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Epidemiology, genome, and clinical features of the pandemic SARSCoV-2: a recent view

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1 Abstract

2 Since the emergence of the Severe Acute Respiratory Syndrome- Coronavirus-2 (SARS-CoV-2) in Chinese Wuhan, the globally confirmed cases according to WHO 3 statistics reached 292,124 in 189 countries by March 22. The deaths cases reached 4 5 12,784 with estimated case-fatality rate ranges from 0.5 to 5.7%. Children are the least affected population by the disease, while the highest rate of death is among 6 elderly and people with comorbidities. The majority of infected individuals are 7 asymptomatic or only with mild symptoms. After the incubation period, the most 8 9 common symptoms are fever, cough, and fatigue. Asymptomatic carrier state is of paramount importance due to their ability to spread the infection and shedding the 10 virus into air and surroundings. Although much is still unknown about SARS-CoV-2, 11 the scientific research progresses in an unprecedented pace toward understanding the 12 nature, effective control, prevention, and treatment of SARS-CoV-2. Various reports 13 14 have suggested an in vivo evolution of the virus which may explain the rapid spread 15 and changing epidemiology of SARS-CoV-2 but further evidences are needed. 16 Unfortunately, no effective treatment or therapeutic drug is available for the disease and only supportive treatment and classical intervention measures are the available 17 choices for confronting SARS-CoV-2 pandemic. 18

19

20 Keywords:

- 21 CoVid-19, epidemic, *Coronavirus*, transmission, asymptomatic, pneumonia, Europe,
- 22 2109-noCoV, quarantine.

23 Abbreviations:

CCDC: Chinese Centre for Disease Control and Prevention, CDC: Centres for
Disease Control and Prevention (USA), ECDC: European Centre for Disease
Prevention and Control, WHO: World Health Organization, ACE2: AngiotensinConverting Enzyme 2, SARS: Severe Acute Respiratory Syndrome, UTR:
Untranslated region, CT: Computerized Tomography.

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40 Introduction

Emerging viral diseases are frequent public health threats owing to their potentials to 41 develop from small outbreaks to epidemics and pandemics. On 31 December 2019, 42 43 Chinese health authorities announced dozens of pneumonia infections in Wuhan city (Hubei province) without a recognized aetiology [1]. The first reported cases of 44 pneumonia in Wuhan had a previous history of visiting or association with a local 45 seafood market where wildlife animals are sold. The infectious agent was 46 subsequently identified on January 12 as a novel coronavirus (2019-nCoV) envisaged 47 to be originated from Huanan seafood market [2]. Due to its high similarity in terms 48 49 of clinical symptoms and biological nature with the causative agent of sever acute respiratory syndrome (SARS), the novel coronavirus named SARS-CoV-2 by the 50 International Committee on Taxonomy of Viruses. After rapid isolation of the virus 51 on January 7, genome sequence became publically available and submitted on 52 January 12 MN908947.2. 53 (GenBank: https://www.ncbi.nlm.nih.gov/nuccore/MN908947.2). Phylogenetic analyses showed 54 55 that SARS-CoV-2 is closely related to two SARS- coronaviruses of bat origin, bat-SL-CoVZC45 and bat-SL-CoVZXC21, but distant from human SARS-CoV (79% 56 sequence homology) and Middle East respiratory syndrome (MERS) coronavirus 57 58 (MERS-CoV) (50%) [3,4]. Epidemiological investigations showed that different animals (Bats, pangolins, snakes) could have been intermediate hosts that facilitate 59 the spill-over of SARS-CoV-2 as a distinct human Betacoronavirus from bats to 60 human population [4–6]. 61

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Since February 26, the reported new cases outside China are surpassing the cases 62 being reported in China mainland [7]. Currently, the numbers are increasing rapidly 63 specially in European region with overwhelming deaths in Italy. Till March 22, the 64 total cases of infections were 292,142 in 189 countries around the globe with 65 approximately 12,784 deaths cases. Reports show that adults and elderly are the most 66 infected by SARS-CoV-2, with slight predominance in men, while only low 67 proportion of paediatrics had contracted the infection [8-10]. Moreover, the presence 68 of previous diseases such as diabetes, cardiovascular or respiratory malfunction 69 significantly affects the outcomes. Indeed, being elderly or delay in diagnosis were 70 found to substantially increase the case-fatality rate [10,11]. The aim of this review is 71 72 to concisely discuss what is currently known about SARS-CoV-2 and its overwhelming pandemic. 73

74 Virology and genome of SARS-CoV-2

SARS-CoV-2 is an enveloped positive-sense unsegmented single-strand RNA virus 75 76 that belong to the genus *Betacoronavirus* (β CoV) (Figure 1A) [12]. The whole-77 genome sequences of SARS-CoV-2 isolated from patients in Wuhan or visited Wuhan showed a genome of 29844 - 29891 nucleotides in size, encoding 78 approximately 9860 amino acids and lacks the hemagglutinin-esterase gene [4,12]. 79 SARS-CoV-2 genome has great sequence similarity (89% - 96.3%) with two bat 80 coronaviruses; SARS-like-CoVZXC21 and bat-SL-CoVZC45, and 79% - 82% with 81 that of human SARS-CoV [4,12,13]. The genome contains 14 open reading frame 82 (ORF) encoding 27 proteins (Figure 1B). The longest ORF is located at the 5'-83

terminus encoding for 15 non-structural proteins collectively involved in viral
replication and possibly in immune evasion. The 3'-terminus of the genome encodes
for structural and accessory proteins [3]. Hypervariable genomic hotspots have been
detected in spike gene and in other ORFs for non-structural proteins [14].

