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### Early insights from statistical and mathematical modeling of key epidemiologic parameters of COVID-19

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1 **Manuscript Number** EID-20-1074

2 **Article Summary Line:** The summary of current knowledge on parameters of disease  
3 transmission will be essential for further planning and response of the COVID -19 epidemic.

4 **Running Title:** Key Epidemiological Parameters of COVID-19

5 **Keywords:** COVID-19; epidemiological parameters; mathematical modelling.

6 **Title** Key Epidemiological Parameters of COVID-19: A Review of Early Insights from  
7 Statistical and Mathematical Modelling

8

9 **Authors:** The WHO COVID-19 Modelling Parameters Group<sup>1</sup>

10 <sup>1</sup> Members of the group are listed at the end of the article.

11 **Abstract**

12 We report key epidemiological parameter estimates for COVID-19 identified in peer-  
13 reviewed publications, pre-print articles, and online reports.

14 Range estimates for incubation period were 1.8 to 6.9 days, serial interval 4.0 to 7.5 days,  
15 and doubling time 2.3 to 7.4 days. The effective reproductive number varied widely, with  
16 reductions attributable to interventions. Case burden and infection fatality ratios increased with  
17 age. Implementation of combined interventions could significantly reduce cases and delay  
18 epidemic peak up to one month.

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19           These parameters for transmission, disease severity and intervention effectiveness are  
20 critical for guiding policy decisions. Estimates will likely change as new information becomes  
21 available.

## 22           **Introduction**

23           On December 31, 2019, Chinese authorities notified the World Health Organization  
24 (WHO) of a pneumonia cluster of unknown etiology in Wuhan. (1); A novel coronavirus was  
25 subsequently isolated. As of March 7, 2020, the disease and causative agent, officially named  
26 COVID-19 and SARS-CoV-2 respectively, had resulted in 101,927 cases and 3,486 deaths in 94  
27 countries spanning 6 continents.(2) The spectrum of illness ranged from asymptomatic infection,  
28 to mild disease (e.g., fever, dry cough and myalgias), pneumonia and death. Roughly 20% of  
29 cases require hospitalization for shortness of breath; death is associated with increasing age and  
30 underlying comorbidities (e.g., hypertension, cardiovascular disease and diabetes).(3)

31           Here, we review important parameters of COVID-19 transmission dynamics from  
32 statistical and mathematical modeling studies using epidemiologic data reported in the first 60  
33 days of the epidemic. We estimate the key components that contribute to future modeling on the  
34 effects of non-pharmaceutical interventions (NPIs) and to inform critical resource allocation  
35 decisions.(4) Data estimates are current as of March 6, 2020, a few days before WHO  
36 characterized COVID-19 as a pandemic on March 11, 2020 (WHO Director General remarks,  
37 <https://www.youtube.com/watch?v=sbT6AANF0m4&feature=youtu.be>), and subject to change  
38 as more information becomes available.

## 39           **Methods and Results**

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40           We reviewed the literature on key epidemiological parameters (Table 1) relating to the  
41 COVID-19 epidemic. This is not a formal systematic review as the epidemic is rapidly  
42 unfolding, and useful data sources exist that have not yet been peer-reviewed. We searched the  
43 peer-reviewed and gray literature, including pre-prints, research reports, and forum posts.  
44 Searches for individual parameters were conducted from February through March 6, 2020 on  
45 PubMed, medRxiv, bioRxiv, arXiv, SSRN, Research Square, Virological, Imperial College  
46 COVID reports, and Wellcome Open Research. Search terms centered on the various names of  
47 the disease and virus over the course of the epidemic (“nCoV”, “COVID”, “SARS-CoV-2”,  
48 “novel coronavirus”), and keywords relating to each of the epidemiologic parameters or  
49 characteristics considered (see Supplementary Table 1). Genetic epidemiology estimates, such as  
50 evolutionary rate and time from last common ancestor were selected from Virological  
51 (<http://virological.org/>). Articles in English and Chinese were included if they used mathematical  
52 or statistical methods for adjustment of different biases and if they were either: i) Peer-reviewed  
53 or ii) non-peer reviewed requiring established methods (i.e., clarity about the data used, known  
54 statistical methods, and reported uncertainty).(5–8)

55

56           For each parameter, characteristics such as study population, assumptions, and analytical  
57 methods were summarized when patterns were discernible across estimates. Estimates were  
58 summarized as ranges to reflect remaining uncertainty. No meta-analyses were performed.

59

60            $R_0$  and  $R$

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61           One of the key early indicators of transmissibility of a novel pathogen is  $R_0$ , the basic  
62 reproduction number, which represents the average number of people infected by an incident  
63 individual in a fully susceptible population. Values for  $R_0$  above one are considered a critical  
64 threshold for epidemic growth. Mean  $R_0$  estimates for Hubei Province, China ranged widely, 2.1-  
65 5.1 (peer-reviewed) and 2.0-7.7 (Majumder and Mandl, unpub. data,  
66 [https://papers.ssrn.com/sol3/papers.cfm?abstract\\_id=3524675](https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3524675); Liu et al., unpub. data,  
67 <https://www.biorxiv.org/content/10.1101/2020.01.25.919787v2>; Mizumoto et al., unpub. data,  
68 <https://www.medrxiv.org/content/10.1101/2020.02.12.20022434v2.full.pdf>; Zhou, unpub. data,  
69 <https://www.medrxiv.org/content/10.1101/2020.02.15.20023440v2.full.pdf>; Sun et al., unpub.  
70 data, <https://www.medrxiv.org/content/10.1101/2020.02.17.20024257v1>), reflecting a variety of  
71 assumptions and methods utilized and data uncertainty (Figure 1).(9–14) A subset of more recent  
72 estimates accounted for the broad restrictions implemented on January 23 in Hubei explicitly and  
73 were lower than earlier estimates (1.0-2.9); Sun et al., unpub. data,  
74 <https://www.medrxiv.org/content/10.1101/2020.02.17.20024257v1>; Xu et al., unpub. data,  
75 <https://www.medrxiv.org/content/10.1101/2020.02.25.20024398v1>; Wan et al., unpub. data,  
76 <https://www.medrxiv.org/content/10.1101/2020.02.16.20023804v1>). Mean  $R_0$  estimates for  
77 provinces outside of Hubei or for all of China were similar to those for Hubei before the  
78 implementation of travel restrictions (peer-reviewed range: 0.4-3.9; preprint range: 0.6-6.4; Liu  
79 et al., unpub. data, <https://www.biorxiv.org/content/10.1101/2020.01.25.919787v2>; Sun et al.,  
80 unpub. data, <https://www.medrxiv.org/content/10.1101/2020.02.17.20024257v1>; Xu et al.,  
81 unpub. data, <https://www.medrxiv.org/content/10.1101/2020.02.25.20024398v1>; Tindale et al.,  
82 unpub. data, <https://www.medrxiv.org/content/10.1101/2020.03.03.20029983v1>; Shen et al.,  
83 unpub. data, <https://www.biorxiv.org/content/10.1101/2020.01.23.916726v1>; Wang et al., unpub.

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84 data, <https://www.medrxiv.org/content/10.1101/2020.02.29.20029421v1.full.pdf>; Ku et al.,  
85 unpub. data, [https://papers.ssrn.com/sol3/papers.cfm?abstract\\_id=3543589](https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3543589); Song et al., unpub.  
86 data, <http://medrxiv.org/lookup/doi/10.1101/2020.02.29.20029421>).(11,14–17)  $R_0$  estimates for China  
87 and cases outside China attributed to exportation (peer-reviewed range: 2.1-3.2; preprint range:  
88 2.1– 5.7; Read et al., unpub. data,  
89 <https://www.medrxiv.org/content/10.1101/2020.01.23.20018549v2.full.pdf>; Zhang and Wang,  
90 unpub. data, <https://www.biorxiv.org/content/10.1101/2020.01.25.919688v3>; Zhou et al., unpub.  
91 data, <https://www.medrxiv.org/content/10.1101/2020.02.06.20020941v1.full.pdf>; Volz et al.,  
92 unpub. data, [https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-](https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College---COVID-19---genetic-analysis-FINAL.pdf)  
93 [fellowships/Imperial-College---COVID-19---genetic-analysis-FINAL.pdf](https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College---COVID-19---genetic-analysis-FINAL.pdf)),(14,18,19),estimates  
94 for the Diamond Princess cruise ship (mean  $R_0$  of approximately 2.2),(20) and estimates for  
95 Singapore and Republic of Korea (range: 2.6-3.2; Tindale et al., unpub. data,  
96 <https://www.medrxiv.org/content/10.1101/2020.03.03.20029983v1>) were generally lower. A  
97 meta-analysis of seven early COVID-19 studies that accounted for uncertainty in assumptions  
98 estimated an  $R_0$  of 2.9 (95% CI: 2.1-4.5; Park et al., unpub. data,  
99 <https://www.medrxiv.org/content/10.1101/2020.01.30.20019877v4>).

