Transmission dynamics and risk factors assessment of the Coronavirus diseases 2019 (COVID-19) in resource limited settings

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A. Abstract

A1. Background

The sudden appearance of SARS CoV 2 has opened a new research horizon to explain any new replication mechanisms and expand what is known already about members of this family of novel Corona viruses so as to assist their control and prophylaxis.

A2. Objectives:

This study was designed to access the risk for acquisition and transmission, of the novel Severe-Acute Respiratory Syndrome Corona Virus 2, (SARS-COV 2) in different geographical communities.

A3. Materials and methods

In this qualitative questionnaire based online survey, randomly selected 136 participants were selected from researcher's mailing lists using a defined inclusion criterion. Using a survey monkey online tool, original emails were sent followed by 4 consecutive follow-up emails in a period of 4-6 weeks during the time of this study. Five Likert scale (Strongly Agree, Agree, Indifferent, Disagree, Strongly Disagree and others) formed the basis for which selected participants were questioned on nine factors (Exposure rate, population density, movement, and timely testing, age, compliance, conflict, and displacement, type of exposure and demographic data of clients) for "COVID-19", transmission. The correlation between questions asked and consenting participant's response were analyzed using the Heatmap software.

A4. Results

One hundred and thirty-six questionnaires were sent out to be answered in 4-6 weeks but 37 were completely filled and returned and Ninety were not retuned while 7 mails bounced and were not delivered giving a response rate of 28.68% and non-response rate of 71.32% respectively. There was no correlation (Heatmap value <50) between all questions asked and strongly disagree, agree and others implying that all respondent were correct if they disagreed with questions suggesting negative relationship between "COVID-19". distribution and all questions.

There was also no correlation between travel reasons types of exposure and indifferent confirmed by the fact that respondents were indifferent on whether travel reasons and type of exposure are risk factors for "COVID-19", distribution. Exposure rate, Age, timely testing, displacement, and population density showed the greatest correlation when compared to strongly agree response rate (Heatmap value >0.5). This means that respondents were correct when the said they strongly agree that exposure rate, age, timely testing, displacement and population densities were all factors for "COVID-19", distribution.

A4. Conclusions

Therefore, this study has shown that exposure rate, population density, timely testing, and

age, were strong factors that significantly affected the distribution of "COVID-19", with a hit map value of greater than 50). Exposures to different strains of Coronaviruses as well as their impact on virus transmission in tropical settings were discussed.

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B. Introduction

The world has seen many pandemics in the past decades (MERS-COV, SARS-Cov,) but none has been so fatal across all countries like this "COVID-19". When the present Coronavirus emerged in 2019 in Wuhan City of China (1-2), the world thought it was one of the usual diseases that can easily be contained like other cases of Corona Viruses that emerged in the past couple of decades. Despite the facts that there were still too many unknowns about the novel virus, on February 11, 2020, the World Health Organization (WHO) named "Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2)" as the virus that causes Coronavirus diseases (COVID-19) due to its resemblance to SARS-CoV (3-5). The emergence of SARSCOV 2 with "COVID-19", amazed the world because of its unprecedented morbidity and mortality and rapidity of distribution even among asymptomatic patients.

Every day, new dimensions and aspects of the Severe-Acute Respiratory Syndrome Corona Virus 2, (SARS-CoV 2) pathogenicity are discovered making it difficult to design and mount effective intervention to contain the present epidemic by SARS-CoV 2. Many known models used to study disease transmission (6) are being put on the drawing board to study the disease epidemiology but it appears they have been found wanting in one way or the other in providing the information needed to design and mount effective containment for the Pandemic caused by the virus [SARS-CoV 2] going by its morbidity and mortality reports worldwide (7). All stakeholders of health and wellbeing are scared to death by [SARS-CoV 2] because of the observed unique and seemingly new fatality rate. There is therefore a huge hunger for information on how to get us out of this mess.

Coronaviruses are enveloped, positive-sense single-stranded RNA viruses with a nucleocapsid of helical symmetry (8). Coronaviruses are members of the, subfamily *Coronavirinae* (family *Coronaviridae*; order *Nidovirales*), which contains four genera: *Betacoronavirus*, *Gammacoronavirus*, and *Deltacoronavirus* *Alphacoronavirus*, (1). Gamma- and delta- coronaviruses normally infect birds, and some of them can cause infection in mammals, whereas, alpha- and beta- coronaviruses are known to harm humans and animals.

