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Is Novel Coronavirus Novel: Covid-19 A Pandemic or An Endemic?

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Abstract

We have analysed the death and recovery rate of Covid-19 disease progression. From the analysis, we have argued that the pandemic is over in certain countries (labelled as group-A) and for other countries (labelled as group-B) the disease appears to remain as endemic. Taking into account the serological survey (sero-survey) test results obtained by certain groups and comparing it with herd immunity threshold value one can infer that the low number of infection for group-B is either due to acquired immunity by some previous infection by other coronavirus or due to innate immunity towards this infection. This effect is stronger for group-B to slow the progress of the disease to such an extent resulting in flattening of the disease progression curve compared to group-A.

Keywords: Covid-19, Herd Immunity Threshold, Corona Virus, Innate immunity, flattening the curve, serological survey.

Introduction:

Several reports were published by several Chinese groups revealing "A Novel Coronavirus" in patients with pneumonia in China around November and December, 2019, [1,2]. They had associated the source of this virus to a wholesale seafood market in Wuhan, China [1,2,3]. This novel coronavirus was named 2019-nCoV and was found to be different from both the earlier known MERS-CoV and SARS-CoV [1,2]. This 2019-nCoV virus was isolated from human airway epithelial cells and was identified under the microscope [1] and phylogenetic analysis of the complete genome was also reported [1]. It was also reported [4] that the 2019-nCoV probably originated from bat due to its 96% identity with a bat coronavirus at the genomic level. The disease associated with this 2019-nCoV virus was called Covid-19. This virus was reported to be new to humans and hence it was expected that the population will have no immunity to it. Thus, it was expected to spread very quickly in humans compared to other existing endemic coronaviruses. The other existing endemic coronaviruses also cause similar symptoms (such as cough, fever, etc.), for which the human population have already developed a certain level of immunity. Because of modern transportation network, the 2019-nCoV virus spread rapidly across the globe. Many countries started taking stringent measures to control the spread of the disease to avoid hospitals from being overburdened with Covid-19 patients. This rigorous measure was for the attempt to "flatten the curve" as it is now known popularly.

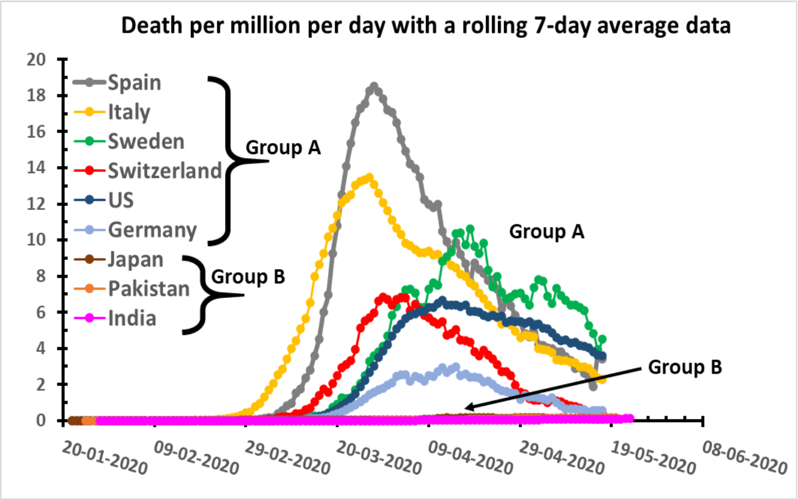
But surprisingly the total number of people reported to be infected is much lower [5] than the herd immunity threshold (HIT) even after the disease progression is showing a decreasing trend after passing through a maximum. The HIT is the critical number of a population that need to be immune in order for an infectious disease to end or remain stable in that population. This low value of reported cases raised serious controversy and to address this shortcoming, surveys of random sample testing of a given population were carried out to test presence of antibodies in the blood (sero-survey) which indicates past 2019-nCoV virus infection [6]. Interestingly these sample surveys showed that no more than 5 percentage of people were infected [6]. This percentage is too low to achieve HIT. The sero-survey results were sometimes found to be more than 50 times greater than the officially reported positive confirmed cases [6]. This low value of infected population obtained through sero-survey tests and the diminishing trend of the disease progression raises doubts regarding the attainment of HIT value that is necessary to curtail the spread of a disease and can only be explained if the remainder of the population are already immune to 2019-nCoV without showing antibodies for the same.