88 Interestingly, the unique aspects of SARS-COV-2 were found in genes of spike 89 glycoprotein, orf8, and orf3b. Spike protein is composed of two subunits; S1 domain of a single polypeptide containing the receptor-binding domain and the S2 composed 90 of highly conserved polypeptides associated with the envelope. The external 91 subdomain of SARS-CoV-2 spike globular head S1 has only 40% similarity with its 92 93 counterparts in bat- and human SARS-CoV virion [12]. The outer portion of the external subdomain responsible for direct contact with the human receptor (ACE2) 94 has the most diversity in amino acids. Such variations are believed to be evolved 95 from homologous recombination between a bat coronavirus and other coronavirus of 96 unknown origin [5]. Orf3b is putative novel protein that seems to play a pivotal role 97 in pathogenesis of SARS-COV-2. The orf8 is an accessory protein shorter than its 98 99 counterparts found in other Betacoronavirus with unknown function.

100 Epidemiology and transmission of SARS-CoV-2

During the past two decades, China has witnessed the emergence of three respiratory viral outbreaks that turned into epidemics; avian influenza H5N1 in 1997 [15], SARS-CoV in 2003 [16], and the ongoing SARS-CoV-2 (in 2019-2020). Only the first cases of SARS-CoV-2 had associations with Huanan seafood market, while the

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subsequent sources of infection were infected individuals. Human-to-human 105 106 transmission is believed to be the major route for disease spreading worldwide [17]. 107 The intermediate host in Wuhan was suspected to be snakes and/or pangolins [5] but it still to be confirmed. Travel and importation played a critical role in delivery of 108 SARS-CoV-2 to Korea, Japan, the Middle East, and Europe [18,19]. During the early 109 weeks of the epidemic, the basic reproductive values (R_0) were calculated between 2 110 and 3.5, which is higher than SARS [20,21]. The R₀ is defined as the expected 111 number of secondary cases infected by a single infectious person in a susceptible 112 population. 113

114 WHO declared SARS-CoV-2 as a Public Health Emergency of International Concern 115 on January 30 and as a controllable pandemic in March 11. According to WHO statistics (March 22), the most reported cases were in China (81,498), Italy (53,578), 116 Spain (24,926), Germany (21,463), Iran (20,610), France (14,296) Korea (8,897), and 117 USA (15,219). Populations of about 54.6% of reporting countries are undergoing 118 local transmission of the infection [22]. Shockingly, more than 160 thousands 119 120 confirmed cases were reported within the last 12 days [7]. Based on reports from the 121 Chinese Centre for Disease Control and Prevention (CCDC), human-to-human 122 transmission via respiratory droplets and contact are the major routes to acquire the 123 infection. So far, no reliable evidence of vertical (intrauterine) transmission has been published. Transmission of infection to healthcare workers resulted in more than 124 125 2000 cases in China and 1423 in Italy (as of March 17) [23,24].

Early March witnessed a rapid increase of cases in Italy, Spain, France, Germany, 126 and Iran. Currently all European countries are affected and thousands of new cases 127 128 are reported on daily basis without known dynamics. Perhaps no pre-existing immunity in the population and all individuals are considered susceptible. The 129 transmission chain might went unnoticed during the incubation period of infected or 130 asymptomatic individuals who are transferring the infection actively. A mutant yet-131 132 unknown new type may be a major factor for the current overwhelming increase in 133 cases despite the pre-emptive implemented precautions and countermeasures taken by at-risk countries. Indeed, genomic analysis of 103 genomes derived from SARS-134 CoV-2 showed that genomes are diverged into two types; S (the ancestor) and L [25]. 135 136 The L type was prevalent during early January 2020, but decreased in later weeks. 137 Furthermore, recent studies support the evolution of the virus by successive mutations and recombination processes [26,27]. Comparative studies of genomes 138 sequenced from European cases compared to previously sequenced genomes in China 139 are needed to verify the previous findings. 140

By March, the number of new cases in China are getting low with time, while Italy and Iran are the new hotspots from which new infections are disseminated to the nearby countries. In the Middle East and central Europe, the reported cases to WHO are growing with time (Figure 2). In the European continent, the total confirmed cases reach 141,858 and 7,319 deaths until March 22 (10:00 CET) [28]. According to the epidemiological data by Italian Higher Institute of Health (ISS), the mortality rate (5.4%) is higher than of China (2.3%) and total deaths in Italy exceeded the number documented in China. This may be attributed to the fact that most infected individualsare the elderly in addition to the incapacity of healthcare system to cope up with the

151 **Turning into a pandemic**

rapid increase of new cases [23].

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152 Unlike its precedent SARS outbreak, SARS-CoV-2 had unique characteristics and chances to become a pandemic. First, the initial case definition set be Chinese CDC 153 (CCDC) was narrow and based solely on pneumonia signs. Subsequent analysis of 154 the first cases showed about 81% of cases have mild disease, which undoubtedly 155 156 increased the transmission within the community by the asymptomatic carrier state 157 [10]. The WHO estimated the mortality rate to be between 3 and 4% with increased value for elderly or individuals with previous comorbidities. Due to the lack of data 158 159 regarding the true number of infected individuals worldwide, it is still early to calculate the exact value of mortality rate. Second, the current definition (March 22) 160 of suspected case set by WHO is a patient with any acute respiratory illness and 161 162 having been in contact with a confirmed or probable SARS-COV-2 case in the last 14 163 days prior to onset of symptoms. The above definition is based on reports calculated 164 the incubation period to range from 1 to 14 days [29]. However, recent reports found an incubation period might be as long as 24 days [30,31]. This period is much more 165 166 than the 14 days used by WHO for guidance the quarantine policies, consequently, truly infected persons may be missed during their long incubation period and 167 contribute to the spread of SARS-CoV-2. Additionally, international surveillance 168 estimated that up to two-thirds of exported case from China went undetected [32]. 169