100

101 High variability in  $R_0$  estimates can result from a mix of data (e.g.s., time period of cases  
102 analyzed; data available by onset date), methods (e.g.s.,  $R_0$  as a component of early exponential  
103 growth; fitting case data to compartmental models), and assumptions (e.g.s., serial intervals; case  
104 ascertainment). In particular, serial interval estimates directly affect  $R_0$ : shorter serial intervals  
105 suggest that fewer transmission events are required for rapid growth. However, most  $R_0$

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106 estimates reviewed here employed serial intervals values between 7.5 (COVID-19) and 8.4  
107 (SARS); these differences likely had limited effects.(7,9)

108

109           Importantly,  $R_0$  reflects average transmission, not individual-level transmission.  
110 Variability (dispersion) among individual-level contacts and transmission potential can lead to  
111 many individuals infecting no additional people, while others infect many as previously observed  
112 for the Severe Acute Respiratory Syndrome (SARS) and the Middle East Respiratory Syndrome  
113 (MERS).(21,22) This pattern has also been observed for COVID-19 with estimates of the  
114 dispersion parameter below one (e.g., 0.5 in Singapore (Tariq et al. unpub. data,  
115 <https://www.medrxiv.org/content/10.1101/2020.02.21.20026435v4.full.pdf>), 0.54 in China (14),  
116 0.58 in Shenzhen (16). This implies that a minority of cases may cause the majority of infections,  
117 e.g., in Shenzhen, 8.9% of cases were found to cause 80% of infections. (16) Rigorous contact  
118 tracing data are needed to improve these estimates and identify opportunities to tailor  
119 interventions accordingly. (23)

120           Explicit estimates of the time-varying or effective reproduction number,  $R$  (often referred  
121 to as  $R_t$  or  $R_E$ ), can identify changes in transmission over time as a result of interventions and  
122 acquired immunity. Mean estimates of  $R$  before January 23 generally fall within the 2.3 to 2.6  
123 range (peer-reviewed) and 3.9 to 6.2 range (preprints; Liu et al., unpub, data,  
124 <https://www.biorxiv.org/content/10.1101/2020.01.25.919787v2>; Wang et al., unpub. data,  
125 <https://www.medrxiv.org/content/10.1101/2020.03.03.20030593v1>).(24,25) Shortly after the  
126 travel restrictions,  $R$  estimates ranging from 0.4-1.0 (peer-reviewed) to 0.2-3.4 (preprints)  
127 indicated a decrease in transmission in Wuhan and other parts of China (Liu et al., unpub data,

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128 <https://www.biorxiv.org/content/10.1101/2020.01.25.919787v2>; Mizumoto et al., unpub. data,  
129 <https://www.medrxiv.org/content/10.1101/2020.02.12.20022434v1.full.pdf>; You et al., unpub.  
130 data, <https://www.medrxiv.org/content/10.1101/2020.02.08.20021253v2.full.pdf>; Wan et al.,  
131 unpub. data, <https://www.medrxiv.org/content/10.1101/2020.02.16.20023804v1>; Ku et al.,  
132 unpub. data, [https://papers.ssrn.com/sol3/papers.cfm?abstract\\_id=3543589](https://papers.ssrn.com/sol3/papers.cfm?abstract_id=3543589); Wang et al., unpub.  
133 data, <https://www.medrxiv.org/content/10.1101/2020.03.03.20030593v1.full.pdf>; Chong et al.,  
134 unpub. data, <https://www.medrxiv.org/content/10.1101/2020.03.02.20028704v1.full.pdf>; Chen et  
135 al., unpub data, <https://arxiv.org/pdf/2003.00305v1.pdf>).(16,24) In Singapore and the Republic of  
136 Korea, declines in  $R$  estimates also suggest decreases in transmission; 1.1 to 0.7 as of February  
137 14 in Singapore, and 1.5 (95% CI: 1.4, 1.6) in Republic of Korea up to February 27 (Tariq et al.,  
138 unpub. data, <https://www.medrxiv.org/content/10.1101/2020.02.21.20026435v6.full.pdf>).(26)  
139 The  $R$  estimate for the Diamond Princess cruise ship suggests high transmission before and  
140 immediately after movement restrictions on the ship (median  $R$  of 12.1 [95% CrI: 8.2, 17.2] on  
141 February 7, two days post-quarantine), with rapid decrease thereafter (median  $R$  of 0.35 [95%  
142 CrI: 0.02, 2.19] as of February 18).(27) Together, these estimates suggest  $R_0$  is high, yet  
143 intensive interventions can reduce transmissibility ( $R$ ) substantially.

144

145 Incubation period

146 The incubation period is the time between infection and symptom onset. Seven studies  
147 (10 estimates) were included in this review; range 1.8 to 9.0 days (Figure 2, Supplemental Tables  
148 2 & 3; Tindale et al., unpub. data,  
149 <https://www.medrxiv.org/content/10.1101/2020.03.03.20029983v1>; Lu et al., unpub. data,



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150 <https://www.medrxiv.org/content/10.1101/2020.02.19.20025031v1>).(9,28–31) Among the  
151 articles in peer-reviewed literature, the mean incubation period was 1.8 to 6.9 days.(9,28–31)

152

153 Serial interval

154 The serial interval is the average time between symptom onset of a primary and  
155 transmission associated secondary case. Seven studies (10 estimates) estimated the mean serial  
156 interval between 4.0 and 7.5 days (Figure 3, Supplemental Tables 2 & 3; Tindale et al., unpub.  
157 data, <https://www.medrxiv.org/content/10.1101/2020.03.03.20029983v1>; Zhao et al., unpub.  
158 data, <https://www.medrxiv.org/content/10.1101/2020.02.21.20026559v1>).(9,31–34) Ganyani et al.  
159 estimated the mean generation interval of 5.21 in Singapore and 3.95 in Tianjin China.(34)

160

161 Doubling time

162 The doubling time is the average time period it takes for the daily case count to double.  
163 Utilizing both genetic and case data over several locations and time periods, 11 studies estimated  
164 a mean doubling time of 2.3 to 7.4 days (Figure 4, Supplemental Tables 2 & 3; Rambaut, unpub.  
165 data, <http://virological.org/t/phylogenetic-analysis-176-genomes-6-mar-2020/356>; Bedford,  
166 unpub. data, <http://virological.org/t/phylogenetic-estimation-of-incidence-and-prevalence-of-novel-coronavirus-ncov-infections-through-time/391>; Pinotti et al., unpub. data,  
167 <https://www.medrxiv.org/content/10.1101/2020.02.24.20027326v1>; Zhao et al., unpub. data,  
168 <https://www.medrxiv.org/content/10.1101/2020.02.06.20020941v1>; Volz et al., unpub. data,  
169

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170 [https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-](https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College---COVID-19---genetic-analysis-FINAL.pdf)  
171 [College---COVID-19---genetic-analysis-FINAL.pdf](https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College---COVID-19---genetic-analysis-FINAL.pdf)).(9,11,15,18,19,35)

172

173 Infectious period

174 The infectious period is the period of time in which an infected host, with or without  
175 symptoms, can transmit to susceptible individuals. One estimate (You et al., unpub. data,  
176 <https://www.medrxiv.org/content/10.1101/2020.02.08.20021253v2>). Based on data from 67  
177 cases, estimated a mean infectious period of 10.91 days (standard deviation, 3.95 days). Little is  
178 known about how characteristics of an infected person, such as age, severity and clinical  
179 progression, affect overall infectious period estimates.

180

181 Severity

182 Clinical progression

183 We did not identify mathematical or statistical models that examine clinical disease  
184 progression. We include empiric findings detailed in the WHO China mission report, which has  
185 been used to inform other models.(36)

186

187 *Within China*

188 The majority of >75,000 cases of COVID-19 reported through March 6 have been from  
189 Hubei province. Among 55,924 confirmed cases in China as of February 20, the median age was

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190 51 years (range 2 days-100 years) with most between 30–69 years (77.8%). The clinical  
191 distribution was: 80.4% mild/moderate, 13.8% severe and 6.1% critically ill (Supplemental  
192 Table 4). Only 2.4% of reported cases were among persons < 19 years old.(36) Severe disease  
193 was reported among those with increased age (over 60) and comorbidities such as hypertension,  
194 diabetes, cardiovascular disease, chronic respiratory disease, and cancer.(37) Fatality estimates  
195 have come primarily from elderly Wuhan residents,(38) suggesting substantially higher lethality  
196 compared with outside Hubei (Figure 5).

### 197 *Outside China*

198 The age-distribution of cases and deaths detected outside China has been wider than that  
199 within China.(38) This difference may result from higher sensitivity surveillance for travelers  
200 compared to cases within China, particularly in countries on high alert, such as Thailand and  
201 Japan, which implemented temperature screening at airports. In general, early severe cases are  
202 more likely to be detected than mild cases resulting in higher severity estimates early on. Cases  
203 among travelers might also generally be younger due to age-specific differences in travel.

