GLOBAL COVID-19 TRANSMISSION AND MORTALITY - INFLUENCE OF HUMAN DEVELOPMENT, CLIMATE AND CLIMATE CHANGE ON EARLY PHASE OF THE PANDEMIC.

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Abstract

Many of the respiratory pathogens show seasonal patterns and association with environmental factors. In this article, we conducted a cross-sectional analysis of the influence of environmental factors, including climate change along with development indicators on the differential global spread and fatality of COVID-19 during its early phase. We used the published COVID-19 data by the WHO for April. Global climate data we used are monthly averaged gridded datasets of Temperature, Humidity and Temperature Anomaly. We used the HDI to account for all other socioeconomic factors that can affect the disease spread and mortality and build a negative binomial regression model. The temperature has a negative association with COVID-19 mortality. However, HDI is shown to confound the effect of temperature on the reporting of the disease. Temperature anomaly, which is being regarded as a global warming indicator, is positively associated with the pandemic's spread and mortality. Viewing newer infectious diseases like SARS-CoV-2 in the perspective of climate change has a lot of public health implications, and it necessitates further research.

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Key points

- Temperature is associated with COVID-19 mortality, though the relationship is weak.
- Human & National development has a significant influence on case detection and reporting of COVID-19, hence can confound the effect of environmental variables.
- Climate change has a significant association with COVID-19 transmission and mortality.
- Specific humidity does not affect COVID-19 transmission and mortality.

ABSTRACT

Many of the respiratory pathogens show seasonal patterns and association with environmental factors. In this article, we conducted a cross-sectional analysis of the influence of environmental factors, including climate change along with development indicators on the differential global spread and fatality of COVID-19 during its early phase. We used the published COVID-19 data by the WHO for April. Global climate data we used are monthly averaged gridded datasets of Temperature, Humidity and Temperature Anomaly. We used the HDI to account for all other socioeconomic factors that can affect the disease spread and mortality and build a negative binomial regression model. The temperature has a negative association with COVID-19 mortality. However, HDI is shown to confound the effect of temperature on the reporting of the disease. Temperature anomaly, which is being regarded as a global warming indicator, is positively associated with the pandemic's spread and mortality. Viewing newer infectious diseases like SARS-CoV-2 in the perspective of climate change has a lot of public health implications, and it necessitates further research.

KEYWORDS:

COVID-19, Environmental factors, Climate change, Temperature, Humidity, Temperature anomaly, Human Development Index

Abbreviations

SAT: Surface Air Temperature, SH: Specific humidity, SATAn: Surface Air Temperature Anomaly, GLM: Generalized Linear Modelling, K: Kelvin

1. INTRODUCTION:

Since its origin in Wuhan, Hubei province, China, the coronavirus disease has spread to more than a hundred and fifty countries across the globe, with a case-fatality ratio of above seven per cent in April, globally. Countries that were known to have a robust health system are now facing several hurdles not only in containing the disease but also in saving their affected population. Although the same pathogen has affected all these countries, there exists a significant variation in the pattern and magnitude of spread, the proportion of patients who require critical care, and fatality among the confirmed cases. This difference can be attributed mostly to the unlikeness among characteristics of either the host or the environment or both, which include general health and well-being of the population, dissimilarities in demographic, environmental & socio-political factors.

