

Host susceptibility to severe COVID-19: a retrospective analysis of 487 case outside Wuhan

Yu Shi

Zhejiang University

Xia Yu

Zhejiang University

Hong Zhao

Zhejiang University

Hao Wang

Zhejiang University

Ruihong Zhao

Zhejiang University

Qun Cai

Zhejiang University

Shanshan Sun

Zhejiang University

Hong Fang

Zhejiang University

Yijie Wang

Zhejiang University

Zhangmin Hu

Zhejiang University

Jinnan Duan

Zhejiang University

Xiaoman Lin

Zhejiang University

Huilan Tu

Zhejiang University

Sheng Tu

Zhejiang University

jifang sheng (✉ jifang_sheng@zju.edu.cn)

Zhejiang University School of Medicine First Affiliated Hospital

Keywords: COVID-2019, Disease severity, Risk factors, Host susceptibility

Posted Date: March 4th, 2020

DOI: <https://doi.org/10.21203/rs.3.rs-16021/v1>

License:   This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Abstract

Background: The recent outbreak of SARS-CoV-2 infection results in a considerable morbidity and mortality, mainly in China. The study is to investigate the intrinsic features of infected patients that associated with severe type of this disease.

Method: A total of 487 laboratory-confirmed COVID-19 patients were included in analysis. The demographic and epidemiological of patients representing as mild and severe at admission were compared. A step-wise multivariate logistic regression analysis were performed to identify significant risk factors associated with severe COVID-19 . A score system incorporating risk factors was established for risk stratification and validated in a small cohort during in-hospital follow-up.

Results: Of all patients, 49 (10.1%) cases are severe at admission. Severe cases are elder [56(17) vs. 45(19), $P<0.001$], with more male (73.5% vs. 50.9%, $P=0.003$). They have a higher incidence of hypertension (53.1% vs. 16.7%, $P<0.001$), diabetes (14.3% vs. 5.0%, $P=0.009$), cardiovascular diseases (8.2% vs. 1.6%, $P=0.003$) and malignancy (4.1% vs. 0.7%, $P=0.025$), and less exposure to epidemic area (49.0% vs. 65.1%, $P=0.027$), but more infected family members($P=0.031$). On multivariate analysis, elder age, male and presence of hypertension are independently associated with severe disease at admission. A host risk score, incorporating age, sex and hypertension history, clearly stratifies risk of developing severe type of COVID-19 both in patients at admission and during in-hospital follow-up.

Conclusions: Elder age, male and presence of hypertension are associated with host susceptibility to developing severe COVID-19. The host risk score may be a useful tool to identify high risk individuals but requires validation.

Introduction

Coronaviruses are positive- sense RNA viruses that typically affect the respiratory tract, but also the gut of mammals and humans[1]. Coronavirus infections in humans generally result in mild symptoms[1], except two zoonotic coronavirus, severe acute respiratory syndrome coronavirus [SARS-CoV][2, 3] and Middle East respiratory syndrome coronavirus [MERS-CoV][4] that crossed species to infect human populations and cause a high mortality in the past two decades. On Dec, 2019, another zoonotic coronavirus, formally named SARS-CoV-2, has been identified in Wuhan, China, in individuals exposed to the Huanan (Southern China) Seafood Wholesale Market and has been demonstrated to be responsible for the recent outbreak of pneumonia originating from Wuhan[5]. This virus, of probable bat origin[6, 7], may be transmitted to humans via intermediate hosts, as SARS-CoV and MERS-CoV do[8], and spread rapidly among human populations by person-to-person transmission[9– 11] with an estimated reproductive number of more than 2[9, 12]. Up to Feb 11, 2020, it is reported that over 70,000 persons has been infected with SARS-CoV-2 in China[13]. Notably, some cases were clinical diagnosed without evidence of nucleic acid test.