204 A broader spectrum of clinical severity has been observed in travel-associated and locally  
205 acquired cases reported outside of China, likely reflecting more robust surveillance for SARS-  
206 CoV-2. Severity ranges from asymptomatic infection, to symptoms such as fever and fatigue, as  
207 well as mild to severe respiratory symptoms including cough and pneumonia. Cases have been  
208 reported in persons with previously good health and no known comorbidities.(39) Differences in  
209 severity have also been observed within transmission chains.(40–43)

210

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## 211 Case and Infection Fatality Ratio

212 The case fatality ratio (CFR) is the proportion of cases which result in death. There are  
213 several variations of CFR, including symptomatic (sCFR), laboratory-confirmed (cCFR),  
214 hospitalization (HFR), and infection (IFR). Eleven studies, estimating either CFR or a variation  
215 of CFR, were included in this review (Figure 5). Most estimates were based on data from China.  
216 However, a few are from outside China or from the Diamond Princess cruise ship (38,44)  
217 Estimates of CFR generally did not include specific case definitions, and ranged from 0.9% to  
218 18.9%. Moreover, CFR is highly variable across situations (i.e., general population, hospitalized  
219 or critically ill). Critically ill patients' central estimates range between 8.0% and 28.7% (Deng et  
220 al., unpub. data, <https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1>). Notably,  
221 IFR seems to be more consistent across studies, with central estimates around 0.6% in two peer-  
222 reviewed studies from mainland China (38,44), yet higher at 3.3% in Hubei, China, 3% in  
223 Northern Italy (Hauser et al., unpub. data,  
224 <https://www.medrxiv.org/content/medrxiv/early/2020/03/30/2020.03.04.20031104.full.pdf>), and  
225 and lower at 0.2% to 1.6% in Asia and Europe (Figure 5 and Supplementary Table 5).

226

227 There was evidence of a strong age-gradient in both CFR and IFR, with the elderly being  
228 at a higher risk.(42) IFR presents a strong age gradient, with an IFR of 0.007% in children,  
229 between 1.9% and 4.6% in those aged 60-69, and between 7.8% and 18% in those aged >80 (38).  
230 Hospitalization rates were also age dependent:<0.04% in children, 11.8% in those aged 60-69  
231 and 18.4% among those aged 80 or more (38).

232

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233           Viral Evolution and Genomic Epidemiology

234           Virus genome sequences from a representative sample of cases can be used for  
235 calculating the evolutionary rate, date of introduction to the human population, size of outbreak,  
236 and estimating the reproduction number.(45–48) The evolutionary rate is the rate at which  
237 mutations accumulate per base pair in the genome over the course of a year. Estimates have  
238 ranged from  $0.8 \times 10^{-3}$  to  $1.2 \times 10^{-3}$  (Table 2; Sciré et al., unpub. data,  
239 <http://virological.org/t/update-2-evolutionary-epidemiological-analysis-of-128-genomes/423>;  
240 Duchene et al., unpub. data, [http://virological.org/t/temporal-signal-and-the-evolutionary-rate-of-](http://virological.org/t/temporal-signal-and-the-evolutionary-rate-of-2019-n-cov-using-47-genomes-collected-by-feb-01-2020/379)  
241 [2019-n-cov-using-47-genomes-collected-by-feb-01-2020/379](http://virological.org/t/temporal-signal-and-the-evolutionary-rate-of-2019-n-cov-using-47-genomes-collected-by-feb-01-2020/379); Hill and Rambaut, unpub. data,  
242 <http://virological.org/t/phylogenetic-analysis-of-sars-cov-2-update-2020-03-06/420>; Rambaut,  
243 unpub. data, <http://virological.org/t/phylogenetic-analysis-176-genomes-6-mar-2020/356>;  
244 Bedford, unpub. data, [http://virological.org/t/phylogenetic-estimation-of-incidence-and-](http://virological.org/t/phylogenetic-estimation-of-incidence-and-prevalence-of-novel-coronavirus-ncov-infections-through-time/391)  
245 [prevalence-of-novel-coronavirus-ncov-infections-through-time/391](http://virological.org/t/phylogenetic-estimation-of-incidence-and-prevalence-of-novel-coronavirus-ncov-infections-through-time/391)). These evolutionary rates  
246 are similar to that of MERS-CoV and SARS-CoV-1. The data suggests that the COVID-19  
247 outbreak was started by a single spillover event occurring in late 2019 (Table 2), and supported  
248 by first case reported data in December 2019 (Sciré et al., unpub. data,  
249 <http://virological.org/t/update-2-evolutionary-epidemiological-analysis-of-128-genomes/423>;  
250 Duchene et al., unpub. data, [http://virological.org/t/temporal-signal-and-the-evolutionary-rate-of-](http://virological.org/t/temporal-signal-and-the-evolutionary-rate-of-2019-n-cov-using-47-genomes-collected-by-feb-01-2020/379)  
251 [2019-n-cov-using-47-genomes-collected-by-feb-01-2020/379](http://virological.org/t/temporal-signal-and-the-evolutionary-rate-of-2019-n-cov-using-47-genomes-collected-by-feb-01-2020/379); Hill and Rambaut, unpub. data,  
252 <http://virological.org/t/phylogenetic-analysis-of-sars-cov-2-update-2020-03-06/420>; Rambaut,  
253 unpub. data, <http://virological.org/t/phylogenetic-analysis-176-genomes-6-mar-2020/356>;  
254 Bedford, unpub. data, [http://virological.org/t/phylogenetic-estimation-of-incidence-and-](http://virological.org/t/phylogenetic-estimation-of-incidence-and-prevalence-of-novel-coronavirus-ncov-infections-through-time/391)  
255 [prevalence-of-novel-coronavirus-ncov-infections-through-time/391](http://virological.org/t/phylogenetic-estimation-of-incidence-and-prevalence-of-novel-coronavirus-ncov-infections-through-time/391); Volz et al., unpub. data,

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256 [https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-](https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College---COVID-19---genetic-analysis-FINAL.pdf)  
257 [College---COVID-19---genetic-analysis-FINAL.pdf](https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College---COVID-19---genetic-analysis-FINAL.pdf).(49) Analysis of viral genomes can also be  
258 used to estimate doubling time and reproduction number.

259

## 260 Effectiveness of Non-Pharmaceutical Interventions (NPIs)

261 NPIs include interventions at individual and community levels. At the individual level, NPIs  
262 examined in modeling studies included voluntary home isolation or quarantine (Supplementary  
263 Table 6). At the community level, NPIs included school and workplace closures and canceling or  
264 postponing large public gatherings (see Supplementary Table 7 for definitions). Modeling can be  
265 used to estimate the effectiveness of components of these interventions (e.g. case detection), the  
266 interventions themselves (e.g. case isolation) or combinations of interventions (e.g. case and  
267 contact isolation). In total, 29 articles were identified; of these, 17 met the inclusion criteria for  
268 this review (Table 3; Pinotti et al., unpub. data,  
269 <https://www.medrxiv.org/content/10.1101/2020.02.24.20027326v1>; Niehus et al., unpub. data,  
270 <https://www.medrxiv.org/content/10.1101/2020.02.13.20022707v2>; Gostic et al., unpub. data,  
271 <https://www.medrxiv.org/content/10.1101/2020.01.28.20019224v2>; Adiga et al., unpub. data,  
272 <https://www.medrxiv.org/content/10.1101/2020.02.20.20025882v2>; Lai et al., unpub. data,  
273 <https://www.medrxiv.org/content/10.1101/2020.03.03.20029843v3.full.pdf>; Zhang et al., unpub.  
274 data, <https://www.medrxiv.org/content/10.1101/2020.03.04.20031187v1>; Clifford et al., unpub.  
275 data, <https://cmmid.github.io/topics/covid19/screening-outbreak-delay.html>; Bhatia et al., unpub.  
276 data

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277 [fellowships/Imperial-College-COVID19-international-surveillance-21-02-](#)

278 [2020.pdf](#)).(11,15,18,50–55)

279

280 Case screening and detection

281 Recent articles have addressed the efficacy of screening and detection by surveillance

282 systems in different countries (Pinotti et al., unpub. data,

283 <https://www.medrxiv.org/content/10.1101/2020.02.24.20027326v1>; Niehus et al., unpub. data,

284 <https://www.medrxiv.org/content/10.1101/2020.02.13.20022707v2>; Bhatia et al., unpub. data

285 [286 \[College-COVID19-international-surveillance-21-02-2020.pdf\]\(#\)\).\(50\) Two studies used data from](https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-</a></p></div><div data-bbox=)

287 Singapore (known for having a reliable health reporting system) as benchmarks to estimate the

288 sensitivity of surveillance systems in other countries (Niehus et al., unpub. data,

289 <https://www.medrxiv.org/content/10.1101/2020.02.13.20022707v2>; Bhatia et al., unpub. data

290 [291 \[College-COVID19-international-surveillance-21-02-2020.pdf\]\(#\)\). Both articles agreed that only a](https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-</a></p></div><div data-bbox=)

292 fraction of cases (22%-64%) are captured by surveillance systems, varying by country. A more

293 recent study found similar results (36% detected cases), and lower ascertainment when

294 repatriations were considered (Pinotti et al., unpub. data,

295 <https://www.medrxiv.org/content/10.1101/2020.02.24.20027326v1>).