Environmental factors are well known to influence infectious disease epidemiology. In diseases of respiratory origin, low temperature, and dry weather favour the survival of droplets and promote rapid transmission (Davis et al., 2016; Yang & Marr, 2012; Mäkinen et al., 2009). Studies have also found that the absolute and relative humidity can modulate influenza virus transmission, survival, and seasonality (Lowen et al., 2007; Shaman & Kohn, 2009). The perceivable relationship between environmental factors and several infectious diseases has also shifted our attention to the problem of climate change. The temperature has been rising on a global perspective, with an accelerated soar of 0.18°C/decade in the past 30 years (Climate Change: Global Temperature | NOAA Climate.Gov, n.d.; Doc_num.Pdf, n.d.-a). The global warming can adversely affect all fields of life; hampered food production, increased occurrences of natural calamities, economic setbacks, impact on key and iconic ecosystems and emerging & re-emerging infectious diseases being only a few among them. WHO had warned the governments that climate change is likely to cause approximately 2.5 Lakhs additional deaths per year, on account of infectious causes and heat stroke. Parameters like monthly surface air temperature anomaly, global annual average temperature anomalies, and global temperature trends are widely being used as indicators of climate change (Doc_num.Pdf, n.d.-b; WMO, n.d.). Research papers which discusses the prospects of infectious disease burden to increase with climate change are many. We found previous studies that identify regions with risk of ENSO, a large-scale ocean surface temperature anomaly related phenomenon, associated with infectious diseases(Fisman et al., 2016; WHO | El Niño Southern Oscillation (ENSO) and Health, n.d.). Climate anomalies, apparently have an effect on the occurrence of outbreaks of diseases like dengue, chikungunya, zika, rift valley fever, cholera & plague(Kovats et al., 2003; Patz et al., 1996; Redding et al., 2017). Hence it is essential to look for any possible association of Covid19 with climatic factors, whatever the result is, and have many public health implications. We used the monthly Surface air temperature anomaly (SATAn) as an indicator of climate change.

Besides all these environmental and climatic variegations, there exist dissimilarities in social factors, economic well-being and national development across the globe which can determine the capacity for case detection, voluntary endorsement of preventive like self-quarantining and self-reporting to the health system and the travel and contact patterns of the citizens. Human Development Index (HDI) is a comprehensive measure of development, used to compare countries worldwide. It gave weightage on three basic dimensions of human development, viz Life expectancy at birth, mean years of schooling and expected years of schooling, and the gross national income per capita. All these factors can have a significant stake in the occurrence and reporting of COVID-19 cases. The proportion of people in older age segments will be higher in countries with high HDI and hence the impact of COVID-19. Similarly, if more and more people are knowledgeable and aware of the pandemic, the reporting will be higher. The knowledge about ways of spreading and strategies to prevent it will help the communities contain the outbreak. The factors contributing to the spread of the pandemic, like international travel, will be more in countries with higher income. In contrast, scarcity of personal protective equipment can be a threat to low-income countries. The ability of a country to purchase test kits can limit the reporting of COVID-19. All the factors explained above should be considered while studying the environmental impact on the disease's spread. So in the current analysis, we believe the HDI of the country as the surrogate measure of all confounders as mentioned heretofore. The study aims to assess the impact of country-specific environmental factors like atmosphere temperature, humidity, and the anomaly of air temperature on reported COVID-19 cases and deaths during the early phase of the pandemic, in countries with significant coronavirus disease transmission.

2. MATERIAL AND METHODS:

The effect of externalities, like meteorological and development factors in the transmission of SARS-CoV2, was explored in our cross-sectional analysis. By April 2020, the pandemic had reached most of the world. We assumed that country-specific disease control strategies have not yet been undertaken widely, since the communities are nascent to the disease. Hence we decided to use the data pertaining to April in our analysis. Our outcome variables are the number of reported cases of and confirmed deaths due to COVID-19 in April 2020. We used the WHO’s COVID-19 data and included all countries with a minimum reported caseload of ten coronavirus disease cases in April. We adjusted the number of reported cases and deaths to the country’s population. For demographic & developmental characteristics, we resorted to the UNDP & world bank database.

Our environmental explanatory variables are the monthly averaged values of Surface Air Temperature (SAT), Specific Humidity (SH), and Surface Air Temperature anomaly (SATAn) for every country reported in this study. The relative humidity is highly dependent on atmospheric temperature and can vary considerably among the indoor and outdoor environment. Absolute humidity is the fraction of water vapour over the air volume, therefore relies on the atmospheric temperature as the air volume changes with temperature. To avoid much of the collinearity between humidity and temperature, we used the specific humidity in our analysis. The SATAn is the difference between the observed temperature of a region and its long-term average reference value. A positive anomaly indicates that the measured temperature is warmer than predicted. In contrast, a negative anomaly means the actual temperature is less than the expected.