Patients with coronavirus Disease 2019 (COVID-19) caused by SARS-CoV-2 infection represents a spectrum of clinical presentations[14– 17]. Some patients are asymptomatic, or only manifest as upper

respiratory tract or gastrointestinal symptoms without pulmonary involvement. However, like outbreaks caused by SARS-CoV and MERS-CoV, SARS-CoV-2 causes pneumonia that can be severe and characterized by fever, cough, dyspnea, bilateral pulmonary infiltrates and acute respiratory injury. It is estimated that approximately 20% of patients developing severe respiratory illness, with the overall mortality around 2.3%[13].

Given the substantial rate of severe cases, it is critical to identify individuals who confer intrinsic susceptibility to become severe or even critically ill upon infected, especially when there is no definite drug directly targeting at SARS-CoV-2 that has been proven to be clinically effective. These patients should be paid particular attention to prevent infection, or under close monitoring when infection is suspected. Also, this population may benefit most from early anti-viral treatment if an effective drug is established. Currently, there is scarce literature on this topic. In the study, we explored potential host risk factors associated with severe cases at admission in a retrospective cohort of 487 patients with community-acquired COVID-19 and attempt to establish a score system to identify high risk individuals.

Patients And Methods

Patients

487 cases with COVID-19, who were referred from January 16, 2020 to Feb 17, 2020 in the designated hospitals in Zhejiang Province, were retrospectively included in the study. All the patients were laboratory-confirmed by nuclei acid test of SARS-CoV-2. The study was conducted according to the principles of the Declaration of Helsinki. The ethics committee of First Affiliated Hospital of Zhejiang University reviewed and approved this study. Written consent was obtained from each patient or his/her authorized representatives following a full explanation of the study.

Diagnostic procedures

The sputum, nasopharyngeal or oropharyngeal swab specimen were collected from suspected patients in the designated hospitals and tested for SARS-CoV-2 by a real-time RT-PCR approach as previously defined[5] in hospital laboratories or local centres for disease control and prevention. Other common respiratory viruses including influenza virus, respiratory syncytial virus, parainfluenza virus and adenovirus were also tested for differential diagnosis. SARS-CoV and MERS-CoV were not detected because infection cases of the two virus had never been reported in Zhejiang Province. In addition, a pulmonary CT scan, as well as whole blood count and biochemical test, were generally performed as an initial evaluation, which would not be delayed awaiting for the result of nucleu acid test. Meanwhile, a pursue for epidemiological history, including recent exposure to epidemic area and suspected/confirmed patients, was also performed.

Data collection and follow-up

Two researchers independently reviewed medical records, laboratory findings, and pulmonary CT scan of each patient with COVID-19, provided by the local health authority. Demographic (age, sex, occupation and smoking history), epidemiological (recent exposure and family cluster) and clinical data (comorbidities, symptoms, laboratory and CT findings, and management) were inputted into a pre-specified, electronic data collection form. All data were checked by another two researcher (). Clinical outcomes were followed up to Feb 17, 2020. Occurrence of death and severe cases are primary endpoint events.

Definition

Severe COVID-19 is diagnosed when one of the following criteria was met: (1) respiratory rate >30 times/min; (2) transcutaneous oxygen saturation <93%; or (3) hypoxaemia defined as arterial oxygen tension (PaO₂) over inspiratory oxygen fraction (FIO₂) of less than 300 mm Hg. Acute respiratory distress syndrome (ARDS).

Statistical analysis

Continuous variables were represented as the mean \pm standard deviation (SD) or the median (interquartile range) and compared via the Mann-Whitney u test. Nominal variables were expressed as a number (percent) and compared by a Chi-square test. Host risk factors associated with severe COVID-19 were explored by a multivariate logistic regression using a backward-forward approach. The entry and removal probability for stepwise was set as 0.5 and 0.10 respectively. A host risk score was calculated by the sum of point of each risk factor that was dichotomized. An optimal cut-off point for dichotomizing continuous variables was determined by the Youden index that indicates a best performance of discriminating severe patients from those mild. A linear-by-linear association test was performed to evaluate the step-wise incidence changes of severe cases when patients were categorized based on the host risk score. Statistical differences were considered significant if a two-sided P-value was less than 0.05. All the Statistical analysis was performed with SPSS 20.0 (SPSS Inc; Chicago, IL, USA) and GraphPad Prism 5 (GraphPad Software Inc; San Diego, CA, USA).