296

297 Case isolation and quarantine of contacts

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298           One study considered different scenarios in which the reproduction number and  
299 transmission before symptom onset were varied to study the controllability of the outbreak.(50)  
300 The authors found that as  $R_0$  increased, the percentage of contacts to be traced increased. The  
301 delay between symptom onset and isolation also affected the controllability of the outbreak. For  
302 values of  $R_0 > 2.5$ , contact tracing and isolation were successful at stopping transmission when <  
303 1% of transmission occurred before symptom onset. For these two parameters, case isolation  
304 alone would be unlikely to control transmission within 3 months.

305

306           Traveler screening

307           Two studies considered models in which passengers are screened before departing an  
308 area with local transmission and upon arrival to destination (Gostic et al., unpub. data,  
309 <https://www.medrxiv.org/content/10.1101/2020.01.28.20019224v2>).(51), demonstrating that a  
310 relatively low number of cases would likely be detected (34%-54%). Different factors affect the  
311 under-detection of cases, including country ability to detect them. Some of those factors include  
312 asymptomatic infections, infections with mild clinical symptoms, limited care-seeking behavior,  
313 case definition, and under-recognition of cases by clinicians. A third study suggests that exit and  
314 entry screening combined with traveler sensitization can delay a local outbreak by  $\geq 83$  days,  
315 with no  $> 1$  infected traveler per week (Clifford et al., unpub. data,  
316 <https://cmmid.github.io/topics/covid19/screening-outbreak-delay.html>).

317

318           Travel restrictions



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319           On January 23, 2020, travel bans were implemented from Wuhan city. Within China, this  
320 resulted in a delay of three days, on average, of disease arrival.(52) Cities, implementing the ban  
321 before their first case was detected observed fewer cases than cities implementing the ban after  
322 their first case.(52) Another study found that 130 cities in China had >50% chance of having a  
323 COVID-19 case imported from Wuhan in the three weeks preceding the implementation of travel  
324 restrictions, suggesting that there were cases outside of Wuhan before the travel ban.(15)  
325 Analysis of the effect of the Wuhan travel ban, including the implementation of long-range travel  
326 restrictions on January 23, showed no noticeable difference for the epidemic trajectory of  
327 Wuhan, while delaying the occurrence of cases for other locations in China by three days.(18)  
328 Another study found that travel restrictions would delay the epidemic spread throughout China  
329 by two days.(53)

330

331           Internationally, several countries implemented travel bans. One modeling study estimated  
332 how travel restrictions from China impacted time of arrival of the infected individuals (Adiga et  
333 al., unpub. data, <https://www.medrxiv.org/content/10.1101/2020.02.20.20025882v2>). It found  
334 that countries in Africa and South America would likely observe the biggest delay, 11 and 9 day,  
335 respectively. Another study found that travel reductions of up to 90% of had only a modest effect  
336 unless paired with public health interventions and behavioral changes to achieve a considerable  
337 reduction in disease transmission.(18)

338

339           Cancellation of events and public gatherings

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340           One study analyzed a range of interventions such as suspending public transport, closing  
341 entertainment venues, and banning public gatherings.(52) Varying by city and number of control  
342 measures adopted, the study found that cities that implemented a Level 1 response (at least two  
343 control measures) before the first case was confirmed had 37% fewer cases in the week after the  
344 first case identified compared with cities that started control thereafter. Locations that closed  
345 entertainment venues and banned public gatherings early in the outbreak reported fewer cases  
346 during the first week.

347

348           Finally, four studies estimated the effects of transmission reduction in China when NPI  
349 mitigation strategies were combined (Lai et al., unpub. data,  
350 <https://www.medrxiv.org/content/10.1101/2020.03.03.20029843v3.full.pdf>).(11) The combined  
351 interventions significantly reduced the number of cases observed and delayed epidemic peak by  
352 ≥1 month. It was found that earlier intervention of social distancing could significantly limit the  
353 epidemic in mainland China. The number of infections could have been reduced up to 98.9%,  
354 and the number of deaths reduced by 99.3% as of Feb 23, 2020 (Zhang et al., unpub. data,  
355 <https://www.medrxiv.org/content/10.1101/2020.03.04.20031187v1>). A different group found  
356 that following the implementation of control measures, growth rates became negative in most  
357 locations, and that drastic control measures implemented in China substantially mitigated  
358 COVID-19 spread.(55)

359

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361 Community behavior modification

362 One research group performed an online survey after the first case of COVID-19 was  
363 reported in Hong Kong. Their results showed that 39%-88% of the people surveyed had adopted  
364 social distancing measures.(54)

## 365 **Discussion**

366 Modeling can provide estimates of disease transmission parameters for planning and  
367 response during epidemics. Investigators around the world have been trying to understand the  
368 transmission dynamics and severity of disease, as well as the effects that different interventions  
369 have had on the course of the epidemic through advanced analytics and modeling. However,  
370 transmission parameter estimates are limited by the availability and comprehensiveness of data  
371 early in the epidemic. Some parameters can be estimated from genetic sequencing data, but these  
372 estimates are heavily influenced by biases in sampling and inaccuracies in sequencing. Although  
373 efforts to collect and share clinical, epidemiological, and sequence data have been remarkably  
374 timely, there remain outstanding gaps in knowledge.

375

376 Several parameters presented in this review are context specific, such as  $R_0$  values or  
377 CFR measurements. Although the characteristics of SAR-CoV-2 are unlikely to change,  
378 responses to transmission will vary. Several factors affect the trajectory of an epidemic in  
379 different locations, such as population density, health system infrastructure, transportation  
380 robustness, cultural practices, and poverty levels.(56) Available data from China may not be

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381 reflective of secular trends elsewhere. As other countries develop more cases, more robust data  
382 will be available for modeling and extrapolation for countries not yet affected.

383

384 Challenges in assessing severity of clinical outcomes during an new emerging epidemic  
385 have been discussed in-depth elsewhere and are not covered here.(7,8) However, there remain  
386 four challenges. First, early in an outbreak, data are heavily biased towards severe cases.  
387 Estimates of the CFR in those patients with known outcomes may be biased upwards until the  
388 extent of clinically milder disease is determined. Second, there is a period between onset of  
389 symptoms and final clinical outcome (death vs survival).(57,58) During a growing epidemic, the  
390 final clinical outcome of most reported cases is typically unknown. This is particularly true with  
391 COVID-19 where severely ill patients may be hospitalized for many days. The crude CFR will  
392 underestimate the fatality risk among early epidemic cases.(7,8,58) Third, while the epidemic is  
393 growing there will be a bias towards having observed cases with recent symptom onset and  
394 outcomes. Therefore, estimates should be adjusted for the growth rate of the epidemic.(8) Fourth,  
395 over-representation of men, elderly people with co-morbidities and people with respiratory risk  
396 factors (smoking, etc.) may result from observation bias or exposure differences and affect CFR  
397 estimates.

398

399 Country preparedness and clinical care capacity will affect patient outcomes. Delayed  
400 diagnosis and treatment, limited knowledge of the natural history of infection, and rapid  
401 escalation of cases can affect clinical outcomes Thus, fatality in patients cared for very early in a  
402 country's epidemic may be greater than for later patients.(7) More information on the proportion

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403 of individuals requiring healthcare, level (outpatient, inpatient and intensive care) and duration  
404 of care required are essential for predicting healthcare needs as the epidemic progresses.

405

406           Pre-symptomatic or asymptomatic transmission, if substantial, might have critical  
407 implications for control efforts. Empiric evidence of such potential transmission includes: i) a  
408 serial interval and generation time that were estimated shorter than the incubation period,  
409 (Tindael et al., unpub.data, <https://www.medrxiv.org/content/10.1101/2020.03.03.20029983v1>;  
410 Lu et al., unpub. data, <https://www.medrxiv.org/content/10.1101/2020.02.19.20025031v1>); ii)  
411 similarly high viral load in asymptomatic and symptomatic cases;(34,59) and iii) documentation  
412 of cases infected by pre-symptomatic or asymptomatic carriers in cluster investigations.(60–63)  
413 If asymptomatic infectious carriers are not characterized appropriately in models, epidemic  
414 infection rates would be underestimated, while the severity and the effectiveness of interventions  
415 would be overestimated, potentially leading to implementation of ineffective interventions.  
416 Serological studies will be critical for understanding the role of asymptomatic transmission.

417

418           Early evidence suggests that travel restrictions result in only modest decreases in the  
419 importation of cases. However, combined with other social distancing measures and behavior  
420 changes, travel restrictions may be a useful addition. Modeling can be extremely valuable in  
421 providing counterfactuals aimed at disentangling the effects of different NPIs. Documentation of  
422 timing, type of NPI, and compliance rate will be needed to estimate the effectiveness of the  
423 different interventions.

424

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425           This paper is subject to additional limitations. To utilize the latest information, we  
426 included a number of pre-print reports that have not been formally peer-reviewed. Additionally,  
427 there is a heavy reliance on data from China, due to the period considered. Given the recent  
428 geographic spread of COVID-19, there may be a range of future estimates that will differ from  
429 those reported here. Finally, we have not performed a formal assessment of possible biases of the  
430 estimates examined in this paper, and therefore cannot exclude that some estimates reported are  
431 affected by unmeasured sources of biases.