We extracted the explanatory environmental variables using a gridded product dataset, simulated from the Noah 3.6.1 model in the Famine Earth Warning Systems Network Land Data Assimilation System, available from the National Aeronautics and Space Administration Goddard Earth Sciences Data and Information Systems – Giovanni Version 4.34 (GES DISC Dataset: FLDAS Noah Land Surface Model L4 Global Monthly Anomaly 0.1 x 0.1 Degree (MERRA-2 and CHIRPS) (FLDAS_NOAH01_C_GL_MA 001), n.d.). The data range from January 1982 to present with global spatial coverage (60S, 180W, 90N, 180E) and 0.10-degree resolution. The LDAS systems (NLDAS and FLDAS) use optimal inputs to produce estimates of water balance and energy balance. We used the global SAT and SH data set, averaged for April, simulated from the FLDAS_Noah Land Surface Model L4 (Fig: 1). The monthly averaged SATan for April, simulated from the same Noah 3.6.1 model in the FLDAS system, describes how the month compares to the 35-year monthly climatology from 1982 to 2016, based on monthly data (Fig: 1). We imported the gridded data set into a GIS platform (QGIS Desktop 3.12.0) and then randomly plotted fourteen lakhs of points across the model. This procedure ensures representation from every 100 - 110Km2 of land area and can account the variabilities present inside a country. We averaged all random data points at the country level, which is the unit of our analysis to arrive at the nation wise mean and standard deviation of all our explanatory variables. The HDI was used in the analysis to adjust confounders reported elsewhere in this article. We used the HDI ranking 2018 and extracted the data from the UNDP's web portal (Human Development Data (1990-2018) | Human Development Reports, n.d.).

Descriptive statistical analyses performed at the baseline. Correlation between the explanatory variables and population-adjusted number of cases and deaths were studied. We used generalized linear modelling (GLM), negative binomial regression with system estimated dispersion parameter to model the number of confirmed cases and deaths due to coronavirus disease. We used IBM SPSS statistics (Trial version 26.0) and R (version 3.6.3) to conduct all statistical analysis.

