Asian Journal of Biochemistry, Genetics and Molecular Biology

Volume 14, Issue 3, Page 29-38, 2023; Article no.AJBGMB.100635
ISSN: 2582-3698

Biomolecular Features of COVID-19 in Hodeidah, Yemen

Mohammed Amood AL Kamarany [a,b#*], Tarik Abdulkarim [bπ] and Mahfouz Nasser [a,cΨ]

[a] Center for Tropical Medicine and Epidemiology Studies, Hodeidah University (CTMES – HU) Hodeidah, Yemen.
[b] Center of Tropical Medicine and Infectious Diseases (CTMID), Al-Thawara Public Hospital Authority, Hodeidah, Yemen.
[c] National Center for Public Health Laboratories (NCPHL), Hodeidah, Yemen.

Authors' contributions

This work was carried out in collaboration among all authors. Author MAAK wrote, revised and edited the final manuscript and responsible for summarizing all data. Author TA analyzed the samples and data collection. Author MN contributed in revision of manuscript. All authors read and approved the final manuscript.

Article Information

DOI: 10.9734/AJBGMB/2023/v14i3317

Open Peer Review History:
This journal follows the Advanced Open Peer Review policy. Identity of the Reviewers, Editor(s) and additional Reviewers, peer review comments, different versions of the manuscript, comments of the editors, etc are available here: https://www.sdiarticle5.com/review-history/100635

Original Research Article

Received: 11/04/2023
Accepted: 13/06/2023
Published: 04/07/2023

ABSTRACT

Background: The biomolecular technique namely Real-Time Polymerase Chain Reaction (RT-PCR) is very important in confirmation of coronavirus disease 2019 (COVID-19) but in progressive infection and predication of the illness severity is not used.
Objective: Therefore, the study aimed to determine the relationship between the viral load of COVID-19 infection and the severity of illness based on cycle threshold (Ct).
Methodology: The research was designed in a case series study. The study included 60 patients that were confirmed by the RT-PCR test with COVID-19 and divided into two major groups. The first major group was mild and moderate cases (n:20) that were treated at home (outpatient) and the second major group was severe and critical cases (n:40) that were treated in the isolation center (inpatient).

[#] Associated Professor in Pharmacology of Infectious, Epidemic Diseases and Tropical Medicine and scientific consultant on COVID-19 humanitarian project in Hodeidah, Yemen and – Dean of CTMES – HU;
[π] Researcher in Master Public Health (MPH) and National Expert in Molecular Biology;
[Ψ] PhD Biotechnology and Lecture in Molecular Biology in CTMES – HU;
**Corresponding author: E-mail: alkamarany@gmail.com;*

Results: The results showed no relationship between the viral load and severity of illness, where the minimum Ct was 14, and the maximum Ct was 36. The mean of Ct was 22 ± 7. On the other hand, the low Ct (high viral load) was reported in early detection cases. In addition , 60% (36 cases) of patients had low Ct (high viral load ; Ct ≤ 15 and ≤ 25) 40% of patients (24 cases) had high Ct (low viral load ; Ct ≤ 26 and ≤ 39) that was more than 25 Ct and less than 39 cycles . On the other mean , 95 % of first group cases (mild and moderate cases) had high viral load based on Ct -values and 42.5 % of second group (severe and critical) had low viral load based on Ct -values. On the other hand, kinetic of viral load–based Ct where the viral load was reported in the first week as very high (low Ct 21) with a longitudinal assessment of RT-PCR test results in individuals requiring third –fourth weeks to clear COVID-19 RNA showed a significant reduction of the viral load in samples (Ct values > 30).

Conclusion: The study concluded that several factors can affect the Ct of RT-PCR (onset date, collection technique, type of swab, sampling method). Briefly, the COVID-19 RT-PCR test cannot be used as a predictor of the severity of illness.

Keywords: COVID -19; bio-molecular; viral load; cycling threshold; Hodeidah; Yemen.

1. INTRODUCTION

"Coronavirus disease 2019 (COVID-19), is a severe acute respiratory syndrome and a new infectious disease that first emerged in Hubei province, China, in December 2019, which was found to be associated with a large seafood and animal market in Wuhan. One of the most important ways of virus transmission is a human-to-human transmission which is primarily achieved through close contact with respiratory droplets, direct contact with the infected individuals, or contact with contaminated objects and surfaces" [1]. "Coronaviruses belong to the order Nidovirales, family Coronaviridae, and subfamily Orthocoronavirinae, are spherical (125nm diameter) and enveloped with club-shaped spikes on the surface giving the appearance of a solar corona. Within the helically symmetrical nucleocapsid is the large positive sense, single-stranded RNA. The coronaviral genome contains four major structural proteins: the spike (S), membrane (M), envelope (E), and the nucleocapsid (N) protein, all of which are encoded within the 3' end of the genome. The S protein mediates attachment of the virus to the host cell surface receptors resulting in fusion and subsequent viral entry. The M protein is the most abundant and defines the shape of the viral envelope. The E protein is the smallest of the major structural proteins and participates in viral assembly and budding. The N protein is the only one that binds to the RNA genome and is also involved in viral assembly and budding" [2,3]. "A novel coronavirus is the seventh member of the coronavirus family to infect humans. Phylogenetic analysis of full-length genome sequences obtained from infected patients showed that severe acute respiratory syndrome coronavirus ***2*** (SARS-CoV-2) is similar to severe acute respiratory syndrome coronavirus (SARS-CoV) and uses the same cell entry receptor, angiotensin-converting enzyme 2 (ACE2), as SARS-CoV" [4,5]. "Many infected individuals develop COVID-19 with fever, cough, and shortness of breath that can progress to pneumonia. Disease progression promotes the activation of immune cells, platelets, and coagulation pathways that can lead to multiple organ failures and death" [6].

