

Estimation of Reproduction Number of SARS-COV-2 Omicron Variant Outbreak in Hong Kong

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Abstract

We present the evolution of time dependent reproduction number across the five different Hong Kong Special Administrative Region of the People's Republic of China (HK) epidemic waves from January, 2020, to March, 2022. We provide reliable estimation of reproduction number of Omicron variant of concern (VOC) by analysing data related to fifth wave to determine its peculiar characteristics with respect to the other VOCs. HK could be considered as the optimal model for the calculation of the dynamics of Omicron VOC transmission in an environment representative of the fully populated cities of the Asian Pacific coast. On the basis of R_t calculated for Omicron VOC in our work, researchers could refine provisional data for the current outbreak which is affecting China.

Introduction

The Hong Kong Special Administrative Region of the People's Republic of China (HK) recorded relatively few cases of coronavirus disease 2019 (COVID-19), especially if compared with other densely populated regions, due to the quick restrictive measures adopted at the beginning of the outbreak, which caused low local transmission rates with few or no local infections, as demonstrated by the mean effective reproductive number between January 23rd, 2020, and May 12th, 2021 [1,2]. As a result, from January 2020, HK had a total cumulative incidence of about 10000 positive tested cases thanks to an “elimination strategy” which supports the so-called “Zero- COVID” regime, albeit it featured formally four different pandemic waves.

However, in January 2022 the sudden increase of new positive tested cases boosted the fifth wave of the epidemic, with such a worrying increase in new cases that it has pushed China's President Xi Jinping to order HK to stabilize its covid-19 fifth wave of the epidemic as “overriding mission” [3]. The new wave was attributed to the B.1.1.529 variant of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), designated as a variant of concern (VOC) Omicron by the World Health Organization (WHO) on November 26th, 2021 [4].

Since HK Chief Executive Carrie Lam decided to track the epidemic through an extensive and enduring contact tracing involv-

ing the entire HK population, the fifth HK wave offered a unique way to determine quantitative epidemiological parameters related to the Omicron VOC only, because most of the recorded infections have been attributed only to Omicron VOC which developed from an environment where a “Zero COVID” regime was present and other VOCs were not existing. Since China's recent COVID-19 outbreak is predominantly led by the Omicron subvariants BA.5.2 and BF.7, which together account for 97.5% of all local infections, the analysis of HK dynamics of the 2022 epidemic could represent an effective model for it [5].

In a previous work, we provided a mapping of the Alpha VOC transmission dynamics spread in all regions of Italy in the first year of the COVID-19 pandemic [6]. With the same methods, we studied the evolution of time-dependent reproduction numbers across the five different HK epidemic waves to obtain an estimation of the reproduction number of Omicron VOC in order to determine its peculiar characteristics with respect to the other VOCs.

Material and Methods

Epidemiological Data

Official data on the COVID-19 pandemic in Hong-Kong has been taken from the complete *Our World in Data* COVID-19 dataset as downloaded by <https://ourworldindata.org/> website. These data are available as open source for all purposes and complemented by vaccination data as implemented by Mathieu et al., 2021 [7]. Data

for the analysis were considered from 2020-01-23 to 2022-03-01, i.e. 769 days from the onset related to the first COVID-19-positive cases recorded in Hong-Kong. In this period, we consider the daily number of new confirmed positive cases defined as “Daily Incidence” and the number of Fully Vaccinated people, i.e. the number of people that received a full vaccination cycle.

Estimation of Time Dependent Reproduction Number R_t

To evaluate the time dependent reproduction number R_t we adopted the method developed by Wallinga and Teunis, 2004 [8]. The transmission probability (p_{ij}) of individual i being infected by individual j at t_i, t_j onsets, respectively, can be described mathematically as [9]:

$$p_{ij} = \frac{N_i \phi(t_i - t_j)}{\sum_{i \neq k} N_i \phi(t_i - t_k)} \quad (1)$$

where ϕ_i is the distribution of the generation time corresponding to the distribution of the serial interval, i.e. the time between when a person gets infected and when they subsequently infect another other people, calculated at the time i within the assumption that the incubation period does not change over the course of the epidemic [10]. We considered that the distribution of the serial the interval was expected to follow a gamma distribution with a mean (\pm SD) of 6.50 ± 4.03 days as reported by the Imperial College COVID-19 Response Team [11].