The viruses SARS-CoV (betacoronavirus), 229E (alphacoronavirus), HKU1 (betacoronavirus), NL63 (alphacoronavirus), and OC43 (betacoronavirus), can all cause infections in humans (1). Beta- coronaviruses are made of pathogenic viruses against humans, including but not limited to: SARS-CoV-2, MERS-CoV, and SARS-CoV (1, 9-10). However, Clade-2 of the *S* genetic region (11-12) (*ORF8* (13), and *ORF3b* in SARS-CoV from bats contain major variations compared to SARS-CoV from humans (13). So it is not clear if this observed variation could hinder the viral transmission through bats.

Coronavirus replication involves ribosome frameshifting during: genome translation, the synthesis of both genomic and multiple subgenomic RNA species, and the assembly of progeny virions (14). Viral transmission is by respiratory and fecal-oral routes and extensive coding capacity of the virus (15) defines the incompletely understood complex gene-expression strategies. CDCP and WHO keeps revising and updating their rules for avoiding infection by including both symptomatic and asymptomatic clients as risk for transmission. This clearly alludes to the facts that viral transmission and risk are far from being completely understood

The sudden appearance of SARS CoV 2 has led to many new research interests to unravel any new replication mechanisms and expand what we know already about members of this family of Corona viral agents. This knowledge is expected to aid the novel viral control and prophylaxis. This may therefore be the right time to again assess and expand what we already know about the virus and what can be deduced from evidence based qualitative studies as we prepare for complex studies that need state of the art hands on facilities. Summing up our collective knowledge about the epidemiology of coronaviruses with emphasis on SARS-COV 2 would ultimately impact the fatality rate of the virus. Undoubtedly, it may take decades to completely translate and incorporate our collective knowledge into to the existing social, economic and environmental systems so as to usher in sustainable development in the long run. It is not too late to start and the best time to start is now

B1. Research Objectives/Questions

This study was designed to build the knowledge base of the risk for acquisition and transmission, of the novel Severe-Acute Respiratory Syndrome Corona Virus 2, (SARS-COV 2) in different geographical communities with the ultimate goal of generating data for effective intervention

C. Materials and Methods

This is a qualitative questionnaire based online survey in which Survey-Monkey online survey software was used to design some questions seeking answers from selected 136 participants through their e-mails. These questions sought to generate real-time evidence-based answers to the topic for use in discussing the participant's views about the topic supported by existing literature.

A brief description of the study was given to participants to seek their informed consent before participation. Adult participants with a minimum of any first degree, that has used his/her email within the past 4 weeks from the time of this study and is aware of the virus were randomly selected from the mailing lists of the researchers. Filling and returning the questionnaire was also taken to imply the participants consented. An original email was sent followed by 4 consecutive emails follow-up in a period of 4-6 weeks during the time of this study. At the end response rates were retrieved and compiled using the survey money software.

Five Likert scale (Strongly Agree, Agree, Indifferent, Disagree, Strongly Disagree and others) formed the basis for which selected participants were questioned on nine factors deemed to be risk for "COVID-19", transmission. The nine factors included . (Exposure rate, population density, movement, and timely testing, age, compliance, conflict, and displacement, type of exposure and demographic data of clients) as shown in Table 1 below. The correlation between questions asked and consenting participant's response were analyzed using the Heatmap software

D. Result:

Table 1: Risk factors for "COVID-19",

One hundred and thirty-six questionnaires were sent out to be answered in 4-6 weeks but 37 were completely filled and returned and Ninety were not retuned while 7 mails bounced and were not delivered giving a response rate of 28.68% and non-response rate of 71.32% respectively.

	Strongly agree	Agree	Indifferent	Disagree	Strongly disagree	Other
Exposure rate	78.4	18.92	0	0	0	2.7
Population density	64.7	32.43	0	0	0	2.9
Travel reasons	48.38	21.62	24.32	0	0	studies
Timely testing	67.57	24.32	5.41	0	2.7	0
Age	75.6	10.81	5.41	0	2.7	2.7
Compliance	40.54	48.65	2.7	5.4	2.7	0
Conflict	43.24	43.24	4.41	0	5.41	0
Displacement	56.76	32.43	2.7	5.4	2.7	0
Type of exposure	32.43	48.65	13.51	2.7	0	0

