INTERNATIONAL JOUNAL OF: SCIENCE RESEARCH AND TECHNOLOGY

TIMBOU-AFRICA ACADEMIC PUBLICATIONS
INTERNATIONAL JOURNAL, NOVEMBER, 2022 EDITIONS
VOL. 11 NO. 9 ISSN: 2623-7861

LOCAL STABILITY ANALYSIS FOR THE MATHEMATICAL MODEL OF COVID-19 DISEASE TRANSMISSION DYNAMICS INCORPORATING NATURAL IMMUNITY.

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ABSTRACT

In this study, we present a compartmental model for the spread of coronavirus in a human population. The Disease Free Equilibrium (DFE), Endemic equilibrium and the basic reproduction number of the model were obtained. The Jacobian matrix stability technique was used to analyzed the local stability of the disease free equilibrium and endemic equilibrium, in terms of the basic reproduction number

INTRODUCTION

The coronavirus disease, caused by the novel coronavirus severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) commonly known as COVID-19 has created a complete chaos across the globe by infecting more than 35,027,546 people and having death more than 1,034,837 people in 235 countries as on October 05, 2020 (World health organisation, 2019). The said virus and its resultant outbreak hit the city of Wuhan first and later affected almost the whole world. It took hundreds of thousands of lives worldwide. It is hard to take a single point of view on this virus's origin. It may be due to a seafood market exchange, or the people's migration from one place to another, or the transmission from animals to humans; it may also be due to human-to-human interactions. So far, the virus has devastated almost everything around the world. Social life, health, economy, education and generally, each segment of human life has been severely affected. Health researchers, governmental policymakers, and health care authorities are puzzled in combating the deadly outbreak. They all have their point of view on the situation (Rahim & Ehrahem 2021). Dry cough, fever and fatigue (tiredness) are the most common symptoms of the novel coronavirus disease. However, other symptoms include shivering (chills), pains, sore throat, difficulty in breathing, headache, skin rashes, runny nose, taste loss, diarrhea and

$R_0 = \frac{\varepsilon\varphi(1-d)(\mu+\kappa-\omega\mu)}{(\mu+\kappa)(\mu+\delta+\tau+\beta)}$. The investigation shows that the disease free equilibrium exist and is locally asymptotically stable ($R_0 < 1$) and also the endemic equilibrium exist and is locally asymptotically stable ($R_0 > 1$).

Keywords: coronavirus, Equilibrium, Basic Reproduction Number, Endemic Equilibrium, Local Stability analysis.

fingers or toes dislocation (Nigeria Centre for Disease Control (NCDC) 2022; Shanafelt, Ripp & Trockel 2020; US Centres for Disease Control and Prevention 2022). COVID-19 is transmitted from human to human via direct contact with contaminated surfaces and through respiratory droplets' inhalation from infected individuals (Bai, Yao & Wei, 2021; World Health Organisation, 2021; W. H. O. 2022). Many researchers such as (Bogoch, Watts, Thomas-Bachli, Huber, Kraemer, & Khan, 2020; Gumel 2004; Wu, Leung & Leung 2020; Zhou, Yang, Wang, Hu, Zhang, Si HR, Zhu, Huang, &Chen 2020) study SARS-CoV-2 with the aim to contribute their best in provide ways and solutions of combating the disease. We will study COVID-19 by incorporating compartment with natural immunity in the model developing by (Nthiiri, 2016) the dynamics of the disease with compartments PSIT: Protected, Susceptible, Infected and Treatment.

MATERIAL AND METHODS

Description and Formulation of Model

The model here consist of five classes: $P(t)$ is the compartment used for those that are protected against the disease over a period of time. Protected individuals are recruited into the population at a rate $\omega\alpha$ and the population decrease by natural death at a rate μ. $S(t)$ is used to represent the number of individuals that are prone to the disease at time t, Susceptible individuals are recruited into the population at the rate $(1-\omega)\alpha$ by birth or emigration and also from treated class by losing temporary immunity at the rate ϕ and from protected class by losing protection at the rate λ, the population decrease by natural death at rate μ and by infection following a contact with infected individuals at a rate γ. $I(t)$ Is the number of individuals who have been infected with the disease and are capable of spreading the disease to those in the susceptible categories, the population decreased by natural death, disease induced death and treatment. $N_i(t)$

Denotes the number of individuals who have been infected but poses natural immunity against the disease. $T(t)$ Is the number of individuals who have been infected with the disease and are treated, the population increases when infected individual get treated and move into the compartment, the population decrease by natural death at a rate μ . In the model we assumed that once an individual is treated, gets recovered from the disease, and there is reinfection once an individual is treated.