The net reproduction number R_j is then then sum of all p_{ij} involving j as the infector $R_j = \sum_j p_{ij}$ and it can be averaged over all cases with same date of onset as $R_t = \frac{1}{N_t} \sum_{\{t_j=t\}} R_j$.

Since R_t are computed by averaging over all transmission networks compatible with observed incidence data, no assumption is made about the time dependence of the epidemic unlike, for example the exponential growth in the well-known Bayesian approach [8,9].

We believe, hence, that this model is particularly suitable to estimate the reproduction number in the post-peak period where the transmission is expected to decrease. All the above data analyses were performed using the R0 package [9] as implemented in the statistical software R (R Core Team; 5 R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <https://www.R-project.org/>), 2017).

Results

The daily incidence of COVID-19 tested positive cases in HK is represented in [Figure 1]. From 2020, January 1st, to 2022, March 1st, HK featured different five pandemic waves. Looking at the smoothed time dependence of effective reproduction number across the waves [Figure 2], we recorded a rather modest variation with only few events weakly deviating from the control $R_t = 1$ regime. However, at the beginning of January, 2022 the sudden increase of daily incidence boosted dramatically the fifth wave of epidemic reaching the 50,000 cases in few days, with maximal R_t and smoothed R_t estimated reaching about 3.5 and 2.2, respectively (see also Figure 2).

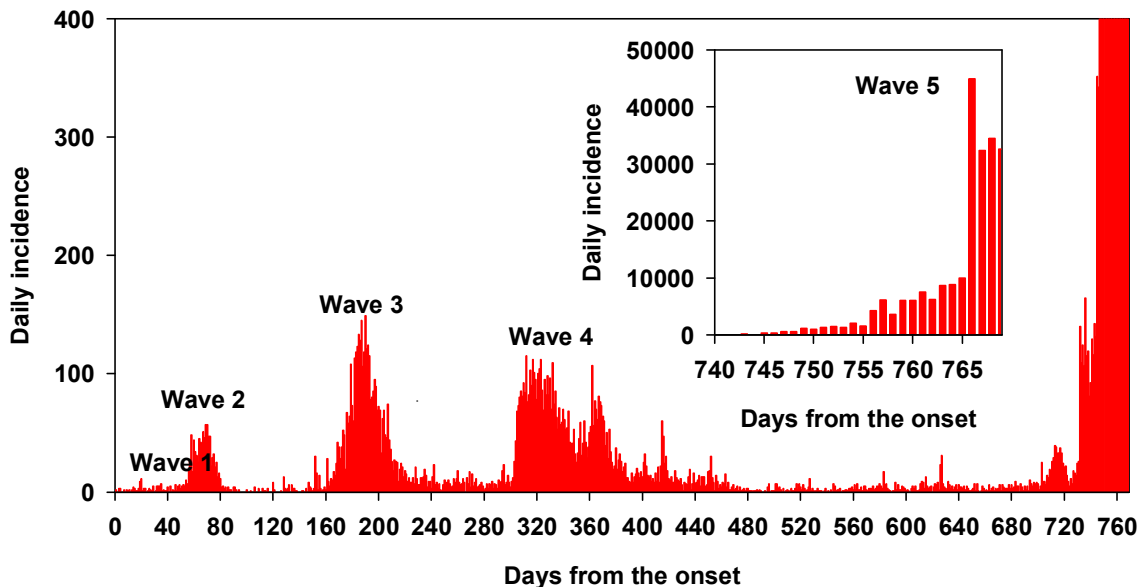


Figure 1: Daily incidence related to confirmed cases in Hong Kong.