Table 2: Professional and institutional distribution of survey participants

S/N	Profession n=37		Institutions n=37	
	Description	No % positive	Description	No % positive
1	Law maker (PA)	1 (2.7)	KIU Uganda	28 (75.7)
2	Microbiologists	5 (13.5)	KAB Uganda	3 (8.1)
3	Med Lab Sc	4 (10.8)	Uni Free State SA	1 (2.7)
4	Physicians	1 (2.7)	Dental center	1 (2.7)
5	Dentist	1 (2.7)	UPDF	1(2.7)
6	Teachers	1 (2.7)	EBSU	1 (2.7)
7	Lecturers	24 (64.9)	Fed Secretariat Nig	1(2.7)
			South Sudan Ministry of Health	1 (2.7)

In Table 2 the randomly selected study participants were from seven professions in seven legal institutions located in four countries which were Uganda, Nigeria South Sudan and South Africa. We found that 64.9% consenting participants were lecturers followed by 13.5% Microbiologists, 10.8% Medical Laboratory Scientists, and 2.7% each of Law Makers, Dentists, Physicians and Teachers respectively. While 75.7% were KIU Uganda lecturers, 8.1% were Kabale University Lectures and the rest 2.7% were from University of Free states South Africa, Uganda Peoples Defense Force (UPDF), Ebony State University Nigeria, Southern Sudan Ministry of Health and Unanimous Private Dental Clinic in Uganda.

Table 3: Age and sex specific distribution of respondents with 3 participants not disclosing their true sex or age

Age	Male	female
<10	-	-
11-20	-	-
21-30	5 (13.5%)	1 (2.7%)
31-40	16 (43.2%)	1 (2.7%)
41-50	8 (21.6%)	0 (0.0%)
51-60	5 (13.5%)	0 (0.0%)
>60	-	-
Total	32	2

Majority (43.2%) of the consenting male participants were within the age range 31-40 years of age followed by 13.5% of males who were 21-30 and 51-60 years of age respectively. About 2.7% females were from the age bracket of 21-30 and 31-40 years old respectively