This could be possible only if the population has already developed the immunity to 2019-nCoV virus. There are two possibilities which could lead to this scenario. (1) The immunity developed due to other coronavirus infections in the past and (2) large portions of the population had already been infected by 2019-nCoV virus earlier which went unnoticed as we did not know the existence of this virus then. With this motivation we present some latest data on death rate and recovery rate from Covid-19 disease below.

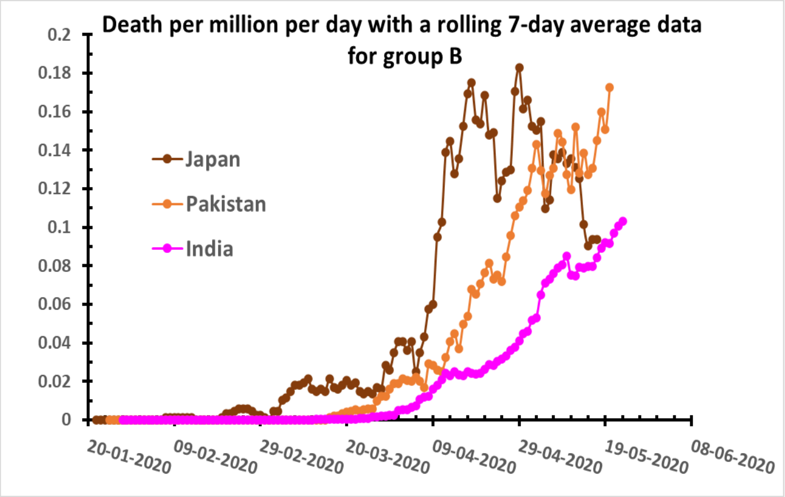
Results:

In our earlier report we had shown daily new confirmed cases per million with a rolling 7-day average data for different countries [5]. We clearly observed two groups: one with a very quick progression of the disease and with almost same rate of decrease (the group A), and another group showing a slower rise in the disease compared to group A and showing no peak till the date of reporting this article (the group B). The group B exhibited much lower number of confirmed cases at all times compared to group A resulting in the disease progression curve appearing flattened. We had attributed it to innate immunity of the population ie., high tolerance to the disease than that of group A [5]. In this article we shall analyse only the death rate and the recovery rate, since these two data are more reliable than the officially reported confirmed positive cases (please see our earlier report [5] on the analysis of the officially released confirmed positive cases data).

In fig. 1 (a, b) we show the death per million per day with a rolling 7-day average data as a function of date. We see a clear peak and the death rate decreases at a slower rate than the rising rate. The curves indicate that the disease is diminishing for group A. In group B the death rate is very low and slowly progressing to achieve its peak value. We see a similar trend in Fig. 2(a, b) for the case of recoveries per million per day with a rolling 7-day average data as a function of date for group A and group B. From these set of data one can clearly conclude that the pandemic is almost coming to an end for group A and for group B the disease appears to remain like an endemic as we will discuss this in the next section. Note: here, by pandemic we mean higher percentage of infection and death in the population spread worldwide and by endemic we mean slow progressing and low percentage of infection and death in a local population.



(a)



(b)

Fig 1(a) and (b) shows the death per million per day with a rolling 7-day average data as a function of date. *(b) is expanded graph for the countries in Group B. Data recovered from reference [7]*

Discussion:

From the above results, we see a group of countries with high mortality rate (Group A) having maximum of 2 to 20 deaths per million per day (with a seven day rolling average to smoothen the curve) and a second group (Group B) of countries with a maximum of 0.2 deaths per million per day. Thus, one can clearly infer that the pandemic outburst was severe in certain geographical regions unlike other regions where the outburst was less intense. Both the figures (fig. 1 and fig. 2) show the death and the recovery curves declining and tending towards zero for group A, indicating clearly the disease is almost on its way out. But, since the number of officially reported infected cases in all these countries are much lower than the HIT value (see table I), it suggests that the pandemic will eventually crossover to endemic and 2019-nCov virus will be present for long time if the HIT value has to be reached.