The model description can be written in the system of differential equations below:

$$\frac{dP}{dt} = \omega\alpha - (\mu + \kappa)P \quad (1)$$

$$\frac{dS}{dt} = (1-\omega)\alpha + \kappa P + \eta N_i + \phi T - (\mu + \gamma)S \quad (2)$$

$$\frac{dI}{dt} = \gamma S - (\mu + \delta + \tau + \beta)I \quad (3)$$

$$\frac{dN_i}{dt} = \tau I - (\mu + \eta)N_i \quad (4)$$

$$\frac{dT}{dt} = \beta I - (\mu + \phi)T \quad (5)$$

With initial condition

$$P(0) = P_0 > 0,\ S(0) = S_0 > 0,\ I(0) = I_0 > 0,\ N_i(0) = N_{i0} > 0,\ T(0) = T_0 > 0$$

Here, $\gamma = \dfrac{\varepsilon\varphi(1-d)}{N}$ is the effective force of infection.

Where ε the transmission probability rate of COVID-19, φ is the contact rate of infection, d is the effective rate of protection against infection.

The total population is given as:

$$N = P(t) + S(t) + I(t) + N_i(t) + T(t) \quad (6)$$

Model parameter and variable description

Table1: Definition of variables

Variables	Description
P	Total number of protected individuals at time t
S	Total number of susceptible individuals at time t
I	Total number of infected individuals at time t
N_i	Total number of individuals with natural immunity against at time t

T	Total number of treated individuals at time t.

Table 2: Definition of parameters

Parameter	Description
$\omega\alpha$	Is the at rate which protected individuals are recruited into the population
μ	Is the natural death rate
η	Is the rate at which natural immune individuals join susceptible class
ϕ	Is the rate of losing temporary immunity after treatment
γ	Is the rate of infection
κ	Is the rate of losing protection from the protected class
δ	**Is the rate of disease** induced death
τ	Is the rate of natural recovery due to immunity after infection
β	Is the rate of treatment

EQUILIBRIUM ANALYSES

By equilibrium of a given set of equation(s), we mean the state of the set of equation(s) remaining the same at all times. Therefore, by equilibrium point, we mean the point in value where the disease level remains the same at all times. This means that the rate of change of any of the compartments in the disease dynamics is equal to zero for all times (Godwin, 2021).

Disease Free Equilibrium Point

Disease free equilibrium point is a steady state solution whereby there is no disease. At this state, an individual has no virus in the body. The disease free equilibrium of the model differential equation (1) to (5) can be obtained by setting the right sides of model equations (1) to (5) equal to zero. That is,

$$\frac{dP}{dt}=\frac{dS}{dt}=\frac{dI}{dt}=\frac{dN_i}{dt}=\frac{dT}{dt}=0$$

$$\omega\alpha-(\mu+\kappa)P=0 \quad (7)$$

$$(1-\omega)\alpha+\kappa P+\eta N_i+\phi T-(\mu+\gamma)S=0 \quad (8)$$

$$\gamma S-(\mu+\delta+\tau+\beta)I=0 \quad (9)$$

$$\tau I-(\mu+\eta)N_i=0 \quad (10)$$

$$\beta I-(\mu+\phi)T=0 \quad (11)$$

Therefore,

TIJSRAT
ISSN: 2623-7861

In the absence of the disease this implies that $I(t) = N_i(t) = T(t) = 0$. Substituting into (7) to (11), we obtained

$$P = \frac{\omega\alpha}{\mu+\kappa},\ S = \frac{(\mu+\kappa-\omega\mu)\alpha}{\mu(\mu+\kappa)}$$

Hence, the disease free equilibrium points E_0 is:

$$E_0 = (P, S, I, N_i, T) = \left(\frac{\omega\alpha}{\mu+\kappa}, \frac{\mu+\kappa-\omega\mu}{\mu(\mu+\kappa)}, 0, 0, 0\right)$$

This implies that the disease will out in the population.