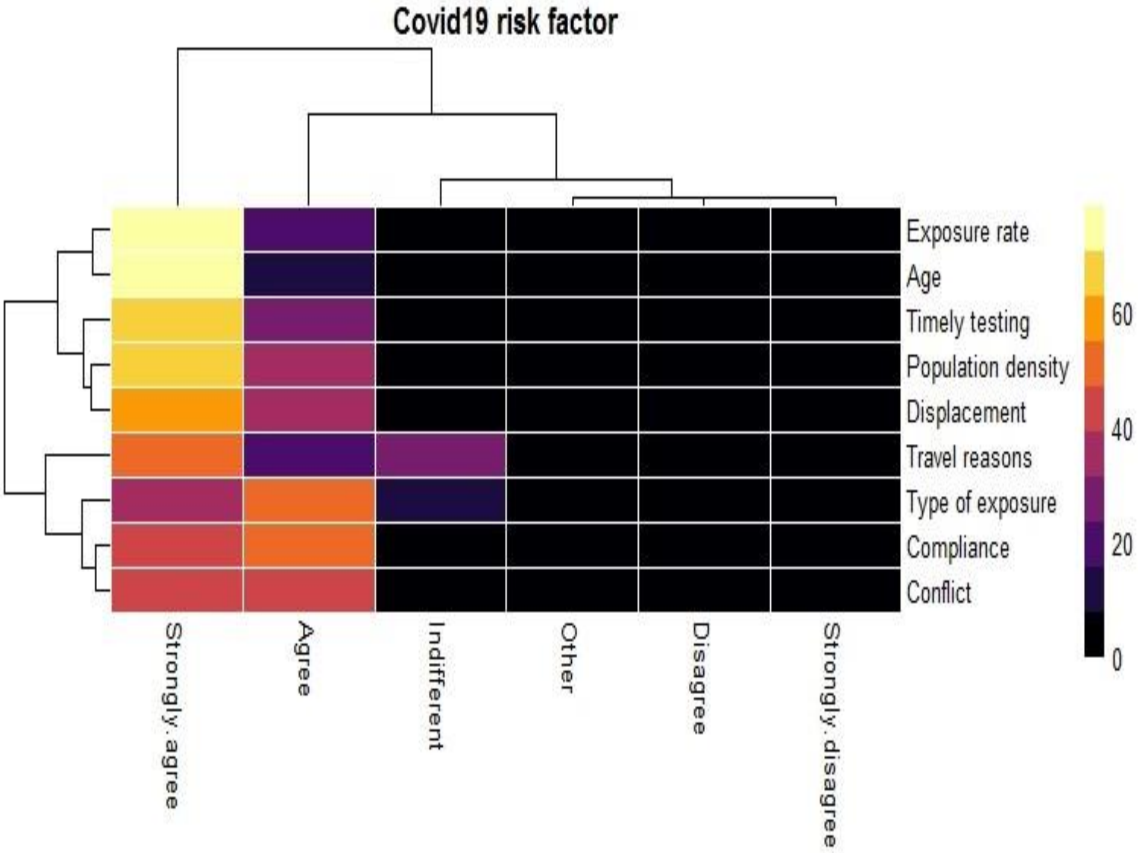

Fig 1. Heatmap correlation plot of consenting participant's view on risk factors of COVID-19 distribution.

From fig 1, The questions asked included if: exposure rate, Population density, Movement, Timely testing, age, compliance, conflict, displacement, type of exposure and demographic data of clients are risk factors for COVID-19 distribution. There was no correlation (Heatmap value <50) between all questions asked and strongly disagree, agree and others implying that all respondent were correct if they disagreed with questions suggesting negative relationship between "COVID-19", distribution and all questions. There was also no correlation between travel reasons types of exposure and indifferent confirmed by the fact that respondents were indifferent on whether travel reasons and type of exposure are risk factors for "COVID-19", distribution. Exposure rate, Age, timely testing, displacement, and population density showed the greatest correlation when compared to strongly agree response rate (Heatmap value >0.5). This means that respondents were correct when the said they strongly agree that exposure rate, age, timely testing, displacement and population densities were all factors for "COVID-19", distribution.

E. Discussion

The outbreak of the novel severe acute respiratory syndrome (SARS) in Guangdong, China in 2002 and 2003 (1-2) revealed a lot of weaknesses in the capacity of existing systems to live to the task of containing emerging or reemerging infectious disease pandemics. Again, the magnitude of the devastation brought by the present novel SARS-CoV 2 also further exposed the weakness of existing health services outlets and the vulnerability of humans facing the onslaught of novel infectious agents of public health importance. We often face aggravated vulnerability when there is any significant gap in the knowledge regarding the epidemiology of such novel agents of disease pandemic. Understanding the risk factors and disseminating the same to the general public is one step while community acceptance and implementing same is another milestone that must be achieved to significantly impact "COVID-19", distribution.

This study recorded a response rate of 28.68% and non-response rate of 71.32% respectively. The pandemic itself led to global economic meltdown making it difficult for people's response to be more than what we observed. Lack of internet data, and airtime to respond to the survey were among the huge challenges noted to drive non response rate high whereas availability of smartphones that can be powered by solar systems up to two days made response rate 28.68%. Outlining what we know about the virus will lay the foundation for understanding what is not clearly understood about the novel virus distribution.

We know that the SARS-CoV infects ciliated bronchial epithelial cells and type-II pneumocytes through angiotensin-converting enzyme 2 (ACE2) as a receptor (1, 16). The transmission of SARS-CoV to humans was based on the facts that its genome sequence exhibits close relatedness (88% identity) with two bat-derived SARS-like coronaviruses (bat-SL-CoVZC45 and bat-SL-CoVZXC21). The zoonotic source of SARS-CoV-2 is not confirmed, but still being debated.

Many unknown about SARS-CoV-2 continue to retard the progress in containing the virus. The instance, the mechanisms associated with the infectiousness of SARS-CoV-2 are not clear, but it is likely that it entered into humans through ACE2 receptor (17). The SARS-CoV strains detected in market civets (18-19) were transmitted from horseshoe bats (11), because the genome sequences of SARS-CoV strains isolated from humans were highly similar to those in bats (18). The newly emerged SARS-CoV-2 also appears to be transmitted to humans from animals used as humans pets (4), because the primary protease is highly conserved between SARS-CoV-2 and SARS-CoV, with a 96% overall identity.

Enough evidence suggest that bats are the most likely source of origin, while an animal sold at the Wuhan seafood market might represent an intermediate host facilitating the emergence of the virus in humans (17, 20). The infectious agent responsible for this atypical pneumonia was confirmed and reported as coronavirus SARS-CoV-2, which caused the first fatality in early January 2020. During the first 6 weeks of the outbreak, several cases were reported in more than 37 countries, including the USA, Japan, Iran, and South Korea (21).