"An effective strategy for controlling the COVID-19 pandemic is to develop highly accurate methods for the rapid identification of COVID-19 infected patients. Many companies and institutes are therefore striving to develop effective methods for the rapid detection of COVID-19 RNA" [7]. "Clinically, nucleic acid-based methods are sensitive but prone to false-positive" [8]. "The primers and probe were designed based on the nucleocapsid protein gene (N gene) sequence of COVID-19. The detection limit was 10 copies per reaction in this assay, which could be conducted within 15 min at a constant temperature (39 °C), without any cross-reaction with other respiratory tract pathogens, such as other coronaviruses" [9]. "The diagnosis of COVID-19 is critically dependent on the detection of COVID-19 RNA from clinical specimens (e.g., nasopharyngeal swabs). While laboratory-developed testing for COVID-19 is an essential component of diagnostic testing for this virus, the majority of clinical microbiology laboratories are dependent on commercially available COVID-19 molecular assays. In contrast to assays approved or cleared by the U.S. Food and Drug Administration (FDA) for in vitro diagnostic use, assays for the detection of COVID-19 nucleic

acids have emergency use authorization (EUA) from the FDA. Outside of highly specialized academic and commercial laboratory settings, clinical microbiology laboratories are likely unfamiliar with the EUA classification, and thus, assay verification can be daunting" [10].

"In clinical practice, the SARS-CoV-2 real-time RT-PCR test reports as negative or positive based on a specific Ct value threshold" [11]. "This cut-off is determined by an algorithm that automatically interprets various amplification process parameters. However, there are some uncertainties, such as whether Ct values should be used to predict the level of infectivity and disease severity in SARS CoV-2 patients. RT-PCR and Ct values have been linked to a more complete picture of viral load in COVID-19 deceased. A lower viral RNA load and a lower risk of infection transmission are represented by higher Ct values" [12].

In our study, we aimed to answer this question, Can the bio-molecular techniques (RT-PCR) determine and predict the severity of the illness of COVID-19.

2. METHODOLOGY

2.1 Study Area

The study was carried out in the COVID-19 isolation department, Molecular Biological Unit, Center of Tropical Medicine and Infectious Diseases (CTMID), AL Thawara Public Hospital Authority, Hodeidah Yemen. In this study area 2020, AL Kamarany et al reported 505 COVID-19 patients in 2020. A total of 49/505 cases (9.70 %) were confirmed and admitted to the isolation department. On the other mean, 386 patients (76.43%) with mild and moderate cases, and 70 patients (13.86%) with severe illnesses were treated at home. 21 patients with severe illness (4.16%) and 28 patients (5.54%) with critical illness were treated in the isolation department. 49 patients (9.7 %; severe and critical) needed admission to an intensive care unit (ICU) that were confirmed based on RT-PCR. Other cases (mild and moderate) were confirmed epidemiologically (epidemiologically linked case: A case in which the patient has/ had contact with one or more persons who have/had the disease, and transmission of the agent by the usual modes of transmission is plausible. A case may be considered epidemiologically linked to a laboratory-confirmed case if at least one case in the chain of transmission is laboratory confirmed [13-15]. The study area is high endemic of vector – borne diseases (VBDs) such as dengue, malaria, Chikungunya, west – Nile virus [16-20].

2.2 Study Design

The research was designed in a pilot study and one-time cross-sectional COVID-19 Ct-based viral load measurement that included 60 participants, divided into two groups: the first group included 20 mild and moderate patients of COVID-19 who were isolated and treated at home. The second group (n:40) was severe cases (n:20) and the third group was critical cases (n:20) that treated at the COVID-19 isolation department, CTMID, AL Thawara Public Hospital Authority, Hodeidah Yemen (Fig. 1).

2.3 Real-Time Polymerase Chain Reaction (RT-PCR) for Detection of the COVID-19 Infection

The RT- PCR of COVID-19 detection was re-validated partially in the Molecular Biological Unit of CTMID, AL Thawara Public Hospital Authority of Hodeidah, Yemen. The assay for molecular detection of COVID-19 on nasopharyngeal swabs was performed using the RT-PCR Bio-System. Norgen's COVID-19 TaqMan RT-PCR kit was designed for the detection of COVID-19-specific RNA [24].