Basic Reproduction Number R_0

The basic reproduction number is one of the fundamental concepts in mathematical biology that determines the future of an epidemic. According to Diekmann & Heesterbeck (2000), the basic reproduction number R_0 is the expected number of secondary cases produced in a completely susceptible population, by a typical infective individual. It is one of the most useful threshold parameters, which characterize mathematical problems concerning infectious diseases. If R_0 is less than unity, this implies that, on average an infected individual produces less than one new infected individual during the infectious period and infection can be wiped out. Conversely if R_0 is greater than unity, then each infected individual produces, on average, more than one new infection, and the disease spreads in the population. For single infected compartment, R_0 is the product of the infection rate and the mean duration of the infection. But for complicated models, this definition of R_0 is insufficient. We therefore compute the basic reproduction number R_0 of the model equations (1) to (5), using next generation operator approach by (Diekmann, Heesterbeek, & Metz 1990; Driessche & Watmough, 2002; Diekmann & Heesterbeck 2000; Diekmann, Heesterbeek & Britton 2012).

$$R_0 = \rho\left(FV^{-1}\right)$$

Where,

$\rho(A)$ is the spectral radius of matrix A(or the maximum modulus of the eigenvalues of A).

$F = \left[\frac{\partial F_i}{\partial x_j}(E_0)\right]$ and $V = \left[\frac{\partial V_i}{\partial x_j}(E_0)\right]$, with $1 \le i,\ j \le m$, where m represents the infected classes.

TIJSRAT
ISSN: 2623-7861

F_i and V_i are the rate of appearances of new infections in compartment *i* and the transfer of individuals into and out of compartment i by all means respectively. Using the linearization method, the associated matrices at disease-fee equilibrium E_0.

Considering the primary infection:

$$F_i = \gamma IS = \frac{\varepsilon\varphi(1-d)IS}{N} \quad (12)$$

Differentiating (12) partial with respect to infection class, substituting the values of N and S at the disease free equilibrium, we obtained

$$F_i = \frac{\varepsilon\varphi(1-d)(\mu+\kappa-\omega\mu)}{(\mu+\kappa)} \quad (13)$$

Similarly, considering the secondary infected class:

$$V_i = (\mu+\delta+\tau+\beta)I \quad (14)$$

Differentiating (14) partial with respect to infection class, we have

$$V_i = (\mu+\delta+\tau+\beta) \quad (15)$$

Taking the inverse of (15), we have

$$V_i^{-1} = \frac{1}{(\mu+\delta+\tau+\beta)} \quad (16)$$

Multiplying matrix (13) by the inverse (16), gives

$$F_i V_i^{-1} = \frac{\varepsilon\varphi(1-d)(\mu+\kappa-\omega\mu)}{(\mu+\kappa)(\mu+\delta+\tau+\beta)} \quad (17)$$

Hence, the basic reproduction number is

$$R_0 = \frac{\varepsilon\varphi(1-d)(\mu+\kappa-\omega\mu)}{(\mu+\kappa)(\mu+\delta+\tau+\beta)}$$

Local Stability Analysis of the Disease Free Equilibrium point E_0.

Theorem 1: The disease free equilibrium of the system of the model equation (1) to (5) is locally asymptotically stable when $R_0 < 1$ or unstable when $R_0 > 1$.

Proof: The criteria for stability or instability of the disease free equilibrium of the model equations (1) to (5) shall be established by solving the characteristic equation of the Jacobian matrix of the model equations at the disease free equilibrium point E_0.The Jacobian matrix of the model equations is given as:

$$J=\begin{pmatrix} -(\mu+\kappa) & 0 & 0 & 0 & 0 \\ \kappa & -(\mu+\gamma I) & -\gamma S & \eta & \phi \\ 0 & \gamma I & \gamma S-(\mu+\delta+\tau+\beta) & 0 & 0 \\ 0 & 0 & \tau & -(\mu+\eta) & 0 \\ 0 & 0 & \beta & 0 & -(\mu+\phi) \end{pmatrix}$$

(18)

Evaluating the Jacobian matrix (18) at the disease free equilibrium point E_0, we have

$$JE_0=\begin{pmatrix} -(\mu+\kappa) & 0 & 0 & 0 & 0 \\ \kappa & -\mu & -\dfrac{\gamma(\mu+\kappa-\omega\mu)\alpha}{\mu(\mu+\kappa)} & \eta & \phi \\ 0 & 0 & \dfrac{\gamma(\mu+\kappa-\omega\mu)\alpha}{\mu(\mu+\kappa)}-(\mu+\delta+\tau+\beta) & 0 & 0 \\ 0 & 0 & \tau & -(\mu+\eta) & 0 \\ 0 & 0 & \beta & 0 & -(\mu+\phi) \end{pmatrix}$$

(19)