Results

Comparisons of demographic and epidemiological data of severe and non-severe COVID-19 patients

A total of 487 COVID-19 patients were included for analysis, with 49 (10.1%) cases were severe at admission. As shown in Table 1, severe cases were elder [56(17) vs. 45(19), P<0.001] and of higher male proportion (73.5% vs. 50.9%, P=0.003). 36.7% of severe patients were agricultural workers, followed by self-employed (32.7%) and retired persons (24.5%), a different constitution from mild cases. No significant difference in smoking history was found between the two groups. As to comorbidities, severe cases have a higher incidence of hypertension (53.1% vs. 16.7%, P<0.001), diabetes (14.3% vs. 5.0%, P=0.009), cardiovascular diseases (8.2% vs. 1.6%, P=0.003) and malignancy (4.1% vs. 0.7%, P=0.025). Regarding to epidemiological history, severe patients had less exposure to epidemic area (49.0% vs.

65.1%, $P=0.027$) and likely confirmed cases (26.5% vs. 39.5%, $P=0.077$), but more high-dense family clusters ($P=0.031$).

Risk factors associated with severe COVID-19 at admission

Next, we explored among demographic and epidemiological factors to identify risk factors associated with severe COVID-19 presenting at admission to hospital, by a multivariate logistic regression. Given that the time from onset of symptoms to admission is a notable confounder, an analysis adjusting this variable was performed as well. As shown in Table.2, on multivariate analysis, host factors including elder age, male and presence of hypertension, were statistically significant risk factors of development of severe diseases, irrespective of adjustment of time to admission. An exposure history to patients, was found to be significant, if the model is unadjusted by time to admission.

The correlation between host risk score and incidence of severe COVID-19

Finally, as shown in Table.3, we defined a host risk score on the basis of the three risk factors, to assess the intrinsic host susceptibility to develop severe cases of COVID-19. Age was dichotomized by the cut-off point of 50 which is determined by Youden index of AuROC. As shown in Figure.1A, a step-wise increase in the incidence of severe COVID-19 at admission was observed with the increment of the host risk score ($P<0.001$). The performance of the score was also validated in 66 patients who presented mild at admission and were under follow-up during hospital stay. 15 patients progressed to severe COVID-19 within a median follow-up time of 15 days. No death was reported by the end of follow-up. A similar trend to the above was confirmed when analyzing the correlating between host risk score and occurrence of severe COVID-19 ($P=0.014$) (see Figure.1B).

Discussion

For the first time, we found that hypertension as a host risk factor, along with other two known factors elder age and male sex, are associated with severe COVID-19. And we constructed a host risk score to reflect the intrinsic susceptibility to develop severe type of this disease, which may provide guidance on tailor of preventive and therapeutic measures.

A major finding that hypertension as a host risk factor for severe COVID-19 may underscore the involvement of renin-angiotensin system (RAS) in the pathogenesis of this disease. The RAS is important in maintaining blood pressure homeostasis, as well as fluid and salt balance[18]. To activate the renin-angiotensin system, ACE cleaves angiotensin I to generate angiotensin II, which acts on Ang II type 1 and type 2 receptors (AT1R and AT2R) and results in a variety of biological effects including vasoconstriction, salt and water reabsorption, oxidative stress and inflammation, whereas ACE2 converts Ang I into Ang 1–9 and Ang II into Ang 1–7, which serves as a physiological mechanism counteracting RAS activation[18]. It has been speculated that, angiotensin-converting enzyme 2 (ACE2), previously known as the receptor

for SARS-Cov [19, 20] and NL63[21], is also the receptor for SARS-CoV-2 infection in human beings[22, 23]. And ACE2, as well as other components of RAS, have also been implicated in the development of severe acute lung injury. Mice studies have shown that ACE, angiotensin II and AT1a, induce lung edemas and thereby promote disease progression[24]. In contrast, ACE2 has been shown to prevent from severe acute lung injury[24]. It thereby implies that an unbalance between ACE and ACE2 expression in lung may predispose the host to severe acute lung injury. Given that such disturbance of RAS may be present in patients with hypertension, it may explain their increased susceptibility to develop severe type of COVID-19. Actually, it has been reported that ACE2 expression at both mRNA and protein level were significantly reduced in hypertensive rat strains[25]. ACE2 or other RAS components therefore may represent potential therapeutic targets in control of COVID-19 severity, although further investigations using human samples are apparently required.