432

433           As the COVID-19 epidemic progresses, ongoing refinement and validation of key  
434 epidemiological parameters will help inform the global public health response. Defining optimal  
435 surveillance methods, laboratory testing, contact tracing parameters, quarantine measures,  
436 hospital acute care capacities, and many other operational factors, depends on estimates of the  
437 epidemiological parameters summarized in this paper. One of the largest knowledge gaps are  
438 those of asymptomatic or pre-symptomatic infectious potential and the occurrence of subclinical  
439 infections. In the absence of efficacious vaccines and therapeutics, developing an evidence-base  
440 for NPIs will remain a critical tool for effective local, national, and global outbreak control.  
441 Better data will enable mathematical and statistical modeling to more precisely predict how  
442 different NPIs can be combined to produce efficient epidemic control.

443

444           Our summary provides estimates through the first 10 weeks of the COVID-19 epidemic  
445 that are needed for operational planning, scenario-building for contingency planning and  
446 forecasting to inform today's preparedness and response efforts. Data from outbreaks in newly

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447 affected countries and new data stemming from sero-prevalence and transmission studies will  
448 provide insights currently unavailable. Documenting and evaluating NPIs will help public health  
449 and government decision makers to implement the most effective epidemic control measures.

#### 450 **Members of the WHO COVID-19 Modeling Parameters Group**

451 Matthew Biggerstaff, Benjamin J. Cowling, Zulma M Cucunubá, Linh Dinh, Neil M Ferguson,  
452 Huizhi Gao, Verity Hill, Natsuko Imai, Michael A. Johansson, Sarah Kada, Oliver Morgan, Ana  
453 Pastore y Piontti, Jonathan A. Polonsky, Pragati Venkata Prasad, Talia M. Quandelacy, Andrew  
454 Rambaut, Jordan W. Tappero, Katelijn A. Vandemaele\*, Alessandro Vespignani, K. Lane  
455 Warmbrod, Jessica Y. Wong

456 \* corresponding author

457 Katelijn A. Vandemaele

458 Health Emergencies Programme, World Health Organization, 20, avenue Appia, 1211 Geneva  
459 27 Switzerland, [vandemaelek@who.int](mailto:vandemaelek@who.int); +41.22.791.4591

460

461

#### 462 **Affiliations**

463 **World Health Organization, Geneva, Switzerland** (KL Warmbrod MS, L Dinh DDS, O  
464 Morgan PhD, JA Polonsky MSc, JW Tappero MD, KA Vandemaele MD); **University of**  
465 **Edinburgh, Edinburgh, UK** (Prof A Rambaut DPhil, V Hill MSc); **Centers for Disease**  
466 **Control and Prevention, Atlanta, Georgia, USA** (PV Prasad, MPH, TM Quandelacy PhD, S  
467 Kada PhD, M Biggerstaff ScD, MA Johansson PhD); **The University of Hong Kong, Hong**  
468 **Kong Special Administrative Region, China** (Prof BJ Cowling PhD, H Gao MPH, JY Wong

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469 PhD); **Imperial College London, UK** (ZM Cucunubá PhD, N Imai PhD, Prof NM Ferguson  
470 DPhil); **Northeastern University, Boston, MA, USA** (A Pastore y Piontti PhD, Prof A  
471 Vespignani); **ISI Foundation, Turin, Italy** (Prof A Vespignani)

472

473

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475 KAV, OM, AV, NMF, NI, ZMC, MB, AR, BJC, MAJ, LD, JAP, KLW developed the  
476 idea for this manuscript. KLW, LD, PVP, TMQ, SK, HG, JYW, ZMC, NI, AV, APP, VH, AR  
477 conducted the literature searches. KLW, LD, PVP, SK, MAJ, JYW, ZMC, AV, APP, VH, AR,  
478 JAP analyzed data. KLW, LD, KAV, JWT, MAJ, JYW, BJC, ZMC, NI, AV, APP wrote the  
479 manuscript. KLW, JT, KAV, OM, JAP, HG, JYW, BJC, ZMC, NI, NMF, MB, MAJ, AV, APP,  
480 AR edited the document.

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#### 488 **Declaration of Interests**



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670

## 671 **Tables**

672 Table 1. Key parameters and definitions

Parameter	Definition
Basic Reproduction Number ( $R_0$ )	The average number of people infected by a single infected individual in a fully susceptible population
Time-varying or effective reproduction number ( $R_t$ , $R_E$ )	The average number of people infected by an infected individual in a population in the context of changing transmission patterns such as those resulting from interventions and acquired immunity
Incubation Period	The time between infection and symptom onset
Serial Interval	The average time between symptom onset of a primary case and symptom onset of linked secondary cases
Generation Interval	The average time between infection of a primary case and infection of linked secondary cases
Doubling Time	The average time period it takes for the daily case count to double
Infectious Period	The period of time in which an infected host, with or without symptoms, can transmit an infectious agent to susceptible individuals, directly or indirectly
Case Fatality Ratio (CFR)	The proportion of cases which result in death (with case defined in numerous ways)
Infection Fatality Ratio (IFR)	The proportion of all infections (including confirmed, symptomatic, asymptomatic, etc.) which result in death
Mean Evolutionary rate	The average rate at which mutations accumulate per base pair in the genome over the course of a year

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674 Table 2. Summary of Estimates of Mean Evolutionary Rate and Most Recent Common Ancestor  
675 (MRCA)

Mean Evolutionary Rate (95% CI)*	MRCA (95% CI)	Number of Genomes in Analysis	Clock Model**	Growth Model	Source
-	29 Nov 2019 (8 Nov 2019 – 16 Dec 2019)	23	Strict	Constant	Rambaut, unpub. data, <a href="http://virological.org/t/phylogenetic-analysis-of-23-ncov-2019-genomes-2020-01-23/335">http://virological.org/t/phylogenetic-analysis-of-23-ncov-2019-genomes-2020-01-23/335</a>
$1.23 \times 10^{-3}$ ( $0.56 \times 10^{-3}$ - $1.98 \times 10^{-3}$ )	21 Nov 2019 (23 Oct 2019 - 13 Dec 2019)	51	Strict	Exponential	Duchene et al., unpub. data, <a href="http://virological.org/t/temporal-signal-and-the-evolutionary-rate-of-2019-n-cov-using-47-genomes-collected-by-feb-01-2020/379">http://virological.org/t/temporal-signal-and-the-evolutionary-rate-of-2019-n-cov-using-47-genomes-collected-by-feb-01-2020/379</a> .
$1.29 \times 10^{-3}$ ( $0.535 \times 10^{-4}$ - $2.15 \times 10^{-3}$ )	14 Nov 2019 (28 Sept 2019- 13 Dec 2019)	51	UNCL***	Exponential	Duchene et al., unpub. data, <a href="http://virological.org/t/temporal-signal-and-the-evolutionary-rate-of-2019-n-cov-using-47-genomes-collected-by-feb-01-2020/379">http://virological.org/t/temporal-signal-and-the-evolutionary-rate-of-2019-n-cov-using-47-genomes-collected-by-feb-01-2020/379</a> .
$0.9 \times 10^{-3}$ ( $0.5 \times 10^{-3}$ - $1.4 \times 10^{-3}$ )	3 Dec 2019 (30 Oct 2019- 17 Dec 2019)	51	Strict	Exponential	Bedford, unpub. data, <a href="http://virological.org/t/phylogenetic-estimation-of-incidence-and-prevalence-of-novel-coronavirus-ncov-infections-through-">http://virological.org/t/phylogenetic-estimation-of-incidence-and-prevalence-of-novel-coronavirus-ncov-infections-through-</a>

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					time/391.
0.92x10 <sup>-3</sup> (0.33x10 <sup>-3</sup> - 1.46x10 <sup>-3</sup> )	29 Nov 2019 (28 Oct 2019 - 20 Dec 2019)	75	Strict	Exponential	Rambaut, unpub. data, <a href="http://virological.org/t/phylogenetic-analysis-176-genomes-6-mar-2020/356">http://virological.org/t/phylogenetic-analysis-176-genomes-6-mar-2020/356</a> . Accessed March 4, 2020
1.04x10 <sup>-3</sup> (0.71x10 <sup>-3</sup> - 1.4x10 <sup>-3</sup> )	3 Dec 2019 (16 Nov 2019 - 17 Dec 2019)	116	Strict	Exponential	Hill and Rambaut, unpub. data, <a href="http://virological.org/t/phylogenetic-analysis-of-sars-cov-2-update-2020-03-06/420">http://virological.org/t/phylogenetic-analysis-of-sars-cov-2-update-2020-03-06/420</a>
7.41x10 <sup>-4</sup> (4.91x10 <sup>-4</sup> - 1.02x10 <sup>-3</sup> )	27 Nov 2019 (7 Nov 2019- 11 Dec 2019)	128	Strict	Birth Death Model	Sciré et al., unpub. data, <a href="http://virological.org/t/update-2-evolutionary-epidemiological-analysis-of-128-genomes/423">http://virological.org/t/update-2-evolutionary-epidemiological-analysis-of-128-genomes/423</a>