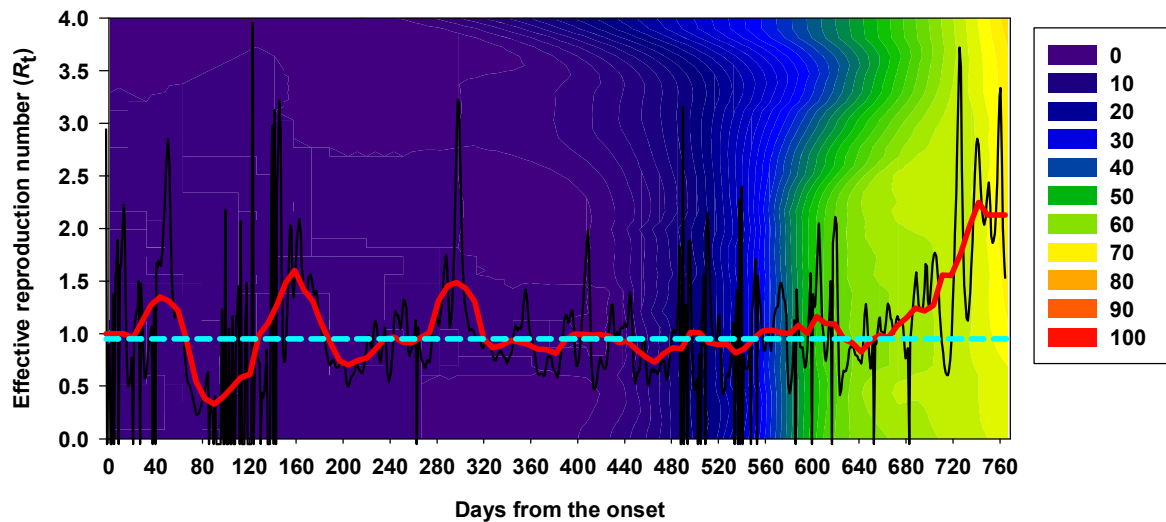


Figure 2: Time evolution of effective reproduction number across the five waves: original series (thinner profile) and moving average smoothing (thicker profile). The false color scale represents the percentage (%) of fully vaccinated people over the total population resident in Hong Kong [7].

Discussion

Based on previous literature, we know that Omicron VOC showed early doubling time consistently shorter than Beta and Delta VOC [12], with a reproduction number expected greater than three times with respect to Delta [13]. However, the Omicron VOC epidemic developed in countries where other VOCs are highly diffused, so it is difficult to derive the contribution of Omicron VOC only from the analysis of cumulative positive cases recorded without an accurate “genomic” tracing able to separate the relative contribution of several VOCs. Hence, only few estimations are available in the literature, based mainly by defining the ratio with respect to Delta VOC or by analyzing small cluster of infected people [14-18].

Despite HK is one of the most densely populated area in the world, before 2022, the effects of restrictive measures imposed by HK government were very satisfactory in limiting the spread of pandemic, despite the virus mutations [19,14], hence the fifth wave in HK offered a different perspective to evaluate intrinsic epidemiological parameters related to Omicron VOC because it developed from a rather unperturbed zero-covid environment.

In this work, we estimated the reproduction number of Omicron VOC by means of the analysis of the fifth wave of the COVID-19 pandemic in HK, featured since January to February, 2022, determining and comparing the evolution of time dependent reproduction number across the five different HK waves in order to obtain the peculiar characteristics of Omicron VOC with respect to the other epidemic waves. We determined for the fifth HK pandemic (highly related to Omicron VOC) a mean R_t approx. 2, in agreement with Kim et al. [20].

Omicron VOC has a growth advantage over the others because of its higher transmissibility, immune evasion, and shorter serial interval [15], which is shorter than or close to its median incubation

period [21]. This suggests that a significant amount of secondary transmission may occur prior to the symptomatic disease onset, thus facilitating the epidemic. In the fifth wave of HK, the effective R_t remained persistently high even in a context with relevant full vaccination coverage [22] (see also the “false colors” contour plot in Figure 1), probably due to the scarce effectiveness of BNT162b2 and CoronaVac against Omicron VOC, especially in children and adolescents [23].

Conclusions

The initial stages of the fifth wave of the COVID-19 pandemic in HK, which occurred in January 2022, could be considered as the optimal model for the calculation of the dynamics of Omicron VOC transmission in an environment representative of the fully populated cities of the Asian Pacific coast.

Moreover, on the basis of R_t calculated for Omicron VOC in our work, researchers could refine provisional data for the current outbreak which is affecting China.

Author contributions

Mattia Allieta: conceptualization (lead); data curation (equal); formal analysis (lead); writing original draft (supporting); writing-review and editing (supporting). **Jelena Komloš:** data curation (equal); writing-review and editing (lead). **Davide Rossi Sebastiano:** writing-original draft (lead); supervision (lead).

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