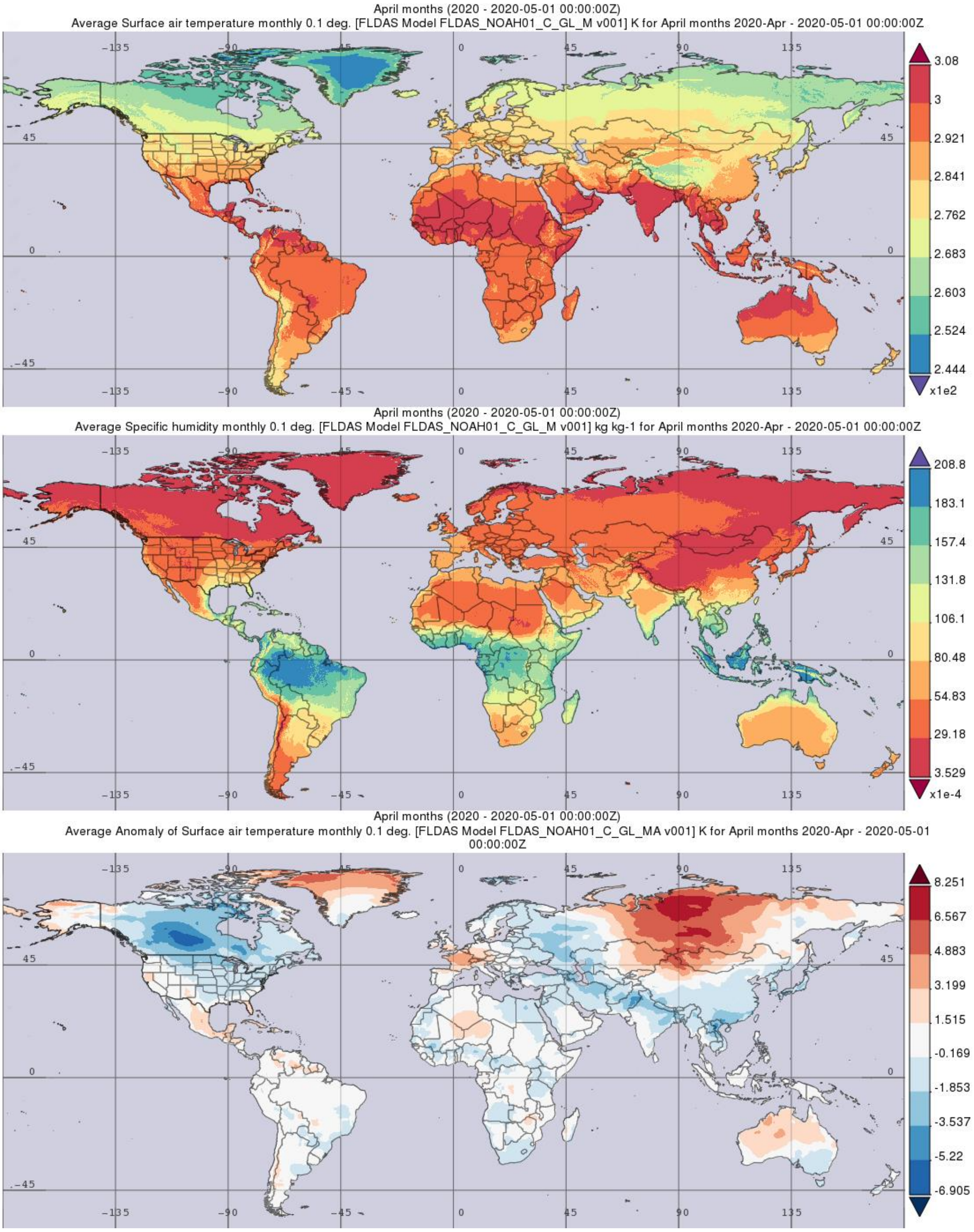

Fig:1 – Monthly Averaged - Surface Air Temperature, Specific Humidity and Anomaly of Surface Air Temperature For April. FLDAS Model - Data source: National Aeronautics and Space Administration Goddard Earth Sciences Data and Information Systems – Giovanni Version 4.34

3. RESULTS:

Among the countries whose HDI data is available in the public domain, one hundred and sixty-eight reported their COVID-19 statistics to WHO. An aggregate of 23,45,549 coronavirus cases and 1,83,313 deaths were reported in April 2020. One hundred fifty-seven countries were eligible to be included in our analysis as they have a reported caseload of ten or more. The population-adjusted cases and deaths yielded a highly positively skewed- distribution. All the explanatory variables (SAT, SH and SATAn) show significant ($p = 0.00$ for all correlations) bivariate correlation with the population-adjusted number of cases and deaths. SAT and SH negatively correlate with country-specific population-adjusted COVID-19 cases and deaths, whereas the HDI values and SATAn show a positive correlation. However, according to the multivariate analysis (GLM), the mean SATAn and the HDI have a statistically significant association with both the COVID-19 caseload and deaths. The mean SAT has a significant association with the fatality, not with the caseload. Humidity was associated neither to the caseload nor to the deaths (Table: 1). The Incidence Risk Ratio (IRR) for SATAn is 1.31 (1.07, 1.62), and 1.75 (1.41, 2.16) for reported cases and confirmed deaths, respectively which translates into 310 (70, 620) additional cases for every 1000 reported cases and 750 (410, 1160) more deaths for every 1000 confirmed deaths over one month for each 1K positive SATAn. Likewise, the IRR of SAT for confirmed deaths, 0.94 (0.90, 0.99) may be comprehended as 60 (100, 10) fewer deaths per 1000 confirmed deaths for every 1K rise in mean SAT