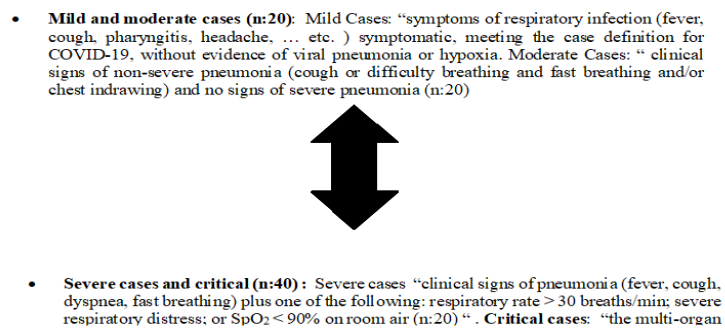

Fig. 1. Study design to determine the relationship between the viral load of COVID-19 infection and severity of illness based on cycle threshold (Ct) in Hodeidah, Yemen [21-23]

2.4 Data Management

A simple statistical process was used, firstly, the RT-PCR was validated to assure the results and secondly, data were collected, checked, and entered in Excel Software 2013, and then the data was analyzed using tables, graphs, percentages, median, range, and average were the main descriptive tools.

3. RESULTS

3.1 Viral Load in Mild, Moderate, Severe and Critical Cases

At symptom onset, the mean Ct - based viral load was 22 ± 7. The viral load change was 1 Ct /day. The highest viral load was 14 Ct on day 2 and the lowest viral load was Ct 36 on day 41. The earliest and latest positive results were on day 1 and day 42. In addition, 60% (36 cases) of patients had low Ct (high viral load ; Ct ≤ 15 and ≤ 25) and 40% of patients (24 cases) had high Ct (low viral load ; Ct ≤ 26 and ≤ 39) (Table 1). On the other mean, 95 % of first group cases had high viral load based on Ct -values and 42.5 % of second group had low viral load based on Ct -values (Figs. 2 and 3).

3.2 Kinetic of Ct-based Viral Load in COVID-19 Patients

Fig. 4 showed the kinetics of viral load–based Ct where the viral load was reported in the first week as very high (low Ct 21) with a longitudinal assessment of RT-PCR test results in individuals requiring fifth - sixth weeks to clear COVID-19 RNA showed a significant reduction of the viral load in samples (Ct values > 30).

Table 1. Viral load in mild, moderate, severe, and critical cases

Ct values	First group (n:20)		Second group (n:40)				Total	
	Mild and Moderate n:20		Severe Cases n: 20		Critical Cases n: 20			
	n	%	n	%	n	%	n	%
15 – 25	19	95	11	55	6	30	36	60
26 – 39	1	5	9	45	14	70	24	40
Total	20	100	20	100	20	100	60	100

- *The chi-square statistic is 18.6678 , the p-value is .0.000088 that is significant at p < .05*