To assess host susceptibility to disease severity is of important clinical relevance. First, individuals with high risk should be identified to take appropriate prevention measures and a priority of pre-exposure vaccination and/or post-exposure antiviral prophylaxis should be given to these persons if an effective vaccine or antiviral drug is developed. Second, individuals with high risk should be informed to seek for medical institutions if any suspected symptom. Third, close monitoring is required to detect early progression, for high risk population with confirmed COVID-19. Finally, as it has been shown that influenza patients of high risk for complication benefit from early antiviral treatment[26], it would be prudent to enroll sufficient COVID-19 patients at high risk of progression in clinical trials evaluating the efficacy of antiviral therapies, not only for the scientific purposes but also as a compassionate treatment[27]. In this regard, our study provides a useful tool to assess host risk to develop severe disease, although it needs be validated.

The present study suffers from several limitations. First, there is no information on the specific time point at which patients develop severe cases before admission and thereby a logistic regression analysis was performed. Nevertheless, it may be alternative to use the time to admission instead and the risk factors remained to be significant when adjusted by the time variable. In addition, considering that patients un-severe at admission may progress during hospitalization, the host risk score was also validated in 66 patients with in-hospital follow-up, albeit the size is not limited. Second, a markedly reduced mortality of Wuhan-outside patients compared to those in Wuhan[16] may indicate a viral evolution towards host adaptation. Therefore, whether the host risk score applies to Wuhan patients is not clear.

In summary, by identifying host risk factors associated with severe COVID-19, this study shed light on the underlying mechanisms of disease progression and provides a useful tool to identify high risk individuals, which is helpful for designing specific strategies for prevention and treatment of this disease. But further studies, particularly those enrolling Wuhan patients, are needed to validate the findings.

Conclusions

This study identifies elder age, male sex and presence of hypertension are associated with host susceptibility to developing severe COVID-19. A host risk score was also established, which is helpful to reflect the intrinsic susceptibility to develop severe type of this disease but requires further validation.

Declarations

Ethics approval and consent to participate

The ethics committee of First Affiliated Hospital of Zhejiang University reviewed and approved this study. Written consent was obtained from each patient or his/her authorized representatives following a full explanation of the study.

Consent for publication: Not applicable.

Availability of data and materials

The datasets and materials used and/or analysed during the current study are available from the corresponding author on reasonable request.

Competing interests

The authors declare that they have no competing interests.

Funding

This work was supported by grants from Chinese National Natural science foundation (No. 81670567 and 81870425) and the Fundamental Research Funds for the Central Universities.

Authors' contributions

J.S and Y.S conceptualized the idea and design the study. Y.S and X.Y draft the manuscript and J.S revised it. X.Y, H.Z, H.W, R.Z, Q.C, S.S, H.F, Y.W, Z.H, X.L, H.T and S.T participated in data collection, analysis and interpretation. All authors read and approved the final manuscript.

Acknowledgements: Not applicable.