Explanatory variables	Reported cases/m		Confirmed deaths/10m	
	Coefficient (95%CI)	Statistical significance (p-value)	Coefficient (95%CI)	Statistical significance (p-value)
SAT Mean	-0.03 (-0.06, 0.006)	0.108	-0.06 (-0.11, -0.02)	0.009
SH Mean	0.04 (-0.03, 0.10)	0.271	0.003 (-0.06, 0.07)	0.925
SATAn Mean	0.27 (0.07, 0.48)	0.010	0.56 (0.34, 0.77)	0.000
HDI	6.9 (5.3, 8.5)	0.000	7.90 (5.83, 9.97)	0.000

Table: 1 Results of GLM – Modelling Population adjusted number of reported cases/deaths - Regression coefficient (95% confidence interval) and their statistical significances are shown in this table.

3.1 HDI:

The impact of HDI on COVID-19 transmission and fatality is found substantial. An increment in the index by 0.01 can result in 71 (54, 89) more cases per 1000 cases and 82 (60, 105) more deaths per 1000 deaths over one month. HDI category-wise (UNDP categorization) distribution of cases and deaths is shown in Fig: 2. We did a univariate analysis of HDI on reported cases and deaths. There is only a single nation with an HDI of less than 0.8 in the top twenty countries with the highest number of cases per million. HDI values show a reasonably good correlation with the number of reported cases and confirmed deaths (R = 0.76)