Third, the containment measure was challenging in the first phase of the outbreak in 170 Wuhan due to its high population, immense trade and wide travel connections within 171 China and the world. Furthermore, the industry, commerce, and travel of China with 172 the rest of the world has doubled since 2000 which aided SARS-CoV-2 quick spread 173 [33,34]. The Spring Festival and Lunar Year events also believed to played a critical 174 role in SARS-CoV-2 spread within China and the region as millions of Wuhan 175 dwellers travelled out of the city before the lockdown measure implementation and 176 just after the outbreak. The same situation applies for Europe where international 177 travel and business are intense and free travel within the Eurozone is permitted. The 178 exact underlying reason(s) for the ongoing rapid spread of SARS-CoV-2 in Europe is 179 180 still unknown. The suspected in vivo evolution of the virus and transmission by asymptomatic carriers may be major factors. [27,35,36]. 181

Fourth, in SARS-CoV-2 infections, shedding of virions starts earlier than clinical 182 manifestations and shedding peak is still unknown [37]. Isolation of individuals after 183 symptoms onset will be too late and transmission to others would already occurred 184 185 during the incubation period [30,38]. Person-to-person transmission of SARS-CoV-2 186 from asymptomatic cases was documented in first clusters in Germany and Vietnam during early February [39,40]. Dependence on temperature for ruling out 187 188 asymptomatic carriers as it used during SARS containment deemed inefficient in SARS-CoV-2 [41]. Additionally, the R₀ value of SARS-CoV-2 is higher than of 189 190 SARS (3.28 vs 2.2) [20,21]. High transmissibility of SARS-CoV-2 is obvious by a

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- 191 global increase of more than 72,000 cases in three days according to WHO reports
- 192 (from March 18 to 20) [7].
- 193

3 **Pathology and clinical features**

SARS-CoV-2 exploits the angiotensin-converting enzyme 2 receptor (ACE2), same 194 195 receptor of SARS, in lower respiratory tract of human for entry into lung cells [42,43]. Cellular surface serine protease TMPRSS2 is also employed by SARS-CoV-196 197 2 for priming of spike protein S to facilities membrane fusion with host cell [42]. ACE2 is also prevalent on other cells outside lung [44]. The exact pathophysiology of 198 199 SARS-CoV-2 and its closely related outbreaks-associated coronaviruses remains 200 elusive. Cytokines storm and viral evasion of cell-mediated immune response play important roles in pathogenesis and disease severity [45]. Higher levels of 201 202 inflammatory chemokines and cytokines (GCSF, IP10, MCP1, MIP1A, TNFa, and other interleukins) result in lung injury that requires urgent admission to intensive 203 care units [8]. 204

Children are the least affected population by the disease, however, this observation might be biased by low number of sampled children in the earlier reports. Moreover, children have less contact with potential sources due to fewer outdoor activities and parental protection. Some scholars believe that immune system of children develops less intense cytokines storm or their respiratory tracts are healthier because they have not been exposed to pollutants as adults, yet supporting evidences are still unavailable.

After an incubation period of 5-14 days, SARS-CoV-2 infected people commonly 212 present by features of pneumonia including fever, dry cough, dyspnoea, myalgia, and 213 fatigue. Acute respiratory distress syndrome (ARDS) is a feature in severe cases. 214 Other symptoms include productive cough, headache, haemoptysis, and diarrhoea 215 were also documented [8]. A report from the CCDC estimated that only 5% are 216 critically ill (e.g., with shock, respiratory failure requiring mechanical ventilation, or 217 multiple organ dysfunction), 14% of patients had severe pneumonia (e.g., shortness 218 219 of breath, low oxygen saturation, or had more than 50% of their lung parenchyma involved on chest imaging within 1-2 days). Meanwhile, most patients (81%) showed 220 no or mild pneumonia [10]. The overall case-fatality rate was 2.3 percent, however, 221 222 case-fatality rate between 5.8 percent in Wuhan to 0.7 percent in the rest of China 223 were reported. Fortunately, no deaths were reported among noncritical cases [46].

224 Leukocyte count in most cases shows lymphopenia, nonetheless, total white cell count may be low or higher than normal. D-dimer, prothrombin time, hepatic 225 transaminases and procalcitonin are high among critically ill patients. Abnormal chest 226 227 radiographic features were seen in almost all patients [8]. Bilateral patchy shadows 228 are frequently seen on chest X-ray, while ground glass opacifications (GGO) are found in cases with ARDS. Typical CT findings include; multiple GGO with or 229 230 without reticular pattern, and parenchymal consolidations involving both lungs [47,48]. Other common CT features include; microvascular dilatation, thick interlobar 231 232 septa and air bronchogram [48]. Interestingly, CT changes have also been seen in 233 patients before the onset of clinical symptoms and before viral RNA detection from upper respiratory specimens [49]. Time required for recovery ranges from 2 weeks in
mild infections to 3-6 weeks in severe disease. Extrapulmonary complications include
acute injuries in heart, liver, and kidneys are known [9,50].