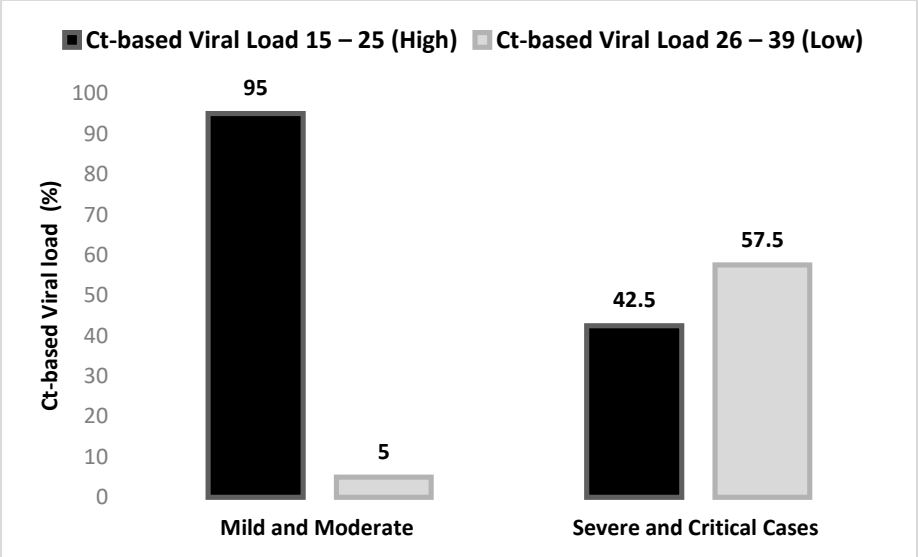

Fig. 2. Viral load in mild, moderate, severe, and critical cases

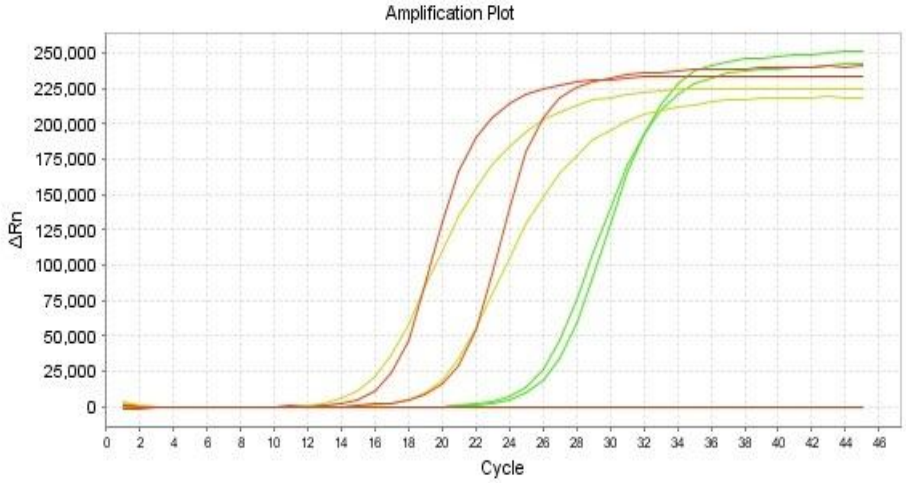

Fig. 3. Amplification plot of Ct-based viral load in COVID-19 patients

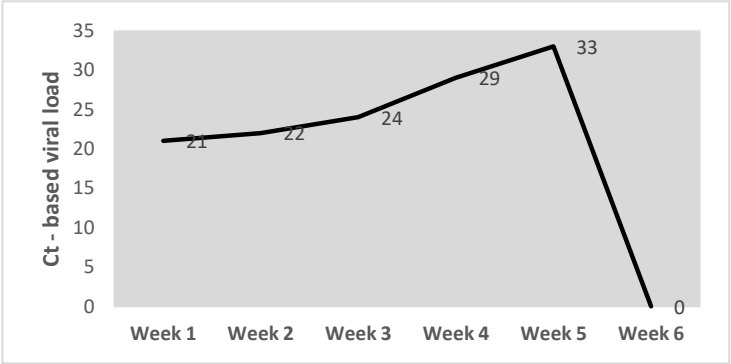

Fig. 4. Kinetic of Ct-based viral load in COVID-19 patient

Table 2. Other factors in in mild, moderate, severe, and critical cases

Risk Factors	Mild and Moderate n:20		Severe Cases n: 20		Critical Cases n: 20	
	n	%	n	%	n	%
Co-morbidity						
Diabetes	1	5	5	25	3	15
Diabetes with chronic diseases	0	0	2	10	3	15
Heart diseases and hypertension	0	0	2	10	3	15
Heart diseases and asthma	0	0	1	5	1	5
Asthma	1	5	2	10	2	10
Renal Failure	1	5	1	5	1	5
Coinfection						
- Tuberculosis	0	0	1	5	1	5
- Hepatitis C	0	0	0	0	1	5
Non	17	85	6	30	6	30
Total	20	100	20	100	20	100

3.3 Other Factors in Mild, Moderate, Severe and Critical Cases

30/40 patients (65.30%) with severe and critical COVID-19 infection were affected significantly by one or more co-morbidity caused by an underlying chronic disease (X^2 = 6.36 and p = 0.0066), the most common of which was diabetes mellitus namely 13 patients (32.5%). 5 (12.5%) of these patients had diabetes alongside other chronic conditions. 5 patients (12.5%) had underlying cardiac disorders and hypertension, of which 2 patients (5.0 %) (also concurrently had respiratory disorders (bronchial asthma). 4 patients (10.0 %) had bronchial asthma without other co-morbidities, and a further 2 patients (5.0 %) suffered from renal failure. 2 patients (5.0%) were identified with coinfections of an infectious disease namely hepatitis C virus (HCV) and tuberculosis (TB). 12 of the patients (30.0 %) did not present with any underlying chronic or infectious disease or related co-morbidity (Table 2).

4. DISCUSSION

"RT-PCR is considered the gold standard confirmatory test for COVID-19. The Ct values are being utilized to diagnose COVID-19 infection" [25,26]. "On the other mean, most RT-PCRs are designed for qualitative COVID-19 reporting (COVID-19 detected or not detected) but have been used for semi-quantitative estimation of viral load based on Ct value" [27,28]. The results showed a significant difference in viral load between mild (outpatients) and severe patients (inpatients needed oxygen therapy) among Hodeidah patients, Yemen. Our results agreed with a previous study by Abdulrahman et al reported that "the viral load, as indicated by Ct values, did not seem to be associated with the requirement for oxygenation on admission" [29]. Another previous study by Shah et al reported that "the patients with mild disease had significantly lower Ct values than patients with severe disease but had also been tested significantly earlier in the illness than those with severe disease. The patients who died had significantly lower Ct values than patients who survived but here again they had a significantly shorter duration of symptoms before testing" [30].

Some authors have demonstrated "an independent relationship between the Ct value (indicative of viral load) of an individual's first positive COVID-19 PCR test, and overall mortality, in which a lower Ct value is associated with greater hazards of death. Ct values may allow for early risk stratification in patients with COVID-19. Further work is required to confirm this association and to assess the utility of including Ct values in early risk stratification" [31].