676 \* confidence interval

677 \*\*The Clock Model is a technique that uses the mutation rate to estimate the time of emergence.  
678 (47)

679 \*\*\*Uncorrelated

680



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681 Table 3. Summary of the studies of non-pharmaceutical interventions (NPI)

Non-pharmaceutical intervention	Summary/Results	Source
Case detection	(27% - 37%) cases detected*	Bhatia et al., unpub. data, <a href="https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College-COVID19-international-surveillance-21-02-2020.pdf">https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College-COVID19-international-surveillance-21-02-2020.pdf</a>
Case detection	38% (22%-64%) cases detected	Niehus et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.02.13.20022707v2">https://www.medrxiv.org/content/10.1101/2020.02.13.20022707v2</a>
Case screening and detection	(36%-65%) cases detected*	Pinotti et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.02.24.20027326v1">https://www.medrxiv.org/content/10.1101/2020.02.24.20027326v1</a>
Case isolation and contact tracing	Delay of onset symptoms to isolation has a high impact on the results, affecting the controllability of the outbreak. Results vary by scenario.	50
Travel screening	34% (20%-50%) travelers identified through both departure and arrival screening using symptoms or risk screening	Gostic et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.01.28.20019224v2">https://www.medrxiv.org/content/10.1101/2020.01.28.20019224v2</a>
Travel screening	46.5% (35.9% - 57.7%) travelers not detected through thermal screening	51

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Travel screening	Syndromic screening and traveler sensitization in combination could delay outbreaks in yet unaffected countries up to 83 days (75% 36 days, 97.5% 8 days)	Clifford et al., unpub. data, <a href="https://cmmid.github.io/topics/covid19/screening-outbreak-delay.html">https://cmmid.github.io/topics/covid19/screening-outbreak-delay.html</a>
Travel reduction (transport suspension)	Delay of 2.91 days (95% CI: 2.54-3.29) for the arrival of the disease to other cities in China.	52
Travel reduction (travel quarantine)	130 cities in China had $\geq 50\%$ chance of having a COVID-19 case imported from Wuhan in the 3 weeks preceding the quarantine	15
Travel restrictions	Travel restriction imposed on Wuhan delay the epidemic for 3 days	18
Travel reduction (airline suspensions)	Travel restriction imposed on China will delay the disease in other countries, the biggest delay being in Africa (11 days) and South America (9 days)	Adiga et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.02.20.20025882v2">https://www.medrxiv.org/content/10.1101/2020.02.20.20025882v2</a> ;
Travel reduction	Travel restriction will delay the epidemic for 2 days.	53
Cancellation of mass gathering	37% fewer cases when the interventions started before the first case.	52
Combination of NPI	66%, 86%, and 95% fewer cases depending on the timing of the interventions	Lai et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.03.03.20029843v3.full.pdf">https://www.medrxiv.org/content/10.1101/2020.03.03.20029843v3.full.pdf</a>
Combination of NPI	50% fewer cases if transmissibility reduced by 25% in all cities in China. Delay of epidemic peak for one month.	11

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Combination of NPI	Drastic control measures implemented in China have substantially mitigated the spread of COVID-19	34
Combination of NPI	Earlier intervention of social distancing could significantly limit the epidemic in mainland China. The number of infections could be reduced up to 98.9%, and the number of deaths could be reduced by up to 99.3% as of Feb 23, 2020	Zhang et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031187v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031187v1</a>
Community behavior modification	At least 42% of the people interviewed have modified daily behavior.	54

682 \*point estimates

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## 684 **Legends for Figures**

685           Figure 1. Basic reproduction number ( $R_0$ ) estimates by date of last reported cases  
686 analyzed and location. Points are mean or median estimates and error bars indicate 90% (12, 13,  
687 18) or 95% bounds (i.e. confidence or credible intervals). International-China estimates are those  
688 using international cases or exported cases from China to infer  $R_0$  in China or Hubei. Estimates  
689 for China refer to  $R_0$  estimates at the national or province level, except for those exclusive  
690 estimating  $R_0$  for Hubei (China-Hubei).

691           Figure 2. Estimated incubation period based on search in peer-reviewed (top) and gray  
692 literature (bottom). Point are mean, triangles are median estimates (if applicable) and error bars  
693 indicate confidence (blue) or credible intervals (red).

694           Figure 3. Estimated serial interval based on search in peer-reviewed literature (top) and  
695 gray literature (bottom). Point are mean estimates, triangles are median estimates (if applicable)  
696 and error bars indicate confidence (blue) or credible intervals (red).

697

698           Figure 4. Estimated doubling time based on search in peer-reviewed literature (top) and  
699 gray literature (bottom). Point are mean estimates and error bars indicate confidence (blue) or  
700 credible intervals (red).

701

702           Figure 5. Summary of CFR and IFR estimates. Point are mean or median estimates and  
703 error bars indicate confidence (dotted line) or credible intervals (full line). Red color refers to  
704 Peer-reviewed and blue to non-Peer-reviewed papers.

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705 **Supplementary Figures and Tables**

706 Supplementary Table 1- Search Terms

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Topic	Search Terms
Virus Evolution	<p>"nCoV", "2019-nCoV", "nCoV-2019", "COVID", "COVID-19", "novel coronavirus", "SARS-CoV-2"</p> <p>AND</p> <p>"evolution*" or "phylogenetics"</p>
Incubation period	<p>In PubMed, medRxiv, bioRxiv and arXiv:</p> <p>#1: "incubation period"</p> <p>#2: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>#3: #1 AND #2</p> <p>In SSRN:</p> <p>#1: "incubation period"</p> <p>#2: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>#3: #1 AND search within each of the term in #2</p> <p>In research square, Virological, and Wellcome Open Research:</p>

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	<p>#1: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>Then read through all the papers</p>
Serial interval	<p>In PubMed:</p> <p>#1: "serial interval" OR "generation interval" OR "generation time" OR "serial distribution" OR "secondary infections" OR "secondary cases"</p> <p>#2: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>#3: #1 AND #2</p> <p>In medRxiv, bioRxiv, and arXiv:</p> <p>#1: "serial interval"</p> <p>#2: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>#3: #1 AND #2</p> <p>In SSRN:</p> <p>#1: "serial interval"</p> <p>#2: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>#3: #1 AND search within each of the term in #2</p> <p>In research square, Virological, and Wellcome Open Research:</p>

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	<p>#1: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>Then read through all the papers</p>
Generation interval	<p>In PubMed and arXiv:</p> <p>#1: "generation interval"</p> <p>#2: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>#3: #1 AND #2</p> <p>In medRxiv and bioRxiv:</p> <p>"generation interval" for full text or abstract or title (match whole all)</p> <p>In SSRN:</p> <p>#1: "generation interval"</p> <p>#2: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>#3: #1 AND search within each of the term in #2</p> <p>In research square, Virological, and Wellcome Open Research:</p> <p>#1: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>Then read through all the papers</p>

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Doubling time	<p>In PubMed, medRxiv, bioRxiv and arXiv:</p> <p>#1: "doubling time" OR "growth rate"</p> <p>#2: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>#3: #1 AND #2</p> <p>In SSRN:</p> <p>#1: "doubling time" OR "growth rate"</p> <p>#2: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>#3: #1 AND search within each of the term in #2</p> <p>In research square, Virological, and Wellcome Open Research:</p> <p>#1: "coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV-2019" OR "SARS-CoV-2"</p> <p>Then read through all the papers</p>
CFR	<p>In PubMed:</p> <p>("coronavirus"[MeSH Terms] OR "coronavirus"[All Fields] OR "2019-ncov"[All Fields] OR "COVID-19"[All Fields] OR "COVID"[All Fields] OR "SARS-COV-2"[All Fields] OR "ncov"[All Fields] OR "ncov-2019"[All Fields]) AND "2019/12/31 00.00"[MHDA] : "2020/03/06 23.59"[MHDA] AND ("fatality"[All Fields] OR "Case Fatality"[All Fields] OR "Infection Fatality"[All Fields])</p> <p>In biorXiv &amp; medrXiv:</p>



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	<p>for title "coronavirus fatality" (match all words) and abstract or title "coronavirus fatality" (match all words) and posted between "01 Jan, 2020 and 07 Mar, 2020"</p> <p>In arXiv:</p> <p>Query: <a href="#">order: -announced date first; size: 50; date range: from 2020-01-01 to 2020-03-07; include cross list: True; terms: AND abstract=coronavirus; AND abstract=fatality</a></p> <p>In ResearchSquare:</p> <p>SARS-CoV-2 Preprints</p> <p>In Wellcome Research:</p> <p>Query: "coronavirus"</p> <p>In WHO Global Research Database:</p> <p>Query: "sever*"</p> <p>Cited by WHO:</p> <p>Imperial College London, IDO</p>
<p>Non-Pharmaceutical Interventions</p>	<p>In all databases:</p> <p>"coronavirus" OR "nCoV" OR "COVID" OR "COVID-19" OR "2019-nCoV" OR "nCoV- 2019" OR "SARS-CoV-2"</p>

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709 Supplementary Table 2. Summary of the published study included in the review of incubation  
710 period, serial interval, doubling time and generation interval.