Applying the formula $\det(JE_0-\lambda I)=0,$ so that,

$$|JE_0-\lambda I|=$$

$$\begin{vmatrix} -(\mu+\kappa)-\lambda & 0 & 0 & 0 & 0 \\ \kappa & -\mu-\lambda & -\dfrac{\gamma(\mu+\kappa-\omega\mu)\alpha}{\mu(\mu+\kappa)} & \eta & \phi \\ 0 & 0 & \dfrac{\gamma(\mu+\kappa-\omega\mu)\alpha}{\mu(\mu+\kappa)}-(\mu+\delta+\tau+\beta)-\lambda & 0 & 0 \\ 0 & 0 & \tau & -(\mu+\eta)-\lambda & 0 \\ 0 & 0 & \beta & 0 & -(\mu+\phi)-\lambda \end{vmatrix}$$

(20)

The characteristic matrix equation of (20) is given as:

$$\{-(\mu+\kappa)-\lambda\}\{-\mu-\lambda\}\left\{\frac{\gamma(\mu+\kappa-\omega\mu)\alpha}{\mu(\mu+\kappa)}-(\mu+\delta+\tau+\beta)-\lambda\right\}$$

$$\{-(\mu+\eta)-\lambda\}\{-(\mu+\phi)-\lambda\}=0$$

Therefore, we have the following eigenvalues:

$$\lambda_1=-(\mu+\kappa),\ \lambda_2=-\mu,\ \lambda_3=\frac{\gamma(\mu+\kappa-\omega\mu)\alpha}{\mu(\mu+\kappa)}-(\mu+\delta+\tau+\beta)$$

$$\lambda_4=-(\mu+\eta),\ \lambda_5=-(\mu+\phi)$$

The eigenvalues λ_1, λ_2, λ_4 and $\lambda_5 < 0$, the eigenvalue λ_3 will be less than zero, if $R_0 < 1$

.

Hence, the disease free equilibrium is locally asymptotically stable when $R_0 < 1$, these implies that, the infection will die in the population and at this point the endemic equilibrium does not exist. The prevalence ratio of COVID-19 infective in the population would decrease and approach the value. Therefore, the COVID-19 disease epidemic would die out of the population with time.

Where, $R_0 = \dfrac{\gamma(\mu+\kappa-\omega\mu)\alpha}{\mu(\mu+\kappa)} - (\mu+\delta+\tau+\beta)$

These complete the proof.

Endemic Equilibrium point (EEP)

Endemic equilibrium point E^* is a state where at least one of the infected compartments is non-zero, or is steady state solutions where the disease persists in the population (Godwin, 2021). The endemic equilibrium point $E^* = (P^*, S^*, I^*, N_i^*, T^*)$ can be obtained by setting rates of changes of variables with respect to time of the model equations to zero. Solving (7) to (11) in terms of E^*, we have

$$P^* = \frac{\omega\alpha}{\mu+\kappa}$$

$$S^* = \frac{\frac{\alpha}{\mu}(\mu+\delta+\tau+\beta)}{\varepsilon\varphi(1-d)}$$

$$I^* = \frac{(\mu+\eta)(\mu+\phi)}{(\mu+\eta)(\mu+\phi)+\tau(\mu+\phi)+\beta(\mu+\eta)}\left[\frac{\alpha}{\mu} - \frac{\omega\alpha}{\mu+\kappa} - \frac{\frac{\alpha}{\mu}(\mu+\delta+\tau+\beta)}{\varepsilon\varphi(1-d)}\right]$$

$$N_i^* = \frac{\tau(\mu+\phi)}{(\mu+\eta)(\mu+\phi)+\tau(\mu+\phi)+\beta(\mu+\eta)}\left[\frac{\alpha}{\mu} - \frac{\omega\alpha}{\mu+\kappa} - \frac{\frac{\alpha}{\mu}(\mu+\delta+\tau+\beta)}{\varepsilon\varphi(1-d)}\right]$$

$$T^* = \frac{\beta(\mu+\eta)(\mu+\phi)}{(\mu+\eta)(\mu+\phi)+\tau(\mu+\phi)+\beta(\mu+\eta)}\left[\frac{\alpha}{\mu} - \frac{\omega\alpha}{\mu+\kappa} - \frac{\frac{\alpha}{\mu}(\mu+\delta+\tau+\beta)}{\varepsilon\varphi(1-d)}\right]$$