Al Dossary et al reported that age, sex, and ethnicity are important predictors of COVID-19 severity. The Ct of the COVID-19 RT-PCR test cannot be used as a predictor of the criticality of illness [32]. Research published by AL Kamarany et al concluded that old age, chronic diseases, and co-infection may be contributing factors to excess morbidity and mortality among COVID-19 patients [13,14].

Our study proved that viral load is reduced with the recovery phase (third week to the fourth week) and the duration of isolation may complete at home. These results agreed with the study of Aranha et al that reported "in the longitudinal assessment of RT-PCR test results in individuals requiring 15-30 days to clear COVID-19 RNA showed a significant reduction of the viral load in samples with high or intermediate viral loads (Ct values ≤ 25 and between 26 and 30, respectively) but the follow-up group with low viral RNA (Ct values ≥ 31) exhibited a stable viral load. Together, these results suggest that COVID-19 positive cases with Ct values more than or equal to 31 require reduced duration to clear COVID-19, and thus, a shorter isolation period for this group might be considered to facilitate adequate space in the COVID Care Centres and reduce the burden on healthcare infrastructure" [33]. The author reported that the viral load reduces with the time of symptoms onset and these results agreed with the study of Boan et al that reported that " COVID-19 viral load declines from the time of symptom onset; at symptom onset, the mean viral load was 4.34 $\log_{10}$ IU/mL with Ct 28.9 cycles and viral load at symptom onset was higher for that reporting fever compared to those not reporting fever [34]. The COVID-19 RT-PCR test and Ct values cannot be used to predict the severity of illness because Ct values are commonly affected by pre-analytic factors such as collection technique, specimen type, time of sample collection, viral kinetics, the difference in viral load between upper respiratory tract (URT) and lower respiratory tract (LRT) samples, transport and storage conditions, and so on. Analytical variables include nucleic acid extraction efficacy, viral RNA load in collected samples, primer

design, nature of the target RNA, real-time PCR efficiency, and Ct value determination method, and post-analytical variables include result interpretation and reporting [35]. "Other techniques can predicate for severity illness of COVID-19 and previous studies were published from Yemen's authors, the radiological techniques have good predictive values on severity and mortality. Also can support the clinicians staff in early detection, early triage, criteria admission, and effective management of COVID-19 infection" [14]. In addition, the hematological parameters namely WBCs, neutrophil and lymphocytes are early indicators in COVID-19 diagnosis and severity illness [36].

On the other hand, several studies reported the fatal outcomes that are particularly associated with certain social determinants, chronic diseases or other communicable disease co-infections [37,38]. The risk of mortality from COVID-19 increases dramatically with age, as well as in those who have underlying comorbidities with diabetes. hypertension and coronary heart disease [39-43].

5. CONCLUSION

Several factors influence the diagnosis of SARS-CoV-2 infection or COVID19, including the selection of appropriate tools and techniques, the most appropriate sample form, appropriate sampling techniques, and the duration of the infection. The RT-PCR technique has been widely used, and Ct values are regarded as indicators of viral load. In addition , study aligns with other epidemiological and clinical studies in highlighting old age and comorbidity with non-communicable diseases and coinfection as key potential contributing factors to excess the severity among COVID-19 patients.

6. LIMITATIONS OF THE STUDY

There are some limitations in this study that needs to be considered. The small sample size in this study and other bio-molecular features are not included.

CONSENT

As per international standards or university standards, Participants' written consent has been collected and preserved in Medical File. The raw data are secured in CTMES – HU and CTMID, Hodeidah, Yemen.

ETHICAL APPROVAL

The studies involving human participants were reviewed and approved by the Ethics Committee of CTMES – HU, Hodeidah, Yemen.

ACKNOWLEDGEMENTS

The authors would like to thank the supervisor and medical staff of the COVID-19 isolation department, Molecular Biology Unit, Center of Tropical Medicine and Infectious Diseases (CTMID), AL Thawara Public Hospital Authority, Hodeidah, Yemen for their fruitful assistance. Also to thank for national center for public health laboratories (NCPHL) staff.

COMPETING INTERESTS

Authors have declared that no competing interests exist.

REFERENCES

1. Yoshimoto FK. The proteins of severe acute respiratory syndrome coronavirus-2 (SARS CoV-2 or n-COV19), the cause of COVID-19. Protein J. 2020 Jun;39(3):198-216.
   DOI: 10.1007/s10930-020-09901-4. PMID: 32447571; PMCID: PMC7245191
2. Malik YA. Properties of coronavirus and SARS-CoV-2. Malays J Pathol. 2020;42(1):3-11.
   PMID: 32342926.
3. Bchetnia M, Girard C, Duchaine C, Laprise C. The outbreak of the novel severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2): A review of the current global status. J Infect Public Health. 2020;13(11):1601-1610.
   DOI: 10.1016/j.jiph.2020.07.011. Epub 2020 Aug 4. PMID: 32778421; PMCID: PMC7402212.
4. Wang H, Li X, Li T, Zhang S, Wang L, Wu X, Liu J. The genetic sequence, origin, and diagnosis of SARS-CoV-2. Eur J Clin Microbiol Infect Dis. 2020 Sep;39(9):1629-1635.
   DOI: 10.1007/s10096-020-03899-4. Epub 2020 Apr 24. PMID: 32333222; PMCID: PMC7180649.
5. Gupta R, Charron J, Stenger CL, Painter J, Steward H, Cook TW, Faber W, Frisch A, Lind E, Bauss J, Li X, Sirpilla O, Soehnlen X, Underwood A, Hinds D, Morris M, Lamb N, Carcillo JA, Bupp C, Uhal BD,