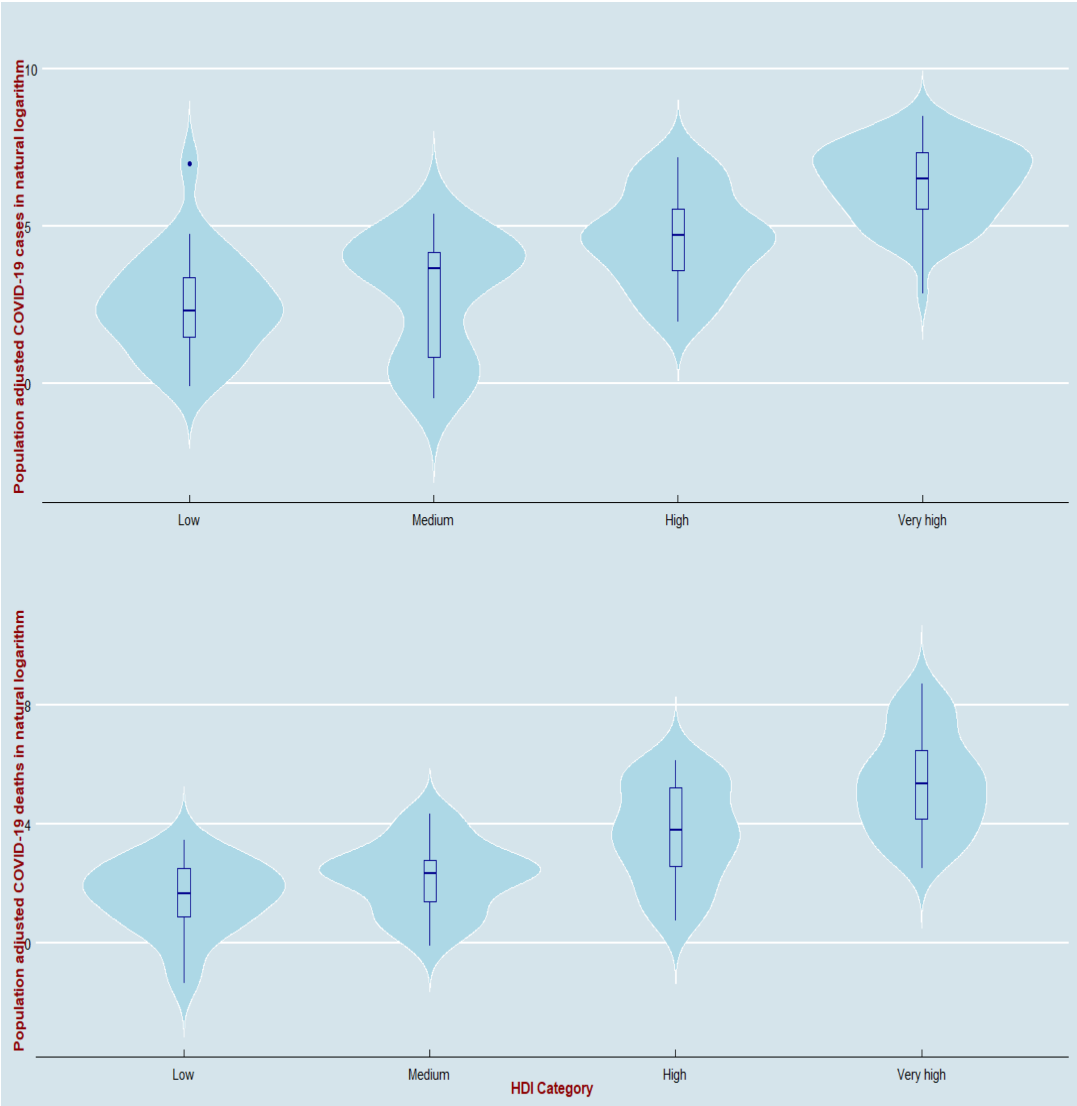

Figure: 2. Distribution of cases and deaths among countries categorized based on HDI - Violin plot showing the distribution of population-adjusted cases and deaths due to COVID-19. Countries were categorized according to UNDP classification based on the Human development index. Natural logarithm of cases and deaths is used for the plot.

3.2 Surface air temperature:

Even though correlated to the number of reported cases (ρ = -0.48), the mean SAT fails to elicit a statistically significant association in the presence of other environmental and development variables. In contrast, it elicits a protective effect in the model for COVID-19 deaths [IRR = 0.94 (0.90, 0.99)]. Most countries with a high caseload have lesser mean SAT and a higher HDI (Fig: 3). As most of the countries with a high HDI are located in temperate regions, and proportionately low HDI countries are in the tropical region, the higher incidence of cases in countries with cold climate is the impact of HDI.

Figure: 3. Scatterplot of population-adjusted COVID-19 cases and SAT mean showing the distribution of HDI. The scatterplot shows a negative correlation between mean surface air temperature and the natural logarithm of population-adjusted COVID-19 cases. Almost all of the countries with high caseload and low temperature have high HDI values.

3.3 Temperature anomaly:

Correlation plot of SATAn with population-adjusted caseload and fatality in COVID-19 portrays a statistically significant positive association for both outcomes (Fig:4). Based on the SATan data, we grouped the countries into two: those with a positive anomaly and a negative anomaly. A positive anomaly is associated with an IRR of 2.71 [(1.63, 4.50), (p = 0.00)] for cases and 5.15 [(2.76, 9.61), (p = 0.00)] for deaths when compared to a negative anomaly. No specific pattern of HDI or temperature couldn't we make out in the distribution of SATAn against reported cases or deaths in stratified analysis.