237 Diagnosis

238 Travel history is no longer valid as a criterion to build the diagnosis on since local transmission account for the majority of infection acquisition expected in locations 239 where no cases have been identified previously. The clinical manifestations 240 accompanied by radiographic evaluation and laboratory diagnosis (detection of viral 241 242 RNA) are the only possible approach for definitive diagnosis [51]. Generalizations 243 regarding symptoms and laboratory indices still cannot be drawn because SARS-CoV-2 pathology and its reflections are still not completely understood. Due to 244 variations in epidemiology and clinical features of SARS-CoV-2 infections, 245 physicians and specialists are highly recommended to continually update their 246 247 management strategies based on WHO interim guidelines for diagnosis and cases 248 definitions (suspected, probable, and confirmed).

The most convenient laboratory tests for SARS-CoV-2 diagnosis is the real-time reverse transcriptase-PCR (rRT-PCR) of nasopharyngeal specimens. A regularly updated source for various protocols based on rRT-PCR assay is available at WHO website [52]. As in any diagnostic test, false positive and false negative results have been reported but at very low frequency [30]. According to CDC recommendations, the accepted clinical specimens are bronchoalveolar lavage fluid, nasopharyngeal swabs (but not throat swabs), and blood [53]. Bronchoalveolar lavage fluid were
found superior to other respiratory specimens (positive rate 93%) followed by sputum
(72%), nasal swab (63%), fibrobronchoscope brush biopsy (46%), pharyngeal swab
(32%), and faeces (29%) [54]. Due to the increasing number of healthcare-associated
infections, strict adherence to usage of personal protective equipment (PPE) and
airborne precautions is highly recommended. A concise guide for healthcare staff,
researcher, and public health workers has been published [55].

262 **Confronting the pandemic**

In the absence of specific therapy and anti-SARS-CoV-2 drugs, the urgent 263 264 implementation of classical public health measures are the only reliable actions to mitigate the pandemic and gradual control of infection spread. A very recent small-265 266 sized clinical trial has found promising results for treatment of SARS-CoV-2 in France. The administration of 600 mg of hydroxychloroquine plus azithromycin on 267 daily basis resulted in effective clearance of the virus from the nasopharynx within 268 six days [56]. The mechanism of action is the alkalinisation of epithelial 269 270 phagolysosome containing the virus. These results are founding the current therapeutic protocol in IHU Méditerranée Infection, France. Further large-sized 271 ongoing clinical trials (including hydroxychloroquine among other drugs) will 272 provide further pieces of evidence for treatment options. 273

The rigorous and gigantic efforts of China in implementing public measures are obviously effective as new cases are declining steeply. Indeed, China have applied 276 the largest quarantine in history to contain the disease, hence, cut of person-to-person transmission chain, isolation, quarantine, social distancing, and community 277 containment are the only promising measures to fight SARS-CoV-2. As a respiratory 278 virus with substantial transmissibility, applying of social distancing to reduce 279 interactions between people in a mass scale is beneficial especially when detection of 280 cases is swift [57]. If the community transmission continued in expansion, social 281 distancing would be insufficient and community containment would be needed. The 282 efficiency of community containment is apparent in China where normal daily life is 283 gradually being sustained recently in Wuhan after a significant decline of cases. 284 Nonetheless, such measure is challenging and requires a partnership with local and 285 286 state officials of different fields. Media should also tap their abilities to communicate 287 with trusted information about containment benefits and pre-empt false rumours and 288 panic.

As the world witnessing a significant decline in new cases in China, the will of 289 political and healthcare authorities should push forward to implement a lockdown of 290 291 hotspot zones and a comprehensive tracing of contacts associated with confirmed 292 cases. The cost of wide tracking and community containment would not be outweighed by the long-term economic losses and disease burden if the transmission 293 294 continued. Additionally, rapid responses and decision making alongside free or at least affordable laboratory testing will facilitate the delineation of hotspot zones. 295 296 Certain community containment procedures such as cancellation of public events and closure of institutions are seen in numerous countries. These precautions will not be 297

298 fruitful unless parallel thorough surveillance accompanied by medical observation 299 and legal actions are taken if quarantine violations occurred. Recently, Italy, France, and Spain, and Philippines started the implementation of lockdown measures, with 300 law enforcement in some cases, to control the overwhelming increase in cases. In 301 third-world countries, lockdown measure is extremely challenging owing to the high 302 proportion of low-wage jobs where workers seek opportunities at daily basis. Finally, 303 efficient deactivation of different coronaviruses (SARS-CoV-2 was not evaluated) 304 was reported with disinfectants such as 62 - 71% ethanol, 0.5% hydrogen peroxide or 305 0.1% sodium hypochlorite within 1 minute and this efficacy is highly expected to 306 apply for SARS-CoV-2 [58]. 307

308 Issues to be investigated

309 Despite the intense research and clinical investigations, certain issues of SARS-CoV-2 pandemic await exploration. Fist, the origin of the virus and the nature of spill-over 310 from its natural reservoir to human is still unanswered. It is known that bats and 311 312 Pangolins are hunted for food in China but this has not be confirmed so far to be the 313 cause [6]. Moreover, viral replication and human immune response to SARS-CoV-2 314 are still largely unknown. Second, the virus was detected in faecal samples from infected patients and its potentials for oral-faecal transmissibility is still unaddressed 315 by researchers [54,59,60]. Third, the phylogenetic analyses have shown genomic 316 variations in SARS-CoV-2 genomes sequenced in different countries through 317 different periods. Whether the in vivo evolution occurs in human or other 318 intermediate animal host is still unproven. Indeed, the existence and identity of an 319