Rajasekaran S, Prokop JW. SARS-CoV-2 (COVID-19) structural and evolutionary dynamicome: Insights into functional evolution and human genomics. J Biol Chem. 2020;295(33):11742-11753.
DOI: 10.1074/jbc.RA120.014873. Epub 2020 Jun 25. PMID: 32587094; PMCID: PMC7450099.

6. Datta PK, Liu F, Fischer T, Rappaport J, Qin X. SARS-CoV-2 pandemic and research gaps: Understanding SARS-CoV-2 interaction with the ACE2 receptor and implications for therapy. Theranostics. 2020;10(16):7448-7464.
DOI: 10.7150/thno.48076. PMID: 32642005; PMCID: PMC7330865.
7. Ji T, Liu Z, Wang G, Guo X, Akbar Khan S, Lai C, Chen H, Huang S, Xia S, Chen B, Jia H, Chen Y, Zhou Q. Detection of COVID-19: A review of the current literature and future perspectives. Biosens Bioelectron. 2020;15(166):112455.
DOI: 10.1016/j.bios.2020.112455. Epub 2020 Jul 21. PMID: 32739797; PMCID: PMC7371595.
8. Li C, Ren L. Recent progress on the diagnosis of 2019 Novel Coronavirus. Transbound Emerg Dis. 2020;67(4):1485-1491.
DOI: 10.1111/tbed.13620. Epub 2020 May 31. Erratum in: Transbound Emerg Dis. 2020;67(6):3076.
PMID: 32395897; PMCID: PMC7272792.
9. Wu T, Ge Y, Zhao K, Zhu X, Chen Y, Wu B, Zhu F, Zhu B, Cui LA. Reverse-transcription recombinase-aided amplification assay for the rapid detection of N gene of severe acute respiratory syndrome coronavirus 2(SARS-CoV-2). Virology. 2020;549:1-4.
DOI: 10.1016/j.virol.2020.07.006. Epub 2020 Jul 29. PMID: 32758712; PMCID: PMC7388781.
10. Mitchell SL, St George K, Rhoads DD, Butler-Wu SM, Dharmarha V, McNult P, Miller MB. Understanding, verifying, and implementing emergency use authorization molecular diagnostics for the detection of SARS-CoV-2 RNA. J Clin Microbiol. 2020;58(8):00796-20.
DOI: 10.1128/JCM.00796-20. PMID: 32381642; PMCID: PMC7383533.
11. Rao SN, Manissero D, Steele VR, Pareja JA. Narrative systematic review of the clinical utility of cycle threshold values in the context of COVID-19. Infect Dis Ther. 2020;9(3):573–586.
Available: https://doi.org/10.1007/s40121-020-00324-3.
12. Skok K, Stelzl E, Trauner M, Kessler HH, Lax SF. Post-mortem viral dynamics and tropism in COVID-19 patients in correlation with organ damage. Virchows Arch. 2021 Feb;478(2):343-353.
DOI: 10.1007/s00428-020-02903-8. Epub 2020 Aug 20. PMID: 32815036; PMCID: PMC7438212.
13. AL-Kamarany, MA, Suhail KA, Majam AS, Abdulabari Alabsi E, Hamoud Dowbalah M, Mohammed Zohairy A. Epidemiological and clinical features of COVID-19 in Hodeidah, Yemen. International Journal of Tropical Disease & Health. 2021;42(21):28-40.
Available:https://Doi.org/10.9734/ijtdh/2021/v42i2130550.
14. Suhail FA, Al Kamarany, MA. Radiological features of COVID-19 patients in Hodeidah, Yemen. Asian Journal of Research in Infectious Diseases. 2021; 8(4):117-127.
Available:https://Doi.org/10.9734/ajrid/2021/v8i430256.
15. Al-Kamarany MA, Abdulkarim T. Immunological features of COVID-19 in Hodeidah, Yemen. Asian Journal of Immunology. 2023;6(1):76–84.
Available:https://journalaji.com/index.php/AJI/article/view/97.
16. Al-Areeqi A, Alghalibi S, Yusuf Q, Al-Masrafi I, Al-Kamarany MA. Epidemiological Characteristic of Malaria Coinfected with Dengue Fever in Hodeidah, Yemen. International Journal of Tropical Disease & Health. 2020;40(3):1–10.
Available:https://Doi.org/10.9734/ijtdh/2019/v40i330230
17. Alahdal M, Al-Shabi J, Ogaili M, Abdullah QY, Alghalibi S, Jumaan A. O, AL-Kamarany MA. Detection of dengue fever virus serotype – 4 by using one-step real-time RT-PCR in Hodeidah, Yemen. Microbiology Research Journal International. 2016;14(6):1–7.
Available:https://Doi.org/10.9734/BMRJ/2016/24380
18. Abdullah QY, Ogaili M, Alahdal M, AL-Kamarany MA. Dengue fever infection in Hodeidah, Yemen: Risk factors and socioeconomic indicators. British Biomedical Bulletin. 2015;3(1):058-065. Google Scholar