711

Study	Study setting	Incubation period (days)	Serial interval (days)	Doubling time (days)	Generation interval (days)
Backer 2020 (28)	88 confirmed cases detected outside of Wuhan from 20 Jan 2020 to 28 Jan 2020	Mean: 6.4, Median: NA, SD: 2.3, 95% CrI: 5.6 to 7.7 based on Weibull distribution	NA	NA	NA
Chinazzi 2020 [18]	Modeling study	NA	NA	4.2 (90% CI: 3.8 to 4.7) based on reporting dates	NA
Du 2020a [15]	Modeling study	NA	NA	7.31 (95% CrI: 6.26 to 9.66) based on onset dates	NA
Ganyani 2020 (34)	Modeling study	NA	Mean: 5.21, Median: NA, SD: 4.32, 95% CrI: -3.35 to 13.94 in Singapore	NA	Mean: 5.20, Median: NA, SD: 1.72, 95% CrI: 3.78 to 6.78 in Singapore

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Ganyani 2020 (34)	Modeling study	NA	Mean: 3.95, Median: NA, SD: 4.24, 95% CrI: -4.47 to 12.51 in Tianjin, China	NA	Mean: 3.95, Median: NA, SD: 1.51, 95% CrI: 3.01 to 4.91 in Tianjin, China
Jung 2020 (19)	Modeling study	NA	NA	2.39 (95% CI: 1.93 to 3.15) from 20 exported cases reported by 24 Jan 2020, calculated by growth rate of 0.29 (95% CI: 0.22 to 0.36) based on reporting dates	
Leung 2020 (30)	175 confirmed patients in China from 20 Jan 2020 to 12 Feb 2020	Mean: 1.8, Median: NA, SD: NA, 95% CI: 1.0 to 2.7 based on travelers to Hubei fitting to Weibull distribution;	NA	NA	
Leung 2020 (30)	175 confirmed patients in China from 20 Jan 2020 to 12 Feb 2020	Mean: 7.2, Median: NA, SD: NA, 95% CI: 6.1 to 8.4 based on non-travelers fitting to Weibull distribution	NA	NA	

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Li 2020 (9)	425 confirmed cases in Wuhan as of 22 Jan 2020	Mean: 5.2, Median: NA, SD: NA, 95% CI: 4.1 to 7.0 based on log-normal distribution	Mean: 7.5, Median: NA, SD: 3.4, 95% CI: 5.3 to 19.0 based on gamma distribution	7.4 (95% CI: 4.2 to 14.0) based on onset dates
Linton 2020 (29)	158 confirmed cases in and outside of Wuhan as of 31 Jan 2020 (52 cases when excluding Wuhan residents)	Mean: 5.6, Median: NA, SD: NA, 95% CrI: 5.0 to 6.3 based on 158 cases;	NA	NA
Linton 2020 (29)	158 confirmed cases in and outside of Wuhan as of 31 Jan 2020 (52 cases when excluding Wuhan residents)	Mean: 5.0, Median: NA, SD: NA, 95% CrI: 4.2 to 6.0 based on 52 cases	NA	NA
Nishiura 2020 (33)	28 infector-infectee pairs from published research articles as of 12 Feb 2020	NA	Mean: 4.7, Median: 4.0, SD: 2.9, 95% CrI: 3.7 to 6.0 based all 28 pairs fitting to log-normal distribution	NA

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Nishiura 2020 (33)	18 pairs with highest certainty from published research articles as of 12 Feb 2020	NA	Mean: 4.8, Median: 4.6, SD: 2.3, 95% CrI: 3.8 to 6.1 based on 18 certain pairs fitting to Weibull distribution	NA
Sanche 2020 (35)	Modeling study	NA	NA	2.4 (95% CI: 1.9, 3.3) based on onset dates
Wu 2020 (11)	Modeling study	NA	NA	6.4 (95% CrI: 5.8 to 7.1) based on onset dates
Zhang 2020 (31)	8579 confirmed cases reported outside Hubei in China as of 17 Feb 2020 (only 49 cases with no travel history to/from Wuhan/Hubei)	Mean: 5.2, Median: NA, SD: NA, 95% CI: 1.8 to 12.4 based on log-normal distribution	Mean: 5.1, Median: NA, SD: NA, 95% CI: 1.3 to 11.6 based on gamma distribution	NA

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713 Supplementary Table 3. Summary of the study included in the review of incubation period, serial  
 714 interval, doubling time based on search in gray literature  
 715

Study	Study setting	Incubation period (days)	Serial interval (days)	Doubling time (days)
Bedford, unpub. data, <a href="http://virological.org/t/phylogenetic-estimation-of-incidence-and-prevalence-of-novel-coronavirus-ncov-infections-through-time/39">http://virological.org/t/phylogenetic-estimation-of-incidence-and-prevalence-of-novel-coronavirus-ncov-infections-through-time/39</a>	53 publicly available nCoV genomes collected between 24 Dec, 2019 and 4 Feb, 2020	NA	NA	7.2 (95% CI: 5.0 to 12.9) based on sample collection dates
Lu et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.02.19.20025031v1">https://www.medrxiv.org/content/10.1101/2020.02.19.20025031v1</a>	265 confirmed cases in Shanghai before 7 Feb 2020 (only 27 had credible contact information)	Mean: 6.4, Median: NA, SD: NA, 95% CI: 5.3 to 7.6 based on Weibull distribution	NA	NA
Pinotti et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.02.24.20027326v1">https://www.medrxiv.org/content/10.1101/2020.02.24.20027326v1</a>	Modeling study	NA	NA	2.67 (95% CI: 2.24 to 3.30) importations from Hubei, calculated by growth rate of 0.26 (95% CI: 0.21 to 0.31) based on reporting dates

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Rambaut, unpub. data, <a href="http://virological.org/t/phylogenetic-analysis-176-genomes-6-mar-2020/356">http://virological.org/t/phylogenetic-analysis-176-genomes-6-mar-2020/356</a>	75 genomes in 12 Feb 2020, 86 genomes in 24 Feb 2020	NA	NA	6.2 (95% CI: 4.1 to 12.3) 75 genomes based on sample collection dates
Rambaut, unpub. data, <a href="http://virological.org/t/phylogenetic-analysis-176-genomes-6-mar-2020/356">http://virological.org/t/phylogenetic-analysis-176-genomes-6-mar-2020/356</a>	75 genomes in 12 Feb 2020, 86 genomes in 24 Feb 2020	NA	NA	7.2 (95% CI: 4.7 to 16.3) 86 genomes based on sample collection dates
Tindale et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.03.03.20029983v1">https://www.medrxiv.org/content/10.1101/2020.03.03.20029983v1</a>	93 confirmed cases in Singapore from 19 Jan 2020 to 26 Feb 2020	Mean: 7.11, Median: 6.55, SD: NA, 95% CI: 6.13 to 8.25 based on Weibull distribution	Mean: 4.56, Median: NA, SD: 0.95, 95% CI: 2.69 to 6.42 based on expectation-maximization approach	NA
Tindale et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.03.03.20029983v1">https://www.medrxiv.org/content/10.1101/2020.03.03.20029983v1</a>	125 confirmed cases in Tianjin from 21 Jan 2020 to 22 Feb 2020	Mean: 9.02, Median: 8.62, SD: NA, 95% CI: 7.92 to 10.2 based on Weibull distribution	Mean: 4.22, Median: NA, SD: 0.4, 95% CI: 3.43 to 5.01 based on expectation-maximization approach	NA

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Zhang et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031187v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031187v1</a>	8579 confirmed cases reported outside Hubei in China as of 17 Feb 2020 (only 49 cases with no travel history to/from Wuhan/Hubei)	Mean: 5.2, Median: NA, SD: NA, 95% CI: 1.8 to 12.4  based on log-normal distribution	Mean: 5.1, Median: NA, SD: NA, 95% CI: 1.3 to 11.6  based on gamma distribution	NA
Volz et al., unpub. data, <a href="https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College-COVID-19-genetic-analysis-FINAL.pdf">https://www.imperial.ac.uk/media/imperial-college/medicine/sph/ide/gida-fellowships/Imperial-College-COVID-19-genetic-analysis-FINAL.pdf</a>	Phylogenetic analysis of 53 SARS-CoV-2 whole genome sequences	NA	NA	7.1 (95% CI: 3.0 to 20.5) based on sample collection dates
Zhao et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.02.21.20026559v1">https://www.medrxiv.org/content/10.1101/2020.02.21.20026559v1</a>	21 infector-infectee pairs in Hong Kong from 16 Jan 2020 to 15 Feb 2020	NA	Mean: 4.4, Median: NA, SD: 3.0, 95% CI: 2.9 to 6.7, based on gamma distribution	NA
Zhao et al., unpub. data, <a href="https://www.medrxiv.org/content/10.1101/2020.02.06.20020941v1">https://www.medrxiv.org/content/10.1101/2020.02.06.20020941v1</a>	Modeling Study	NA	NA	2.9 (95% CrI: 2 to 4.1) based on onset dates

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718 Supplementary Table 4. Frequency of different case severities