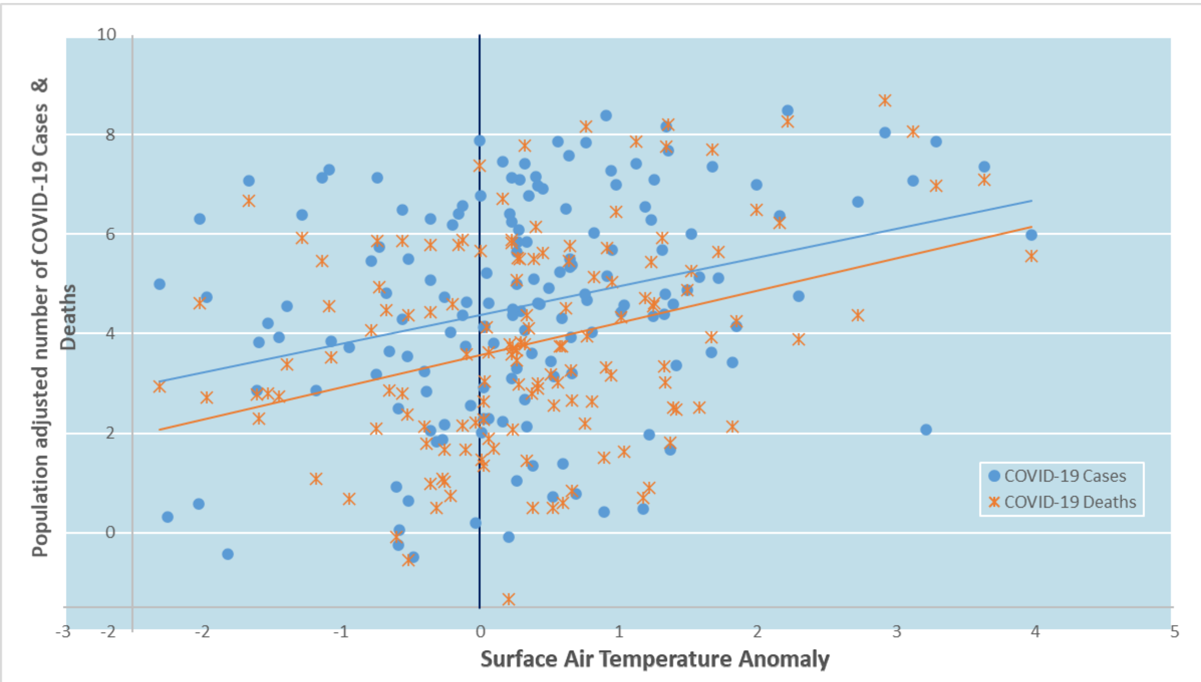

Fig: 4. Scatterplot showing the distribution of SAT anomaly and COVID-19 Cases & deaths in natural logarithm - The scatterplot shows the population-adjusted number of COVID-19 cases and deaths are increasing in countries with the increasing temperature anomaly.

4. DISCUSSION:

It is evident from this analysis that the overall social and economic development is a powerful determinant of the reported morbidity and mortality due to SARS-Co-V-2 infection. It may be due to either the better case detection & reporting efforts taken by these countries or a higher rate of infection in these societies because of the higher degree of social interactions among their citizens exhibiting a contact culture with very close interpersonal distances.

4.1 Temperature:

Many studies have analyzed and reported the impact of meteorological factors on the transmission and fatality of respiratory viruses, including Covid19, the most commonly studied being the influenza virus and RSV(Bloom-Feshbach et al., 2013; Shaman & Kohn, 2009). A Hong Kong-based study on SARS-CoV-1 proves that a higher risk of the SARS epidemic is linked to a lower temperature(Lin et al., 2006). Thermal inactivation of viruses at a higher temperature is a known fact(Polozov et al., 2008; Woese, 1960). Host innate immunity and adaptive immunity can get impaired at a low temperature. (Abram et al., 2017; Foxman et al., 2015; Kokolus et al., 2013). Even though a cold predominance hypothesis is statistically proven, the closeness to the null value of the coefficient's confidence interval may also recount that the effect of temperature on COVID-19 mortality compared to other factors is relatively less.

4.2 Humidity

In addition to altering host viral defence mechanisms, humidity can affect the survival of many viruses(Harper, 1961; Tang, 2009). A study conducted in the US reports that a drop in absolute humidity precedes seasonal outbreaks of influenza(Shaman et al., 2010). Since we used SH, which is the mass of water vapour over the mass of air, to avoid its dependency on atmospheric temperature, the effect of water vapour content of air alone on disease characteristics uninfluenced by atmospheric temperature, is modelled in our analysis. We could not establish a significant association of specific humidity with COVID-19 transmission or mortality.