References

1. Su S, Wong G, Shi W, Liu J, Lai ACK, Zhou J, Liu W, Bi Y, Gao GF: Epidemiology, Genetic Recombination, and Pathogenesis of Coronaviruses. *Trends Microbiol* 2016, 24(6):490-502.
2. Drosten C, Günther S, Preiser W, van der Werf S, Brodt H-R, Becker S, Rabenau H, Panning M, Kolesnikova L, Fouchier RAM et al: Identification of a novel coronavirus in patients with severe acute respiratory syndrome. *N Engl J Med* 2003, 348(20):1967-1976.
3. Ksiazek TG, Erdman D, Goldsmith CS, Zaki SR, Peret T, Emery S, Tong S, Urbani C, Comer JA, Lim W et al: A novel coronavirus associated with severe acute respiratory syndrome. *N Engl J Med* 2003, 348(20):1953-1966.
4. Zaki AM, van Boheemen S, Bestebroer TM, Osterhaus ADME, Fouchier RAM: Isolation of a novel coronavirus from a man with pneumonia in Saudi Arabia. *N Engl J Med* 2012, 367(19):1814-1820.
5. Zhu N, Zhang D, Wang W, Li X, Yang B, Song J, Zhao X, Huang B, Shi W, Lu R et al: A Novel Coronavirus from Patients with Pneumonia in China, 2019. *N Engl J Med* 2020, 382(8):727-733.
6. Zhou P, Yang X-L, Wang X-G, Hu B, Zhang L, Zhang W, Si H-R, Zhu Y, Li B, Huang C-L et al: A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 2020:10.1038/s41586-41020-42012-41587.
7. Lu R, Zhao X, Li J, Niu P, Yang B, Wu H, Wang W, Song H, Huang B, Zhu N et al: Genomic characterisation and epidemiology of 2019 novel coronavirus: implications for virus origins and receptor binding. *Lancet* 2020:S0140-6736(0120)30251-30258.
8. Ji JS: Origins of MERS-CoV, and lessons for 2019-nCoV. *Lancet Planet Health* 2020:S2542-5196(2520)30032-30032.
9. Li Q, Guan X, Wu P, Wang X, Zhou L, Tong Y, Ren R, Leung KSM, Lau EHY, Wong JY et al: Early Transmission Dynamics in Wuhan, China, of Novel Coronavirus-Infected Pneumonia. *N Engl J Med* 2020:10.1056/NEJMoa2001316.
10. Liu Y-C, Liao C-H, Chang C-F, Chou C-C, Lin Y-R: A Locally Transmitted Case of SARS-CoV-2 Infection in Taiwan. *N Engl J Med* 2020:10.1056/NEJMc2001573.
11. Phan LT, Nguyen TV, Luong QC, Nguyen TV, Nguyen HT, Le HQ, Nguyen TT, Cao TM, Pham QD: Importation and Human-to-Human Transmission of a Novel Coronavirus in Vietnam. *N Engl J Med* 2020:10.1056/NEJMc2001272.
12. Wu JT, Leung K, Leung GM: Nowcasting and forecasting the potential domestic and international spread of the 2019-nCoV outbreak originating in Wuhan, China: a modelling study. *Lancet* 2020:S0140-6736(0120)30260-30269.
13. Novel Coronavirus Pneumonia Emergency Response Epidemiology T: The epidemiological characteristics of an outbreak of 2019 novel coronavirus diseases (COVID-19) in China. *Zhonghua Liu Xing Bing Xue Za Zhi* 2020, 41(2):145-151.