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Classification	Definition	Proportion *
Mild/Moderate	non-pneumonia and pneumonia cases	80.9%
Severe	dyspnea, respiratory frequency $\geq 30$ /minute, blood oxygen saturation $\leq 93\%$ , PaO <sub>2</sub> /FiO <sub>2</sub> ratio $< 300$ , and/or lung infiltrates $> 50\%$ within 24–48 hours	13.8%
Critical	respiratory failure, septic shock, and/or multiple organ dysfunction/failure	6.1%

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721 \* Proportion out of 55,924 cases until Feb 20th

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725 Supplementary Table 5- Summary of CFR and IFR Estimate Sources

Author	Place	Metric	Estimate	Uncertainty type	Peer-reviewed	Source
Russell et al	China	IFR	0.6 (0.2-1.3)	95% CI	Yes	<a href="https://www.ncbi.nlm.nih.gov/pubmed/32234121">https://www.ncbi.nlm.nih.gov/pubmed/32234121</a>
Hauser et al	China Hubei	IFR	3.3 (2-4.7)	95% CrI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031104v2.full.pdf">https://www.medrxiv.org/content/10.1101/2020.03.04.20031104v2.full.pdf</a>
Famulare	China Wuhan	IFR	0.9 (0.4-2.9)	95% CI	No	<a href="https://institutefordiseasemodeling.github.io/nCoV-public/analyses/first_adjusted_mortality_estimates_and_risk_assessment/2019-nCoV-preliminary_age_and_time_adjusted_mortality_rates_and_pandemic_risk_assessment.html">https://institutefordiseasemodeling.github.io/nCoV-public/analyses/first_adjusted_mortality_estimates_and_risk_assessment/2019-nCoV-preliminary_age_and_time_adjusted_mortality_rates_and_pandemic_risk_assessment.html</a>
Mizumoto et al	China Wuhan	IFR	0.2 (0.2-0.3)	95% CrI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.02.12.20022434v1">https://www.medrxiv.org/content/10.1101/2020.02.12.20022434v1</a>
Russell et al	Diamond Princess	IFR	1.3 (0.4-3.6)	95% CI	Yes	<a href="https://www.ncbi.nlm.nih.gov/pubmed/32234121">https://www.ncbi.nlm.nih.gov/pubmed/32234121</a>
Hauser et al	Italy Northern	IFR	3 (2.6-3.4)	95% CrI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031104v1.full.pdf">https://www.medrxiv.org/content/10.1101/2020.03.04.20031104v1.full.pdf</a>
Nishiura et al +	mainland China	IFR	NA (0.3-0.6)	95% CI	Yes	<a href="https://www.mdpi.com/2077-0383/9/2/419">https://www.mdpi.com/2077-0383/9/2/419</a>
Verity et al	mainland China	IFR	0.7 (0.4-1.3)	95% CrI	Yes	<a href="https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30243-7/fulltext">https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30243-7/fulltext</a>
Russell et al	China	CFR	1.2 (0.3-2.7)	95% CI	Yes	<a href="https://www.ncbi.nlm.nih.gov/pubmed/32234121">https://www.ncbi.nlm.nih.gov/pubmed/32234121</a>
Deng et al	China Hubei	CFR	5.4 (5.3-5.6)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1</a>
Mizumoto et al	China Hubei not Wuhan	CFR	0.9 (0.6-1.3)	95% CrI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.02.19.20025163v1">https://www.medrxiv.org/content/10.1101/2020.02.19.20025163v1</a>
Deng et al	China not Hubei	CFR	0.9 (0.8-1.1)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1</a>
Deng et al	China not Wuhan	CFR	3.5 (3.4-3.8)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1</a>
Deng et al	China Wuhan	CFR	6.2 (6.1-6.4)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1</a>
Mizumoto et al	China Wuhan	CFR	18.9 (17.1-20.8)	95% CrI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.02.19.20025163v1">https://www.medrxiv.org/content/10.1101/2020.02.19.20025163v1</a>
Russell et al	Diamond Princess	CFR	2.6 (0.9-6.7)	95% CI	Yes	<a href="https://www.ncbi.nlm.nih.gov/pubmed/32234121">https://www.ncbi.nlm.nih.gov/pubmed/32234121</a>
Deng et al	mainland China	CFR	4.5 (4.5-4.7)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1</a>
Wang et al	China Hubei	sCF R	7.2 (6.6-8)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.02.17.20023630v4">https://www.medrxiv.org/content/10.1101/2020.02.17.20023630v4</a>
Wang et al	China not Hubei	sCF R	1 (0.9-1.2)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.02.17.20023630v4">https://www.medrxiv.org/content/10.1101/2020.02.17.20023630v4</a>
Verity et al	mainland China	sCF R	1.4 (1.2-1.5)	95% CrI	Yes	<a href="https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30243-7/fulltext">https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30243-7/fulltext</a>
Famulare	China Wuhan	cCF R	33 (29-37)	95% CI	No	<a href="https://institutefordiseasemodeling.github.io/nCoV-public/analyses/first_adjusted_mortality_estimates_and_risk_assessment/2019-nCoV-preliminary_age_and_time_adjusted_mortality_rates_and_pandemic_risk_assessment.html">https://institutefordiseasemodeling.github.io/nCoV-public/analyses/first_adjusted_mortality_estimates_and_risk_assessment/2019-nCoV-preliminary_age_and_time_adjusted_mortality_rates_and_pandemic_risk_assessment.html</a>
Jung et al *	mainland China	cCF R	5.3 (3.5-7.5)	95% CI	Yes	<a href="https://www.ncbi.nlm.nih.gov/pubmed/32075152">https://www.ncbi.nlm.nih.gov/pubmed/32075152</a>
Jung et al **	mainland China	cCF R	8.4 (5.3-12.3)	95% CI	Yes	<a href="https://www.ncbi.nlm.nih.gov/pubmed/32075152">https://www.ncbi.nlm.nih.gov/pubmed/32075152</a>
Verity et al	outside mainland China (non-parametric)	cCF R	4.1 (2.1-7.8)	95% CrI	Yes	<a href="https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30243-7/fulltext">https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30243-7/fulltext</a>
Verity et al	outside mainland China (parametric)	cCF R	2.7 (1.4-4.7)	95% CrI	Yes	<a href="https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30243-7/fulltext">https://www.thelancet.com/journals/laninf/article/PIIS1473-3099(20)30243-7/fulltext</a>

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<b>Wu et al</b>	China Wuhan	HFR	14 (3.9-32)	95% CI	Yes	<a href="https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2020.25.3.2000044">https://www.eurosurveillance.org/content/10.2807/1560-7917.ES.2020.25.3.2000044</a>
<b>Deng et al</b>	China Hubei	ciCF R	25.7 (25.4-26.5)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1</a>
<b>Deng et al</b>	China not Hubei	ciCF R	8 (7.5-9.6)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1</a>
<b>Deng et al</b>	China not Wuhan	ciCF R	28.8 (28-31)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1</a>
<b>Deng et al</b>	China Wuhan	ciCF R	26.9 (26.6-27.9)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1</a>
<b>Deng et al</b>	mainland China	ciCF R	24.2 (23.9-25)	95% CI	No	<a href="https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1">https://www.medrxiv.org/content/10.1101/2020.03.04.20031005v1</a>

726

727 +. Range based on ~10% ascertainment

728 \*. Fitted to epidemic growth alone

729 \*\*. Fitted to epidemic growth along with other parameters

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732 Supplementary Table 6- Types of NPIs that could be implemented at the individual and  
733 community level

	<b>Non-pharmaceutical intervention</b>
<b>Interventions for individuals</b>	<b>Voluntary home isolation.</b> Separation of ill people with contagious diseases from non-infected persons
	<b>Voluntary home quarantine.</b> Restriction of people who are presumed to have been exposed to a contagious disease but are not ill, either because they did not become infected or because they are still in the incubation period.
<b>Community level</b>	<b>School closure</b> (closure of day care facilities, schools and higher education)
	<b>Workplace closure</b> (closure of non-essential services)
	<b>Cancel or postpone large public gatherings</b>

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737 Supplementary Table 7- Definition of NPIs search key words

Topic	Definition
' <i>case detection</i> ', ' <i>case detected</i> '	Detection of cases imported from an affected area
' <i>case isolation and contact tracing</i> '	Isolation of an identified positive case.
' <i>travel screening</i> '	Screening of passengers at port of exit/entry
' <i>travel reduction</i> ', ' <i>reduced travel</i> ', ' <i>airline suspension</i> '	Mobility reduction of individuals, intra- or inter- city/country.
' <i>school closure</i> '	Closing schools to prevent further transmission
' <i>Cancellation of events and mass gatherings</i> ', ' <i>Lockdown</i> '	Cancellation of events and mass gatherings in order to prevent further transmission.
' <i>Community response</i> '	People's psychological and behavioral responses during an outbreak

738 In Table 7 we present a short definition of the search keywords related to the non-pharmaceutical  
739 intervention we are interested in. As there are not specific terms to describe these interventions,  
740 or there are different terms to describe the same kind of intervention, we considered them to be  
741 equivalent.

742