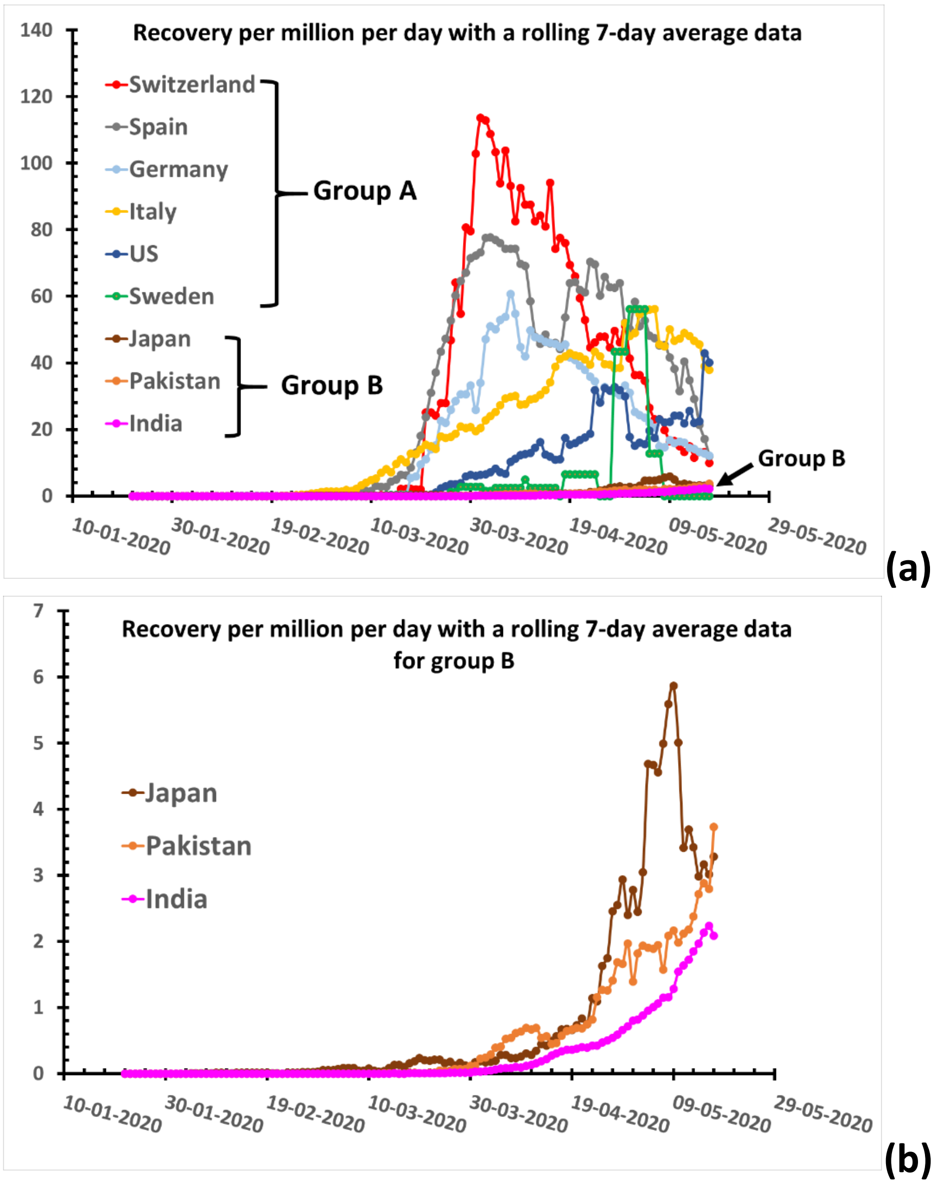


Fig 2(a) and (b) shows the recovery per million per day with a rolling 7-day average data as a function of date. (b) is expanded graph for the countries in Group B. Data recovered from reference [7]