Moreover, asymptomatic persons are thought to be potential sources of SARS-CoV-2 infection (22), which may have caused the rapid spread of SARS-CoV-2. This asymptomatic spread may be one reason that the control strategy based on the isolation of patients has not been fully successful. To overcome these problems, a complete quarantine is necessary, allowing all of the infected individuals to develop symptoms without spreading the virus randomly. Thus, the direct and indirect contacts of infected individuals can be easily identified and isolated.

Societal cooperation with government guidance to mitigate the effects of the pandemic is closely tied to trust in the government. A government's reputation for transparency engenders trust and a sentiment of solidarity and reinforces a belief among citizens that restrictions are being applied fairly. If the public or international bodies do not trust the data on transmission rates, then they are less likely to cooperate, contributing to alternate narratives of the severity of the disease.

Clinical features associated with patients infected with SARS-CoV-2 range from mild respiratory illness to severe acute respiratory disease (23). All SARS patients in later stages develop respiratory distress and renal failure (23). Coronaviruses cause acute and chronic respiratory, enteric, and central nervous system (CNS) diseases in many species of animals, including humans (24). Pneumonia appears to be the most frequent manifestation of SARS-CoV-2 infection, characterized primarily by fever, cough, dyspnea, and bilateral infiltrates on chest imaging (8). The period from infection to appearance of symptoms varies. Generally, it is thought to be between 14 days and 24days. In a family cluster of infections, the onset of fever and respiratory symptoms occurred approximately 3 to 6 days after presumptive exposure (25).

From Fig 1, there were positive correlation between "COVID-19", risk factors and timely testing of vulnerable population. Existing public health system can only test for "COVID-19", for identifying, isolating, and treating those infected—so as to reduce the impact in the society. The primary concern of developing counties is to protect their professional healthcare service providers if they can maintain the sustainability of the diagnostic workforce in their region (26). Advocacy for best practice and adaptation needs also to be communicated to the society. The worst-case scenario is to have a system that have no enough testing system thereby exacerbating the rate of diseases transmission.

From fig 1, there were positive correlation between "COVID-19", risk factors and population density of vulnerable population. Densely populated area creates conditions where viruses can spread quickly and undetected in crowded settlements. Built-up areas of tropical Africa have higher population densities than those in temperate zones. "COVID-19", appears to thrive in cities where it can be transmitted quickly at close range through the movement and frequent contact between people. Communities with higher urban populations are faced with the logistical and communication challenge of informing, monitoring, and possibly isolating a larger pool of at-risk people (27). Stay-at-home orders will be particularly difficult to maintain in African cities where many residents lack adequate shelter, sanitation, and the monetary means to stock up on supplies and to stop work.

Yet lock down and social distancing helps disperse the population and prevent them from exposure to the virus. From fig 1, there were positive correlation between "COVID-19", risk factors and the age of vulnerable population. Approximately 80 percent of "COVID-19", fatalities have been among people over the age of 60. Since over 50% of Africa's population are under the age of 30. it then means that this age advance may be a buffer against the most devastating human costs of the disease on the continent. This may quickly be neutralized by other underlying health factors facing many African populations such as malaria, malnutrition, tuberculosis, and HIV/AIDS (28-33).

From fig 1, there were no correlation (Heatmap<) between "COVID-19", risk factors and the conflict in the location of vulnerable population. Respondents were right as all responses from strongly agree to strongly disagree depicts no relationship. This disturbs public health systems and limits access to basic goods like food, water, and medical supplies.

From fig 1, also showed positive correlation between "COVID-19", risk factors and displaced population. Refugees and internally displaced populations may be congregated in large camps with inadequate access to water, soap, or sanitation (34). Health services are often overstretched and inaccessible. The close quarters typical of such settlements greatly facilitates the spread of any infection once it is introduced. This multilayered risk portfolio underscores the vulnerability these countries face and the importance of trying to identify and limit the spread of the virus at the early stages before it becomes entrenched in the high density urban or displaced person areas.

While each risk factor is relevant depending on the context, the pattern of reported cases for the onset of "COVID-19", in Africa is highly correlated with just a few: international exposure, size of urban population, and strength of health sector. The latter, importantly, reflects the capacity to conduct timely testing. The strong correlation shows the influence of international exposure on generating initial cases. This may reflect relatively effective efforts to contain the spread of the virus—or lagged reporting of cases. Accordingly, these countries will be important to watch.