320 intermediate host is highly expected with few evidences but not experimentally proven. Fourth, the period for which SARS-CoV-2 virion retains its infectivity when 321 322 shed and deposited on surfaces and environment is also unclear. Indeed, the efficacy of hand washing in deactivating SARS-CoV-2 virion has not been tested. Fifth, the 323 reason of predominance of SARS-CoV-2 infections in men is also not known. 324 Smoking habit in Asian men populations was expected to be the underlying cause, 325 but no solid evidence is yet available [61]. Sixth, the initial administration of 326 327 corticosteroids during early stage of SARS epidemic was justified by their mitigation of inflammatory response but subsequently halted due to delay in viral clearance [62]. 328 Lately, a small-sized (n=201) observational study reported that methylprednisolone 329 330 treatment was associated with decrease in death risk of patients with ARDS [63]. Whether the same effects of corticosteroids happen in SARS-CoV-2 infection are still 331 unclear. 332

333 Conclusion

The epicentres of SARS-CoV-2 globally is expected to multiply especially in poor 334 335 nations. Genomic, virological, and medical analyses are progressing in unprecedented 336 strides. Such analyses are expected to contribute to understanding of epidemiology, 337 pathogenesis, treatment, and prevention. Suspected case definition is expected to get revised at any moment, hence, medical staff and epidemiologists should be keep 338 339 updated for better control of the pandemic. Moreover, they are also highly advised to 340 employ protective measures since they are at-risk populations due to exposure to infection nosocomially. The clinical manifestations varied widely and mild or 341

342	asymptomatic cases may not seek a medical care and go undetected and exacerbate
343	transmission scenario. The exact routes of pathogenesis, transmission and pandemic
344	dynamics of the SARS-CoV-2 are under intense investigation. Till now, classical
345	public health measures and control intervention are the only way to fight SARS-CoV-
346	2 pandemic.
347	Conflicts of interest
348	The authors declare no conflicts of interest.
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351 **References**

- 352 [1] World Health Organization. Novel Coronavirus (2019-nCoV) situation report -
- 353 1. Geneva: 2020.
- 354 [2] Zhu N, Zhang D, Wang W, Li X, Yang B, Song J, et al. A Novel Coronavirus
- from Patients with Pneumonia in China, 2019. N Engl J Med 2020.
- 356 https://doi.org/10.1056/nejmoa2001017.
- 357 [3] Wu A, Peng Y, Huang B, Ding X, Wang X, Niu P, et al. Genome Composition
- and Divergence of the Novel Coronavirus (2019-nCoV) Originating in China.
- 359 Cell Host Microbe 2020;27:325–8.
- 360 https://doi.org/10.1016/j.chom.2020.02.001.

361	[4]	Lu R, Zhao X, Li J, Niu P, Yang B, Wu H, et al. Genomic characterisation and
362		epidemiology of 2019 novel coronavirus: implications for virus origins and
363		receptor binding. Lancet 2020;395:565-74. https://doi.org/10.1016/S0140-
364		6736(20)30251-8.
365	[5]	Ji W, Wang W, Zhao X, Zai J, Li X. Cross
366		identified coronavirus 2019 nCoV - Ji - 2020 - Journal of Medical Virology -
367		Wiley Online Library. J Med Virol 2020;92:433–40.
368	[6]	Cyranoski D. Mystery deepens over animal source of coronavirus. Nature
369		2020;579:18–9. https://doi.org/10.1038/d41586-020-00548-w.
370	[7]	World Health Organization. Situation reports 2020.
371		https://www.who.int/emergencies/diseases/novel-coronavirus-2019/situation-
372		reports (accessed March 17, 2020).
373	[8]	Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, et al. Clinical features of
374		patients infected with 2019 novel coronavirus in Wuhan, China. Lancet
375		2020;395:497–506. https://doi.org/10.1016/S0140-6736(20)30183-5.
376	[9]	Guan W, Ni Z, Hu Y, Liang W, Ou C, He J, et al. Clinical Characteristics of
377		Coronavirus Disease 2019 in China. N Engl J Med 2020:NEJMoa2002032.
378		https://doi.org/10.1056/NEJMoa2002032.
379	[10]	Wu Z, McGoogan JM. Characteristics of and Important Lessons From the
380		Coronavirus Disease 2019 (COVID-19) Outbreak in China: Summary of a
381		Report of 72 314 Cases From the Chinese Center for Disease Control and

Journal Pre-proof

382		Prevention. JAMA 2020. https://doi.org/10.1001/jama.2020.2648.
383	[11]	Yang S, Cao P, Du P, Wu Z, Zhuang Z, Yang L, et al. Early estimation of the
384		case fatality rate of COVID-19 in mainland China: a data-driven analysis. Ann
385		Transl Med 2020;8:128–128. https://doi.org/10.21037/atm.2020.02.66.
386	[12]	Chan JF-W, Kok K-H, Zhu Z, Chu H, To KK-W, Yuan S, et al. Genomic
387		characterization of the 2019 novel human-pathogenic coronavirus isolated
388		from a patient with atypical pneumonia after visiting Wuhan. Emerg Microbes
389		Infect 2020;9:221-36. https://doi.org/10.1080/22221751.2020.1719902.
390	[13]	Paraskevis D, Kostaki EG, Magiorkinis G, Panayiotakopoulos G, Sourvinos G,
391		Tsiodras S. Full-genome evolutionary analysis of the novel corona virus
392		(2019-nCoV) rejects the hypothesis of emergence as a result of a recent
393		recombination event. Infect Genet Evol 2020;79:104212.
394		https://doi.org/10.1016/j.meegid.2020.104212.
395	[14]	Wen F, Yu H, Guo J, Li Y, Luo K, Huang S. Identification of the hyper-
396		variable genomic hotspot for the novel coronavirus SARS-CoV-2. J Infect
397		2020. https://doi.org/10.1016/j.jinf.2020.02.027.
398	[15]	Alexander DJ, Brown IH. History of Highly Pathogenic Avian Influenza. Rev
399		Sci Tech 2009;28:19–38. https://doi.org/10.20506/rst.28.1.1856.
400	[16]	Chan-Yeung M, Seto WH, Sung joseph JY. Severe acute respiratory
401		syndrome: Patients were epidemiologically linked. BMJ 2003;326:1393.
402		https://doi.org/10.1136/bmj.326.7403.1393.