HIT is related to the basic reproduction number (R0) which is a measure of transmission potential of a disease by a single infected individual to a susceptible population [8]. R0 is proportional to mainly three factors such as (1) the rate of contacts in the host population, (2) the probability of infection being transmitted during contact and (3) the duration of infectiousness. In general, for an epidemic to occur in a susceptible population R0 must be >1, hence the number of cases will increase exponentially. In the n^{th} generation of new infections, the number of infected people will be $(R0)^n$. For example, assuming that a person can be infectious only for a week, the time taken to infect one billion individuals with R0=2 will be 30 weeks and to infect the entire world population (~ 7.8 billion) will take 33 weeks. This simple calculation is not correct and looks unrealistic and thus more sophisticated models are used to predict the course of the disease. HIT requires that at least (1-1/R0) percentage of the population should be immune to the disease. In most real-life situations we deal with, the effective reproduction number is denoted as R, which is the average number of individuals an infected person can infect in a population where some are already immune (or some other interventions and protections are made) i.e., not all contacts will be susceptible to infection.

We know that in real world we find groups of population having different susceptibility due to different innate immunity to infection and this varies geographically as suggested by us earlier [5]. This tolerance to infection can be due to innate immunity acquired genetically [9-12], or as a result of immunity acquired by previous infections or immunisation. Therefore, not all contacts will become infected and the average number of secondary cases per infectious case will be lower than the basic reproduction number (R0). The effective reproduction number (R) now gives a better understanding of the situation because the number of susceptible people is incorporated within R. When R>1, the number of cases will increase, which happens at the start of an epidemic. When R=1, the disease is endemic, and when R<1 there will be a decline in the number of cases. R can be estimated by the product of R0 (which is fixed) and the fraction of the host population that is susceptible (S) (which can vary due to immunity developed). Hence R = R0×S. For example, if R0 for 2019-nCov is 2.5 in a population where quarter of the population is immune, the effective reproductive number for 2019-nCov is 2.5 x 0.75 = 1.875. Under these circumstances, a single case of 2019-nCov would produce an average of 1.875 new secondary cases. To successfully eliminate a disease from a population, R needs to be less than 1, which can be achieved by reducing the value of S. For R to be < 1 we require the value of S to be < 0.4 i.e., susceptible to be less than 40% of the population. In other words, the amount of immune population should be greater than 60% by either getting the population infected or by immunization, which is the value required for HIT for the case of Covid-19. But the value of positive cases officially reported by each country are nowhere near this HIT value as mentioned earlier. The small value of S can only be accounted for if some portion of the population are already immune to this 2019-nCoV virus because of previous exposure to the virus or have acquired immunity to 2019-nCov by previous infection from other coronaviruses. This small value of S realised by the trend of the curves (data) in Fig. 1 and 2 does not rule out the possibility that the disease is not ‘novel’ to the human population. This has to be investigated further and we should also take into account of mortality due to "influenza-like illness" (ILI) along with other illnesses, such as pneumonia, that cause similar symptoms, notably fever, dry cough, nausea, body aches, and nausea and compare it with covid-19 mortality for more clear understanding.

Following the discussion above, we can now address the main issue i.e., why the officially reported infected cases are very low when we can clearly see that the disease is already coming to an end. As we have mentioned above, the sero-survey antibody testing revealed that positive cases can be as large as 50 times more and so, if we consider the actual infected cases is 50 times than the reported cases, it is still far below the HIT value. Further, if we exaggerate and consider the actual infected cases to be 100 times more than the reported value, then some countries are close to HIT value as can be seen from Table I. The last column of Table 1 reflects the nature of the susceptibility of the population and the stringent measures taken towards delaying the spread of the disease This requirement of inflating the number of infected case or reducing the value of S to fulfil HIT for the disease which is getting over can only be answered by invoking the propositions mentioned in the introduction. But the group B countries are far behind in achieving HIT and are also yet to reach the peak in the disease progression with the exception of Japan. The interesting observation in case of Japan is that we see a clear peak and a decreasing trend in both the death and the recovery rate, which implies that Japan will have to go through several peaks before it achieves the HIT or will have to wait for vaccine to fulfil the HIT criteria to end the disease.