While international exposure, size of urban population, and capacity for testing may drive the reported number of cases initially, subsequent stages are likely to also exploit other vulnerabilities such as weak health systems, densities of urban populations, conflict, size of displaced populations, trust in government, and openness of communications channels.

Since exposure rates and population density stood out among outstanding risk factors for the viral agent of this pandemic, we briefly discuss possible reservoir for viral distribution among the animals. Before SARS-CoV emerged, there were two model human coronaviruses, OC43 and 229E, both etiologic agents of the common cold (24). Since the identification of SARS-CoV, there have been reports of two new human coronaviruses associated with respiratory disease. HKUI is a group II coronavirus isolated from an elderly patient with pneumonia (35). HCoV-NL63 is a group I coronavirus isolated from a 7-month-old bronchiolitis and conjunctivitis (36-37).

It has subsequently been reported in other parts of the world (38-42). HCoV-NL63 is associated with serious respiratory symptoms, including upper respiratory infection, bronchiolitis, croup, and pneumonia in children and immunocompromised (41). The commonly used laboratory murine coronavirus, or MHV, strains infect primarily the liver and the brain (43). It is clear that the level of virulence as well as the tropism of MHV strains results from the interplay of viral gene products and the host immune response.

Mechanism for evading the immune response.

Transmissible gastroenteritis virus (TGEV) is a major cause of viral enteritis and fetal diarrhea in swine; it is most severe in neonates, with mortality (44). In neonates, TGEV infects epithelial cells of the small intestines, leading to potentially fatal gastroenteritis. Infection also occurs in the upper respiratory tract and, less often, in the lungs (45). In adults, TGEV causes mild disease. Porcine respiratory virus (PRCoV) is an attenuated variant of TGEV. PRCoV infects lung epithelial cells, and antigen is found in type I and type II pneumocytes as well as alveolar macrophages; infection is followed by interstitial pneumonia. A relatively new group I porcine coronavirus is PEDV. Interestingly, PEDV antibodies do not neutralize TGEV.

Avian coronavirus causes a highly contagious disease in chickens; it is spread by aerosol. Avian coronavirus replicates in upper respiratory tissues, with infection of bronchi and severe disease in young animals. Some strains cause more systemic infections, replicating in other tissues, including the kidney (causing nephritis), the oviduct (causing decreased egg production), and the gut (46-47). While chickens of all ages are susceptible, very young chicks exhibit more severe respiratory signs and much higher mortality than older birds (48). Maternal antibodies have also been shown to protect against IBV infection during the first 2 weeks of life. Adoptive transfer of CD8$^+$ T cells has been shown to protect against IBV challenge (46).

The feline coronaviruses are composed of two biotypes. Feline enteric coronavirus (FeCoV), commonly found in multicast environments in an asymptomatic carrier state, causes seroconversion. FIPV, a less common variant of FeCoV, has the ability to replicate in macrophages, causing a severe and lethal disease. FIPV may be viewed as a virulent variant of FeCoV that is selected for during persistent infection (47). FIPV replicates initially in pharyngeal respiratory or intestinal epithelial cells. Infection of macrophages then leads to viremia and systemic spread of the virus, including inflammation of the abdominal and thoracic cavities and causing occasional ocular and neurological disorders (49-50).

Bovine CoV is a ubiquitous virus worldwide as measured by serology. BCoV causes both respiratory and enteric disease, including calf diarrhea, winter dysentery in adults, and respiratory infections in cattle of all ages, including those with shipping fever. Viruses isolated from cattle with either respiratory or enteric disease are antigenically similar.

Contribution to sustainable development

Sustainable development is about today and tomorrow and about us and our children. Understanding the mode of transmission and outlining the associated risk factors of this novel “COVID-19”, will be of profound significance in designing and implementing effective intervention both for COVID-19 and allied novel pandemics which invariably impacts on sustainable development.

F. Limitation

Online survey should be supported by onsite survey to increase the response rates of suture studies. Extensive randomized online surveys including pre-survey piloting and follow-up phone calls to increase the response rates and broaden the survey impacts in future studies.

G. Conclusions

Therefore, from the above discussions, exposure rate, population density, timely testing, and age, were strong factors that significantly affected the distribution of “COVID-19”, with a hit map value of greater than 50. Exposures to different strains of Coronaviruses as well as their impact on virus transmission in tropical settings were discussed.

H. Conflict of Interest: None

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