403	[17]	Guo Y-R, Cao Q-D, Hong Z-S, Tan Y-Y, Chen S-D, Jin H-J, et al. The origin,
404		transmission and clinical therapies on coronavirus disease 2019 (COVID-19)
405		outbreak - an update on the status. Mil Med Res 2020;7:11.
406		https://doi.org/10.1186/s40779-020-00240-0.
407	[18]	Giovanetti M, Benvenuto D, Angeletti S, Ciccozzi M. The first two cases of
408		2019-nCoV in Italy: Where they come from? J Med Virol 2020;92:518–21.
409		https://doi.org/10.1002/jmv.25699.
410	[19]	Bernard Stoecklin S, Rolland P, Silue Y, Mailles A, Campese C, Simondon A,
411		et al. First cases of coronavirus disease 2019 (COVID-19) in France:
412		surveillance, investigations and control measures, January 2020. Euro Surveill
413		2020;25. https://doi.org/10.2807/1560-7917.ES.2020.25.6.2000094.
414	[20]	Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of
414 415	[20]	Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. J Travel Med 2020.
414 415 416	[20]	Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. J Travel Med 2020. https://doi.org/10.1093/jtm/taaa021.
414 415 416 417	[20]	Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. J Travel Med 2020. https://doi.org/10.1093/jtm/taaa021. Lipsitch M, Cohen T, Cooper B, Robins JM, Ma S, James L, et al.
414 415 416 417 418	[20]	Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. J Travel Med 2020. https://doi.org/10.1093/jtm/taaa021. Lipsitch M, Cohen T, Cooper B, Robins JM, Ma S, James L, et al. Transmission dynamics and control of severe acute respiratory syndrome.
414 415 416 417 418 419	[20]	 Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. J Travel Med 2020. https://doi.org/10.1093/jtm/taaa021. Lipsitch M, Cohen T, Cooper B, Robins JM, Ma S, James L, et al. Transmission dynamics and control of severe acute respiratory syndrome. Science (80-) 2003;300:1966–70. https://doi.org/10.1126/science.1086616.
414 415 416 417 418 419 420	[20]	 Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. J Travel Med 2020. https://doi.org/10.1093/jtm/taaa021. Lipsitch M, Cohen T, Cooper B, Robins JM, Ma S, James L, et al. Transmission dynamics and control of severe acute respiratory syndrome. Science (80-) 2003;300:1966–70. https://doi.org/10.1126/science.1086616. World Health Organization. Coronavirus disease 2019 (COVID-19) Situation
414 415 416 417 418 419 420 421	[20] [21] [22]	 Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. J Travel Med 2020. https://doi.org/10.1093/jtm/taaa021. Lipsitch M, Cohen T, Cooper B, Robins JM, Ma S, James L, et al. Transmission dynamics and control of severe acute respiratory syndrome. Science (80-) 2003;300:1966–70. https://doi.org/10.1126/science.1086616. World Health Organization. Coronavirus disease 2019 (COVID-19) Situation Report – 51. Geneva: 2020.
414 415 416 417 418 419 420 421 422	[20] [21] [22]	 Liu Y, Gayle AA, Wilder-Smith A, Rocklöv J. The reproductive number of COVID-19 is higher compared to SARS coronavirus. J Travel Med 2020. https://doi.org/10.1093/jtm/taaa021. Lipsitch M, Cohen T, Cooper B, Robins JM, Ma S, James L, et al. Transmission dynamics and control of severe acute respiratory syndrome. Science (80-) 2003;300:1966–70. https://doi.org/10.1126/science.1086616. World Health Organization. Coronavirus disease 2019 (COVID-19) Situation Report – 51. Geneva: 2020. Istituto Superiore di Sanità. Sorveglianza Integrata COVID-19 in Italia. 2020.

424	[The epidemiolo	cical characteristics	of an outbreak	of 2019 novel	coronavirus
-----	-----------------	-----------------------	----------------	---------------	-------------

- 425 diseases (COVID-19) in China]. Zhonghua Liu Xing Bing Xue Za Zhi
- 426 2020;41:145–51. https://doi.org/10.3760/cma.j.issn.0254-6450.2020.02.003.
- 427 [25] Tang X, Wu C, Li X, Song Y, Yao X, Wu X, et al. On the origin and

428 continuing evolution of SARS-CoV-2. Natl Sci Rev 2020.

- 429 https://doi.org/10.1093/nsr/nwaa036.
- 430 [26] Yi H. 2019 novel coronavirus is undergoing active recombination. Clin Infect
 431 Dis 2020. https://doi.org/10.1093/cid/ciaa219.
- 432 [27] Shen Z, Xiao Y, Kang L, Ma W, Shi L, Zhang L, et al. Genomic diversity of
- 433 SARS-CoV-2 in Coronavirus Disease 2019 patients. Clin Infect Dis 2020.
- 434 https://doi.org/10.1093/cid/ciaa203.
- European Centre for Disease Prevention and Control. Situation update for the
 EU/EEA and the UK, as of 17 March 2020 08:00 2020.
- 437 https://www.ecdc.europa.eu/en/cases-2019-ncov-eueea (accessed March 17,
 438 2020).
- 439 [29] Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y, et al. Early Transmission
- 440 Dynamics in Wuhan, China, of Novel Coronavirus–Infected Pneumonia. N
- 441 Engl J Med 2020. https://doi.org/10.1056/nejmoa2001316.
- [30] Bai Y, Yao L, Wei T, Tian F, Jin D-Y, Chen L, et al. Presumed Asymptomatic
 Carrier Transmission of COVID-19. JAMA 2020.
- 444 https://doi.org/10.1001/jama.2020.2565.