Table I: *List of countries with their populations, confirmed covid-19 cases (CC) as on 25th May 2020, cases multiplied by 100 (CC100) (in millions) and percentage of CC100 w.r.t total population (Data adapted from reference [13])*

Country	Total population in millions [13]	Confirmed case (CC) in millions as on 25th May 2020 [13]	100 times the Confirmed case (CC100) in millions (100 × CC)	Percentage of CC100 w.r.t total population
US	331.0	1.701	170.1	51.4
Italy	60.5	0.230	23.0	38.0
Spain	46.75	0.283	28.0	59.9
Germany	83.8	0.181	18.1	21.6
Sweden	10.1	0.034	3.4	33.7
Switzerland	8.65	0.031	3.1	35.8
Japan	126.5	0.017	1.7	1.3
India	1,380.0	0.145	14.5	1.05
Pakistan	220.9	0.056	5.6	2.5

Conclusion:

To summarize, we have shown that the covid-19 pandemic is almost over in most of the strongly affected countries such as the Group A countries inferred from the radical drop in the death rate and the recovery rate simultaneously because of the decrease in the number of new cases. Some countries where the progression of disease is very slow are yet to achieve the peak in the disease progression but favourably show very small death rate. If herd immunity is to be achieved by every country then the countries falling under group B are far behind and will take longer time to reach the HIT value. It appears that the group B is already protected by some previous infection by other coronavirus or by a previous infection by 2019-nCoV or by innate immunity resulting in flattening their disease progression curve. In, countries falling in group B, covid-19 seems to be endemic rather than pandemic. If mortality due to Flu, pneumonia and ILI are included in the analysis and compare it with covid-19 mortality a clearer understanding can be obtained.

Ethical approval: This study did not require ethical approval

Conflict of interest: None

Declarations of interest: None

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References:

[1] Na Zhu et. al., “A Novel Coronavirus from Patients with Pneumonia in China, 2019”, N Engl J Med **382**:727-33 (2020).

[2] Chaulin Huang et. al., “Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China”, Lancet **395**: 497–506 (2020)

[3] Hongzhou Lu, Charles W. Stratton and Yi-Wei Tang, “Outbreak of pneumonia of unknown etiology in Wuhan, China: The mystery and the miracle”, J Med Virol., **92**: 401–402 (2020)

[4] Peng Zhou et. al., “A pneumonia outbreak associated with a new coronavirus of probable bat origin”, Nature **579**: 270 (2020).

[5] S. Banerjee, “Can innate immunity flatten the curve? Covid-19 – A case study”, Preprints (www.preprints.org) Posted: 19 April 2020, doi:10.20944/preprints202004.0353.v1

[6] Eran Bendavid et. al., “COVID-19 Antibody Seroprevalence in Santa Clara County, California”, medRxiv preprint doi: https://doi.org/10.1101/2020.04.14.20062463.

[7] Data used from : https://data.humdata.org/dataset/novel-coronavirus-2019-ncov-cases

[8] Paul L. Delamater et. al., “Complexity of the Basic Reproduction Number (R0)”, Emerging Infectious Diseases Vol. 25, No. 1, pg 1 (2019). Rothman KJ, Lash T, Greenland S. Modern Epidemiology (3rd ed.), Lippincott Williams & Wilkins, 2013

[9] Scott Alper, Rebecca Laws, Brad Lackford, Windy A. Boyd, Paul Dunlap, Jonathan H. Freedman, and David A. Schwartz, “Identification of innate immunity genes and pathways using a comparative genomics approach”, PNAS, 7016–7021 105(19) (2008).

[10] Massimo Mangino, Mario Roederer, Margaret H. Beddall, Frank O. Nestle, and Tim D. Spector, “Innate and adaptive immune traits are differentially affected by genetic and environmental factors”, Nature Communications|8:13850| (2017).

[11] Z Du, SK Sharma, S Spellman, EF Reed and R Rajalingam, “KIR2DL5 alleles mark certain combination of activating KIR genes”, Genes and Immunity, 470–480 9(2008).

[12] JL. McCarville and JS Ayres “Disease tolerance: concept and mechanisms”, Current Opinion in Immunology 88–93, 50(2018).

[13] https://www.worldometers.info/coronavirus/#countries