Hence, the endemic equilibrium points E^* are:

$$E^* = \begin{pmatrix} P^* \\ S^* \\ I^* \\ N_i^* \\ T^* \end{pmatrix} = \begin{pmatrix} \dfrac{\omega\alpha}{\mu+\kappa} \\ \dfrac{\dfrac{\alpha}{\mu}(\mu+\delta+\tau+\beta)}{\varepsilon\varphi(1-d)} \\ \dfrac{(\mu+\eta)(\mu+\phi)}{(\mu+\eta)(\mu+\phi)+\tau(\mu+\phi)+\beta(\mu+\eta)}\left[\dfrac{\alpha}{\mu}-\dfrac{\omega\alpha}{\mu+\kappa}-\dfrac{\dfrac{\alpha}{\mu}(\mu+\delta+\tau+\beta)}{\varepsilon\varphi(1-d)}\right] \\ \dfrac{\tau(\mu+\phi)}{(\mu+\eta)(\mu+\phi)+\tau(\mu+\phi)+\beta(\mu+\eta)}\left[\dfrac{\alpha}{\mu}-\dfrac{\omega\alpha}{\mu+\kappa}-\dfrac{\dfrac{\alpha}{\mu}(\mu+\delta+\tau+\beta)}{\varepsilon\varphi(1-d)}\right] \\ \dfrac{\beta(\mu+\eta)(\mu+\phi)}{(\mu+\eta)(\mu+\phi)+\tau(\mu+\phi)+\beta(\mu+\eta)}\left[\dfrac{\alpha}{\mu}-\dfrac{\omega\alpha}{\mu+\kappa}-\dfrac{\dfrac{\alpha}{\mu}(\mu+\delta+\tau+\beta)}{\varepsilon\varphi(1-d)}\right] \end{pmatrix}$$

(21)

Equation (21), implies that COVID-19 infection will persist in the population.

Local Stability Analysis of the Endemic Equilibrium point E_0 .

Theorem2: The disease endemic equilibrium asymptotically stable if $R_0 > 1$ and unstable if $R_0 > 1$.

Proof: Applying the method developed by Routh-hurwitz, the endemic equilibrium point of the model equations (1) to (5) will be locally asymptotically stable provided the trace of the Jacobian matrix (18) is less than zero, evaluated at the endemic equilibrium point E^* and the determinant of the of (18) is greater than zero also evaluate at the endemic equilibrium point E^*. Evaluating (18) at the endemic equilibrium point E_0, we have

$$JE^* = \begin{pmatrix} -(\mu+\kappa) & 0 & 0 & 0 & 0 \\ \kappa & ((1-R_0)a_0-\mu) & -(\mu+\delta+\tau+\beta)_1 & \eta & \phi \\ 0 & -(1-R_0)a_0 & 0 & 0 & 0 \\ 0 & 0 & \tau & -(\mu+\eta) & 0 \\ 0 & 0 & \beta & 0 & -(\mu+\phi) \end{pmatrix}$$

(22)

Where $a_0 = \left(1+\frac{\mu+\eta}{\tau}+\frac{\mu+\phi}{\beta}\right)$

Applying the formula $\det(JE_0 - \lambda I) = 0,$ so that,

$$\left|JE^* - \lambda I\right| =$$

$$\begin{vmatrix} -(\mu+\kappa)-\lambda & 0 & 0 & 0 & 0 \\ \kappa & [(1-R_0)a_0-\mu]-\lambda & -(\mu+\delta+\tau+\beta)_1 & \eta & \phi \\ 0 & -(1-R_0)a_0 & 0-\lambda & 0 & 0 \\ 0 & 0 & \tau & -(\mu+\eta)-\lambda & 0 \\ 0 & 0 & \beta & 0 & -(\mu+\phi)-\lambda \end{vmatrix}$$

(23)

To compute the trace and determinant of the matrix (23), we used computer software maple 17 and we have:

$$\text{Trace}\left(JE^*\right) = = -4\mu - \kappa + (1-R_0)a_0 - \eta - \phi \qquad (24)$$

$$\text{Det}\left(JE^*\right) = -(-\mu-\kappa)(1-R_0)a_0\begin{pmatrix} -\eta\mu^2 - \eta\mu\phi - \eta\mu\beta - \eta\mu\delta - \eta\phi\delta - \mu^3 \\ -\mu^2\phi - \mu^2\tau - \mu^2\beta - \mu^2\delta - \mu\phi\tau - \mu\phi\delta \end{pmatrix}$$

(25)

From (25) and (24), it is observed that the $\det\left(JE^*\right) > 0$ and the $\text{tra}\left(JE^*\right) < 0$ if and only if $R_0 > 1,$ we therefore conclude that the endemic equilibrium is asymptotically stable.This implies that COVID-19 infection incidences are increasing thus, the epidemic would certainly develop.