19. Malik MR, Mnzava A, Mohareb E, Zayed A, Al Kohlani A, Thabet AA, El Bushra H. Chikungunya outbreak in Al-Hudaydah, Yemen. 2011: epidemiological characterization and key lessons learned for early detection and control. J Epidemiol Glob Health. 2014 Sep;4(3): 203-11.
DOI: 10.1016/j.jegh.2014.01.004. Epub 2014 Mar 15. PMID: 25107656; PMCID: PMC7333817.
20. Yusuf Q, Al-Masrafi I, Al-Mahbashi A, Al-Areeqi A, Al-Kamarany MA, Khan AS. First evidence of west nile virus in Hodeidah, Yemen: Clinical and epidemiological characteristics. International Journal of TROPICAL Disease & Health. 2019;38(4):1-9. Available:https://Doi.org/10.9734/ijtdh/2019/v38i430190
Available:https://journalijtdh.com/index.php/IJTDH/article/view/30190
21. World Health Organization (WHO), WHO COVID-19: Case Definitions. Available: file:///C:/Users/nt/Downloads/WHO-2019-nCoV-Surveillance_Case_Definition-2020.2-eng.pdf [Accessed December 16, 2020]
22. World Health Organization (WHO). Operation Consideration for Case Management of COVID - 19 Health Facility.
Available:https://apps.who.int/iris/bitstream/handle/10665/331492/WHO-2019-nCoV-HCF_operations-2020.1-eng.pdf?sequence=1&isAllowed=y [Accessed March 19, 2020].
23. Ministry of Public Health and Population (MOPHP), Therapeutic Sector, Administration of Service and Emergency, National Guideline for Case Management of Mild and Moderate at Home of Coronavirus Disease 2019 (COVID-19); 2020.
24. Norgen Biotek Corp. Norgen's 2019-nCoV TaqMan RT-PCR Kit; 2020.
25. Rabaan AA, Tirupathi R, Sule AA, Aldali J, Mutair AA, Alhumaid S, Muzaheed, Gupta N, Koritala T, Adhikari R, Bilal M, Dhawan M, Tiwari R, Mitra S, Emran TB, Dhama K. Viral Dynamics and Real-Time RT-PCR Ct Values Correlation with Disease Severity in COVID-19. Diagnostics (Basel). 2021 Jun 15;11(6): 1091.
DOI: 10.3390/diagnostics11061091. PMID: 34203738; PMCID: PMC8232180.
26. Álvarez-Díaz DA, Franco-Muñoz C, Laiton-Donato K, Usme-Ciro JA, Franco-Sierra ND, Flórez-Sánchez AC, Gómez-Rangel S, Rodríguez-Calderon LD, Barbosa-Ramirez J, Ospitia-Baez E, Walteros DM, Ospina-Martinez ML, Mercado-Reyes M. Molecular analysis of several in-house rRT-PCR protocols for SARS-CoV-2 detection in the context of genetic variability of the virus in Colombia. Infect Genet Evol. 2020 Oct;84:104390.
DOI: 10.1016/j.meegid.2020.104390. Epub 2020 Jun 4. PMID: 32505692; PMCID: PMC7272177.
27. Rattan A, Ahmad H. Can quantitative RT-PCR for SARS-CoV-2 help in better management of patients and control of coronavirus disease 2019 pandemic. Indian J Med Microbiol. 2020;38(3& 4):284-287.
DOI: 10.4103/ijmm.IJMM_20_380. PMID: 33154236; PMCID: PMC7709651.
28. Li D, Zhang J, Li J. Primer design for quantitative real-time PCR for the emerging Coronavirus SARS-CoV-2. Theranostics. 2020;10(16):7150-7162.
DOI: 10.7150/thno.47649. PMID: 32641984; PMCID: PMC7330846
29. Abdulrahman A, Mallah SI, Alqahtani M. COVID-19 viral load not associated with disease severity: findings from a retrospective cohort study. BMC Infect Dis. 2021;21(1):688.
DOI: 10.1186/s12879-021-06376-1. PMID: 34271860; PMCID: PMC8284033.
30. Shah S, Singhal T, Davar N, Thakkar P. No correlation between Ct values and severity of disease or mortality in patients with COVID 19 disease. Indian J Med Microbiol. 2021;39(1):116-117.
DOI: 10.1016/j.ijmmb.2020.10.021. Epub 2020 Nov 3. PMID: 33610241; PMCID: PMC7667391.
31. Waudby-West R, Parcell BJ, Palmer CNA, Bell S, Chalmers JD, Siddiqui MK. The association between SARS-CoV-2 RT-PCR cycle threshold and mortality in a community cohort. Eur Respir J. 2021;58(1):2100360.
DOI: 10.1183/13993003.00360-2021. PMID: 34172468; PMCID: PMC8246006.
32. Al Dossary R, Alnimr A, Aljindan R, Alkharsah KR, Al-Qurayn AK, Eltreifi O, Alkuwaiti FA, Almashouf AB, Alsahlawi AM, Alshammari A, Hudhaiah D, Alshahrani MS, Bukhari H. Predictors of

