Dis 15:1377-1384.

8. Vassilara F, Spyridaki A, Pothitos G, Deliveliotou A, Papadopoulos A (2018) A Rare case of human Coronavirus 229E associated with acute respiratory distress syndrome in a healthy adult. Hindawi 6796839:1-4.

9. Golda A, Malek N, Dudek B, Zeglen S, Wojarski J, et al. (2011) Infection with human Coronavirus NL63 enhances streptococcal adherence to epithelial cells. J Gen Virol 92:1358-1368.

10. Zhao M, Li G, Zhang D, Zhou H, Wang H, et al. (2017) Clinical evaluation of a new single-tube multiplex reverse transcription PCR assay for simultaneous detection of 11 respiratory viruses, Mycoplasma pneumoniae and Chlamydia in hospitalized children with acute respiratory infections. Diag Microbiol Infect Dis 88:115-119.

11. Liu DX, Liang JQ, Fung TS (2020) Human Coronavirus-229E, -OC43, -NL63, and -HKU1. Ref Mod Life Sci 1-13.

12.

50. Korea Centers for Disease Control and Prevention (2015) Middle East respiratory syndrome Coronavirus outbreak in the Republic of Korea, 2015. Osong Pub Health Res Persp 6:269-278.

51. Li Z, Tomlinson ACA, Wong AHM, Zhou D, Desforges M, et al. (2019) The human Coronavirus HCoV-229E S-protein structure and receptor binding. eLIFE 8:e51230.

52. Kizilbash SJ, Ahrens SP, Bruce BK, Chelimsky G, Driscoll SW, et al. (2014) Adolescent Fatigue, POTS, and Recovery: A Guide for Clinicians. Curr Prob Pediat Adol Health Care 44:108-133.

53. Woo P, Lau S, Yip C, Huang Y, Yuen KY, et al. (2009) More and more Coronaviruses: Human Coronavirus HKU1. Viruses 1:57-71.

54. Pan Y, Li X, Yang G, Fan J, Tang Y, et al. (2020) Serological immunochromatographic approach in diagnosis with SARS-CoV-2 infected COVID-19 patients. J Infect 81:e28-e32.

55. Clark A, Jit M, Warren-Gash C, Guthrie B, Wang HHX, et al. (2020) Global, regional, and national estimates of the population at increased risk of severe COVID-19 due to underlying health conditions in 2020: A modeling study. Lancet Glob Health 8: e1003-e1017.

56. Simmons G, Reeves JD, Rennekamp AJ, Amberg SM, Piefer AJ, et al. (2004) Characterization of severe acute respiratory syndrome-associated Coronavirus (SARS-CoV) spike glycoprotein-mediated viral entry. PNAS 101:4240-4245.