445	[31]	Guan W, Ni Z, Hu Y, Liang W, Ou C, He J, et al. Clinical Characteristics of
446		Coronavirus Disease 2019 in China. N Engl J Med 2020:NEJMoa2002032.
447		https://doi.org/10.1056/NEJMoa2002032.
448	[32]	Bhatia S, Imai N, Cuomo-Dannenburg G, Baguelin M, Boonyasiri A, Cori A,
449		et al. Report 6: Relative sensitivity of international surveillance. 2020.
450	[33]	Wilson ME, Chen LH. Travellers give wings to novel coronavirus (2019-
451		nCoV). J Travel Med 2020;27. https://doi.org/10.1093/jtm/taaa015.
452	[34]	Bogoch II, Watts A, Thomas-Bachli A, Huber C, Kraemer MUG, Khan K.
453		Potential for global spread of a novel coronavirus from China. J Travel Med
454		2020;27. https://doi.org/10.1093/jtm/taaa011.
455	[35]	Zhang L, Shen F, Chen F, Lin Z. Origin and Evolution of the 2019 Novel
456		Coronavirus. Clin Infect Dis 2020. https://doi.org/10.1093/cid/ciaa112.
457	[36]	Angeletti S, Benvenuto D, Bianchi M, Giovanetti M, Pascarella S, Ciccozzi M.
458		COVID-2019: The role of the nsp2 and nsp3 in its pathogenesis. J Med Virol
459		2020;n/a. https://doi.org/10.1002/jmv.25719.
460	[37]	Wilder-Smith A, Chiew CJ, Lee VJ. Can we contain the COVID-19 outbreak
461		with the same measures as for SARS? Lancet Infect Dis 2020;0.
462		https://doi.org/10.1016/S1473-3099(20)30129-8.
463	[38]	Yu P, Zhu J, Zhang Z, Han Y. A Familial Cluster of Infection Associated With
464		the 2019 Novel Coronavirus Indicating Possible Person-to-Person
465		Transmission During the Incubation Period. J Infect Dis 2020.

466	https://doi.org	g/10.1093/infdi	s/jiaa077.

- 467 [39] Phan LT, Nguyen T V., Luong QC, Nguyen T V., Nguyen HT, Le HQ, et al.
- 468 Importation and human-to-human transmission of a novel coronavirus in
- 469 Vietnam. N Engl J Med 2020;382:872–4.
- 470 https://doi.org/10.1056/NEJMc2001272.
- 471 [40] Rothe C, Schunk M, Sothmann P, Bretzel G, Froeschl G, Wallrauch C, et al.
- 472 Transmission of 2019-nCoV Infection from an Asymptomatic Contact in
- 473 Germany. N Engl J Med 2020. https://doi.org/10.1056/nejmc2001468.
- 474 [41] Quilty BJ, Clifford S, Flasche S, Eggo RM. Effectiveness of airport screening
- 475 at detecting travellers infected with novel coronavirus (2019-nCoV).

476 Eurosurveillance 2020;25:2000080. https://doi.org/10.2807/1560-

- 477 7917.ES.2020.25.5.2000080.
- 478 [42] Hoffmann M, Kleine-Weber H, Schroeder S, Krüger N, Herrler T, Erichsen S,
- 479 et al. SARS-CoV-2 Cell Entry Depends on ACE2 and TMPRSS2 and Is
- 480 Blocked by a Clinically Proven Protease Inhibitor. Cell 2020.
- 481 https://doi.org/10.1016/j.cell.2020.02.052.
- 482 [43] Zhou P, Yang X-L, Wang X-G, Hu B, Zhang L, Zhang W, et al. A pneumonia
- 483 outbreak associated with a new coronavirus of probable bat origin. Nat 2020
 484 5797798 2020;579:270–3. https://doi.org/10.1038/s41586-020-2012-7.
- 485 [44] Gu J, Gong E, Zhang B, Zheng J, Gao Z, Zhong Y, et al. Multiple organ
 486 infection and the pathogenesis of SARS. J Exp Med 2005;202:415–24.

487	https://doi.or	g/10.1084/	jem.20050828.
-----	----------------	------------	---------------

- 488 [45] Channappanavar R, Perlman S. Pathogenic human coronavirus infections:
- 489 causes and consequences of cytokine storm and immunopathology. Semin
- 490 Immunopathol 2017;39:529–39. https://doi.org/10.1007/s00281-017-0629-x.
- 491 [46] Organization WH. Report of the WHO-China Joint Mission on Coronavirus
 492 Disease 2019 (COVID-19). Geneva: 2020.
- 493 [47] Chung M, Bernheim A, Mei X, Zhang N, Huang M, Zeng X, et al. CT Imaging
- 494 Features of 2019 Novel Coronavirus (2019-nCoV). Radiology 2020;295:202–

495 7. https://doi.org/10.1148/radiol.2020200230.