Illness Severity in COVID-19 Cases in Saudi Arabia. Infect Drug Resist. 2021 Oct 5;14:4097-4105.
DOI: 10.2147/IDR.S333300. PMID: 34675555; PMCID: PMC8502032.

33. Aranha C, Patel V, Bhor V, Gogoi D. Cycle threshold values in RT-PCR to determine dynamics of SARS-CoV-2 viral load: An approach to reduce the isolation period for COVID-19 patients. J Med Virol. 2021;93(12):6794-6797.
Doi: 10.1002/jmv.27206. Epub 2021 Jul 23. PMID: 34264527; PMCID: PMC8426941.
34. Boan P, Jardine A, Pryce TM. Clinical associations of SARS-CoV-2 viral load using the first WHO International Standard for SARS-CoV-2 RNA. Pathology. 2022; 54(3):344-350.
DOI: 10.1016/j.pathol.2021.11.006. Epub 2022 Feb 10. PMID: 35153071; PMCID: PMC8829673.
35. Watson J, Whiting PF, Brush JE. Interpreting a covid-19 test result. BMJ. 2020;369:m1808.
DOI: 10.1136/bmj.m1808. PMID: 32398230.
36. AL Kamarany Amood M. Validation of Neutrophils - Lymphocytes Ratio for Monitoring of Therapeutic Efficacy of COVID -19 in Hodeidah, Yemen. The Second Conference for Laboratory Medicine. 2021;20–23:43-44.
37. Lipsitch M, Swerdlow DL, Finelli L. Defining the Epidemiology of Covid-19 - Studies Needed. N Engl J Med. 2020 26;382(13):1194-1196.
DOI: 10.1056/NEJMp2002125. Epub 2020 Feb 19. PMID: 32074416.
38. Zhang C, Shi L, Wang FS. Liver injury in COVID-19: Management and challenges. Lancet Gastroenterol Hepatol. 2020 May; 5(5):428-430.
DOI: 10.1016/S2468-1253(20)30057-1. Epub 2020 Mar 4. PMID: 32145190; PMCID: PMC7129165.
39. Zhou F, Yu T, Du R, Fan G, Liu Y, Liu Z, Xiang J, Wang Y, Song B, Gu X, Guan L, Wei Y, Li H, Wu X, Xu J, Tu S, Zhang Y, Chen H, Cao B. Clinical course and risk factors for mortality of adult inpatients with COVID-19 in Wuhan, China: A retrospective cohort study. Lancet. 2020 Mar 28;395(10229):1054-1062.
DOI: 10.1016/S0140-6736(20)30566-3. Epub 2020 Mar 11. Erratum in: Lancet. 2020 Mar 28;395(10229):1038. Erratum in: Lancet. 2020;395(10229):1038.
PMID: 32171076; PMCID: PMC7270627.
40. Li D, Chen Y, Liu H, Jia Y, Li F, Wang W, Wu J, Wan Z, Cao Y, Zeng R. Immune dysfunction leads to mortality and organ injury in patients with COVID-19 in China: insights from ERS-COVID-19 study. Signal Transduct Target Ther. 2020 May 5;5(1):62.
DOI: 10.1038/s41392-020-0163-5. PMID: 32371949; PMCID: PMC7198844.
41. Du RH, Liang LR, Yang CQ, Wang W, Cao TZ, Li M, Guo GY, Du J, Zheng CL, Zhu Q, Hu M, Li XY, Peng P, Shi HZ. Predictors of mortality for patients with COVID-19 pneumonia caused by SARS-CoV-2: A prospective cohort study. Eur Respir J. 2020;55(5):2000524.
DOI: 10.1183/13993003.00524-2020. Erratum in: Eur Respir J. 2020;56(3).
PMID: 32269088; PMCID: PMC7144257.
42. AL Kamarany MA, Al-Masrafi I, Ghouth AB, Suhail K, Majam A, Zuhairy A, Alabsi E. Outbreak Investigation: First Ten COVID – 19 Infection Related Deaths in Hodeidah, Yemen. Asian Journal of Research in Infectious Diseases. 2023; 13(3):19–27.
Available:https://doi.org/10.9734/ajrid/2023/v13i3268
43. Majam A and AL Kamarany Amood M. COVID -19 and dengue coinfection, predication for increasing the mortality rate: Case report. The First Scientific Annual Conference of AL Thawara Public General Authority; 2021.

Peer-review history:
The peer review history for this paper can be accessed here:
https://www.sdiarticle5.com/review-history/100635