This completes the proof.

CONCLUSION

From the investigation carried out on the disease free equilibrium, endemic disease equilibrium and local stabilities of analysis of the disease free and endemic equilibrium points, in terms of basic reproduction number $R_0 = \frac{\varepsilon\varphi(1-d)(\mu+\kappa-\omega\mu)}{(\mu+\kappa)(\mu+\delta+\tau+\beta)}$, the

investigation shows that the disease free equilibrium exist and is locally asymptotically stable($R_0 < 1$) and the endemic equilibrium also exist and is locally asymptotically stable($R_0 > 1$). We will investigate the global stability analysis of the disease free equilibrium and endemic-equilibrium, sensitivity analysis and numerical simulation in future.

REFERENCES

Bai, Y., Yao, L. and Wei, T.(2021). Presumed asymptomatic carrier transmission of COVID-19. *JAMA,* 14 (323), 1406-1407.

Bogoch, I.I., Watts, A., Thomas-Bachli, A., Huber, C., Kraemer, M.U., Khan, K.(2020). Pneumonia of unknown aetiology in Wuhan, China. *potential for international spread via commercial air travel. J Travel Med.* 27(2).

Diekmann, O.; Heesterbeek, J. A. P. & Metz, J. A. J. (1990). On the Definition and the Computation of the Basic Reproduction Ratio R_0 in Models for Infectious Diseases in Heterogeneous Populations. *Journal of Mathematical Biology*, 28 (4), 365–382.

Diekmann O, Heesterbeck JAP.(2000). Mathematical epidemiology of infections disease. Wiley series in mathematical and computational biology. John Wiley & Sons. West Sussex, England.

Diekmann, O. H., Heesterbeek, and Britton,T.(2012). Mathematical Tools for Understanding Infectious Disease Dynamics Princeton .University Press, Princeton, NJ, USA.

Driessche Van Den, P. and Watmough, J. (2002). Reproduction Numbers and Sub-threshold Endemic Equilibria for Compartmental Models of Disease Transmission. *Mathematical Biosciences*, 2(1), 29–48.

Godwin, C. E. M.(2021). Lecture Note on formulation of Analyses and Application of Differential equations in Mathematical Modelling. Presented at the national Mathematical centre Abuja for the foundation postgraduate program in Mathematical model.

Gumel A.B.(2004). Modelling strategies for controlling SARS out breaks. *Proc R Soc Lond B.,* 271(1554), 2223–22232.

Nthiiri,T.K.(2016). Mathematical modelling of typhoid fever disease incorporating protection against infection. *British Journal of Mathematics & Computer Sciences*. 2(6), 1-10.

Nigeria Centre for Disease Control (NCDC).(2022). https://covid19.ncdc.gov.ng/faq/ (July 12 2022).

Rahim, U.D. & Ehrahem, A. A.(2021). Mathematical analysis of COVID-19 by using SIR model with convex incidence rate. *Published by Elsevier B.V,* (4), 2211-3797.

Shanafelt, T., Ripp, J. A & Trockel, M.(2020): Understanding and addressing sources of anxiety among health care professionals during the COVID-19 pandemic. *J. Am. Med. Assoc.,* 323(21), 2133–2134. https://doi.org/ 10.1001/ jama.2020.5893.

US centres for Disease Control and Prevention(2022). Symptoms of Novel Corona virus (2019- ncov). Retrieved on 16th October, 2022.

World Health Organization (WHO) on coronaviruses (COVID-19). https://www.who.int/ emergencies/diseases/novel-coronavirus-2019/question-and-answers-hub/q-a-detail/q-a-coronaviruses. Accessed on July 16 2020).

W.H.O.(2019). Corona virus disease outbreak review. World Health Organization. https://www.who.int/emergencies/diseases/novel-coronavirus-2019.

World Health Organisation (2021) Questions and answers on Corona virus. Retrieved on 16th October, 2021.

World Health Organization (2022). Novel Corona virus in China. Retrieved on 20 September, 2022.

Wu, J.T., Leung, K., & Leung, G.M.(2020). Now casting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China. *A modelling study Lancet,* 395(10225), 689–97.

Zhou P, Yang, X.L., Wang, X. G., Hu B, Zhang L, Zhang, W., Si HR, Zhu, Y., Li, B., Huang, C.L., & Chen, H.D.(2020).A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature,* 579(7798), 270–3.