- [48] Zhou S, Wang Y, Zhu T, Xia L. CT Features of Coronavirus Disease 2019
 (COVID-19) Pneumonia in 62 Patients in Wuhan, China. Am J Roentgenol
 2020:1–8. https://doi.org/10.2214/AJR.20.22975.
- 499 [49] Shi H, Han X, Jiang N, Cao Y, Alwalid O, Gu J, et al. Radiological findings
- from 81 patients with COVID-19 pneumonia in Wuhan, China: a descriptive
 study. Lancet Infect Dis 2020. https://doi.org/https://doi.org/10.1016/S14733099(20)30086-4.
- 503 [50] Wang D, Hu B, Hu C, Zhu F, Liu X, Zhang J, et al. Clinical Characteristics of
- 504 138 Hospitalized Patients with 2019 Novel Coronavirus-Infected Pneumonia in
- 505 Wuhan, China. JAMA J Am Med Assoc 2020.
- 506 https://doi.org/10.1001/jama.2020.1585.
- 507 [51] Zu ZY, Jiang M Di, Xu PP, Chen W, Ni QQ, Lu GM, et al. Coronavirus

508		Disease 2019 (COVID-19): A Perspective from China. Radiology
509		2020:200490. https://doi.org/10.1148/radiol.2020200490.
510	[52]	WHO. Coronavirus disease (COVID-19) technical guidance: Laboratory
511		testing for 2019-nCoV in humans 2020.
512		https://www.who.int/emergencies/diseases/novel-coronavirus-2019/technical-
513		guidance/laboratory-guidance.
514	[53]	Centers for Disease Control and Prevention. Interim Guidelines for Collecting,
515		Handling, and Testing Clinical Specimens from Persons for Coronavirus
516		Disease 2019 (COVID-19) 2020. https://www.cdc.gov/coronavirus/2019-
517		nCoV/lab/guidelines-clinical-specimens.html (accessed March 17, 2020).
518	[54]	Wang W, Xu Y, Gao R, Lu R, Han K, Wu G, et al. Detection of SARS-CoV-2
519		in Different Types of Clinical Specimens. JAMA 2020.
520		https://doi.org/10.1001/jama.2020.3786.
521	[55]	Jin Y-H, Cai L, Cheng Z-S, Cheng H, Deng T, Fan Y-P, et al. A rapid advice
522		guideline for the diagnosis and treatment of 2019 novel coronavirus (2019-
523		nCoV) infected pneumonia (standard version). Mil Med Res 2020;7:4.
524		https://doi.org/10.1186/s40779-020-0233-6.
525	[56]	Gautret P, Lagier J-C, Parola P, Hoang VT, Meddeb L, Mailhe M, et al.
526		Hydroxychloroquine and azithromycin as a treatment of COVID-19: results of
527		an open-label non-randomized clinical trial. Int J Antimicrob Agents
528		2020:105949. https://doi.org/10.1016/j.ijantimicag.2020.105949.

529	[57]	Wilder-Smith A, Freedman DO. Isolation, quarantine, social distancing and
530		community containment: pivotal role for old-style public health measures in
531		the novel coronavirus (2019-nCoV) outbreak. J Travel Med 2020;27.
532		https://doi.org/10.1093/jtm/taaa020.
533	[58]	Kampf G, Todt D, Pfaender S, Steinmann E. Persistence of coronaviruses on
534		inanimate surfaces and their inactivation with biocidal agents. J Hosp Infect
535		2020;104:246-51. https://doi.org/10.1016/j.jhin.2020.01.022.
536	[59]	Zhang J, Wang S, Xue Y. Fecal specimen diagnosis 2019 novel coronavirus-
537		infected pneumonia. J Med Virol n.d.;n/a. https://doi.org/10.1002/jmv.25742.
538	[60]	Holshue ML, DeBolt C, Lindquist S, Lofy KH, Wiesman J, Bruce H, et al.
539		First Case of 2019 Novel Coronavirus in the United States. N Engl J Med
540		2020. https://doi.org/10.1056/nejmoa2001191.
541	[61]	Burki T. Outbreak of coronavirus disease 2019. Lancet Infect Dis
542		2020;20:292-3. https://doi.org/10.1016/S1473-3099(20)30076-1.
543	[62]	Stockman LJ, Bellamy R, Garner P. SARS: Systematic Review of Treatment
544		Effects. PLoS Med 2006;3:e343.
545		https://doi.org/10.1371/journal.pmed.0030343.
546	[63]	Wu C, Chen X, Cai Y, Xia J, Zhou X, Xu S, et al. Risk Factors Associated
547		With Acute Respiratory Distress Syndrome and Death in Patients With
548		Coronavirus Disease 2019 Pneumonia in Wuhan, China. JAMA Intern Med
549		2020. https://doi.org/10.1001/jamainternmed.2020.0994.



Figure 1. Structure and genome organization of SARS-CoV-2. (A) General structure of SARS-CoV-2 virion. (B) Genome composition of SARS-CoV-2 showing fourteen open reading frames exist in SARS-CoV-2 genome. The first two ORFs at the 5'- UTR are coding for polyprotein (pp1a/ab) required for viral replication

followed by structural proteins for Spike (S), membrane (M), Nucleoprotein (N). At the 3'-terminus accessory genes (3a, 3b, p6, 7a, 7b, 8b, 9b, and orf14) are located with flanking ORFs. Accessory proteins not required for viral replication or other known functions (adopted from reference [3] with permission).



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Figure 2. Reported cases of SARS-CoV-2 from March 1 -21. (A) Total confirmed cases in all regions of the world. (B) Newly reported cases of SARS-CoV-2 in most affected countries (with cases > 8,000). (The numbers are retrieved from WHO situation reports).



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