4.3 Temperature anomaly

Climate changes and its relation to infectious diseases have become an essential point of debate for ecologists, climate scientists, and epidemiologists worldwide. This article is the first of its kind that has studied the association between SATAn and COVID -19. Climate extremes were believed as essential contributors to evolution. They are shown to cause genetic disquietudes in lower animals. Exposure to artificial heatwaves simulating global warming could result in differed gene expressions(Bergmann et al., 2010). Rodrı´guez-Trelles et al. demonstrated that the extent of the genetic anomaly was analogous with the temperature anomalies(Rodríguez-Trelles et al., 2013). Roberts et al. studied the effect of temperature on species susceptibility to RNA virus and found out that temperature may cause host shifts for viruses(Roberts et al., 2018) and increases the susceptibility of more susceptible species. Curtailing the likelihood of survival of an infectious agent, caused by a reduction in biodiversity, changing phenology including the geographic expansion of living organisms triggered by the changing climates, and ever-increasing human-wildlife interactions may act as potentiating contributors for such a host-species jump. Many of the emerging infectious diseases including Ebola, viral influenza, Nipah and the SARS-Cov are considered to originate from an animal host. Novel approaches in this regard, like modelling the likelihood of host - human spillover of Lassa virus infections attributes a large extent of such events to the climate change(Redding et al., 2016). Changes in the agent and host behaviours can result in unpredictable outcomes like epidemics and pandemics. We could make out from our study, a positive association for SATAn with the number of confirmed cases and deaths due to COVID-19 contrasted to the protective effect by Surface air temperature on coronavirus mortality. We were not able to make out any specific pattern of distribution of SAT in its anomaly. Hence we think, it is not unwise to assume that climate change has diverse causal pathways on the differential spread of and mortality due to COVID-19. The human costs and economic costs of emerging infectious events, being on the rise point towards better reasoning of the present scenario.

4.4 HDI:

Latitude specific spread of coronavirus disease pandemic across the temperate countries seem to have followed the pattern of other respiratory infections. However, It is an observable fact that temperate countries where the mean temperature is less when compared to tropical countries are mostly developed nations. As discussed earlier, HDI is a composite measure counting development in a couple of areas. The association between development parameters and coronavirus disease transmission is not astounding. Nations with better per capita income have robust surveillance systems. Only a capable surveillance system can distinguish a significant proportion of the undetected cases, primarily mildly symptomatic and asymptomatic, which get reflected in the number of reported cases. Identifying all those persons who had contacted a confirmed patient, strict observance of them under the health system for any COVID-19 related symptoms, and time-bound testing for the virus's presence depends heavily on the robustness of the surveillance system and the economic well-being of the state. The disease transmission is also determined by the population awareness of the disease, modes of transmission, and its symptoms, where literacy has a principal role. Those countries with a higher life expectancy at birth are expected to harbour a higher proportion of older adults, thus causing the reporting of cases and deaths on the more upper side. Hence it is essential to say that the rampant spread across a few geopolitical areas, in pandemic proportions cannot be accredited solely to the environmental factors.

5. CONCLUSION

Human development, differential across the globe, is a determinant of detecting and reporting cases and deaths due to COVID-19. This fact should be considered while quantifying the impact of climate factors on any infectious disease with a cross-border spread.

A good understanding of how the climate anomalies are associated to and interact with other contributing factors resulting in the emergence of newer infectious diseases and their propagation is necessary to use them for improved and sustainable health outcomes, which warrants the need for further research in this arena.

Limitations:

Our analysis, based on country-wise data, could have missed some of the microclimate variegations and regional spread of the disease.

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Availability of data and materials

All data used for the analysis are available in the following data repository. https://data.mendeley.com/datasets/svtjypr3pz/draft?a=7a1119be-91fb-4852-9616-64c70bdbb6ee

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Ethics approval and consent to participate

Not applicable

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