14. Chen N, Zhou M, Dong X, Qu J, Gong F, Han Y, Qiu Y, Wang J, Liu Y, Wei Y et al: Epidemiological and clinical characteristics of 99 cases of 2019 novel coronavirus pneumonia in Wuhan, China: a descriptive study. *Lancet* 2020, 395(10223):507-513.
15. Huang C, Wang Y, Li X, Ren L, Zhao J, Hu Y, Zhang L, Fan G, Xu J, Gu X et al: Clinical features of patients infected with 2019 novel coronavirus in Wuhan, China. *Lancet* 2020, 395(10223):497-506.
16. Xu X-W, Wu X-X, Jiang X-G, Xu K-J, Ying L-J, Ma C-L, Li S-B, Wang H-Y, Zhang S, Gao H-N et al: Clinical findings in a group of patients infected with the 2019 novel coronavirus (SARS-Cov-2) outside of Wuhan, China: retrospective case series. *BMJ* 2020, 368:m606-m606.
17. Chen L, Liu HG, Liu W, Liu J, Liu K, Shang J, Deng Y, Wei S: Analysis of clinical features of 29 patients with 2019 novel coronavirus pneumonia. *Zhonghua Jie He He Hu Xi Za Zhi* 2020, 43(0):E005-E005.
18. Patel VB, Zhong J-C, Grant MB, Oudit GY: Role of the ACE2/Angiotensin 1-7 Axis of the Renin-Angiotensin System in Heart Failure. *Circ Res* 2016, 118(8):1313-1326.
19. Li W, Moore MJ, Vasilieva N, Sui J, Wong SK, Berne MA, Somasundaran M, Sullivan JL, Luzuriaga K, Greenough TC et al: Angiotensin-converting enzyme 2 is a functional receptor for the SARS coronavirus. *Nature* 2003, 426(6965):450-454.
20. Kuba K, Imai Y, Rao S, Gao H, Guo F, Guan B, Huan Y, Yang P, Zhang Y, Deng W et al: A crucial role of angiotensin converting enzyme 2 (ACE2) in SARS coronavirus-induced lung injury. *Nat Med* 2005, 11(8):875-879.
21. Hofmann H, Pyrc K, van der Hoek L, Geier M, Berkhout B, Pöhlmann S: Human coronavirus NL63 employs the severe acute respiratory syndrome coronavirus receptor for cellular entry. *Proc Natl Acad Sci U S A* 2005, 102(22):7988-7993.
22. Wrapp D, Wang N, Corbett KS, Goldsmith JA, Hsieh C-L, Abiona O, Graham BS, McLellan JS: Cryo-EM structure of the 2019-nCoV spike in the prefusion conformation. *Science* 2020:eabb2507.
23. Chen Y, Guo Y, Pan Y, Zhao ZJ: Structure analysis of the receptor binding of 2019-nCoV. *Biochem Biophys Res Commun* 2020:S0006-0291X(0020)30339-30339.
24. Imai Y, Kuba K, Rao S, Huan Y, Guo F, Guan B, Yang P, Sarao R, Wada T, Leong-Poi H et al: Angiotensin-converting enzyme 2 protects from severe acute lung failure. *Nature* 2005, 436(7047):112-116.
25. Crackower MA, Sarao R, Oudit GY, Yagil C, Kozieradzki I, Scanga SE, Oliveira-dos-Santos AJ, da Costa J, Zhang L, Pei Y et al: Angiotensin-converting enzyme 2 is an essential regulator of heart function. *Nature* 2002, 417(6891):822-828.
26. Jain S, Kamimoto L, Bramley AM, Schmitz AM, Benoit SR, Louie J, Sugerman DE, Druckenmiller JK, Ritger KA, Chugh R et al: Hospitalized patients with 2009 H1N1 influenza in the United States, April-June 2009. *N Engl J Med* 2009, 361(20):1935-1944.
27. Holshue ML, DeBolt C, Lindquist S, Lofy KH, Wiesman J, Bruce H, Spitters C, Ericson K, Wilkerson S, Tural A et al: First Case of 2019 Novel Coronavirus in the United States. *N Engl J Med* 2020:10.1056/NEJMoa2001191.

Tables

Table.1 Demographic, epidermological characteristics and underlying comorbidities of patients with confirmed 2019-ncov infection

Variables	Total (N=487)	Mild (N=438)	Severe (N=49)	P value
Age (years)	46(19)	45(19)	56(17)	<0.001
Sex				
Male	259(53.2%)	223(50.9%)	36(73.5%)	0.003
Female	228(46.8%)	215(49.1%)	13(26.5%)	
Occupation				
Agricultural worker	140(28.7%)	122(27.9%)	18(36.7%)	<0.001
Self-employed	219(45.0%)	203(46.3%)	16(32.7%)	
Employee	82(16.8%)	79(18.0%)	3(6.1%)	
Retired	38(7.8%)	26(5.9%)	12(24.5%)	
Students	8(1.6%)	8(1.8%)	0(0%)	
Smoking history				
Yes	40(8.2%)	34(7.8%)	6(12.2%)	0.331
No	434(89.1%)	391(89.3%)	43(87.8%)	
Unknown	13(2.7%)	13(2.7%)	0(0%)	
Comorbidities				
Hypertension	99(20.3%)	73(16.7%)	26(53.1%)	<0.001
Diabetes	29(6.0%)	22(5.0%)	7(14.3%)	0.009
Cardiovascular disease	11(2.3%)	7(1.6%)	4(8.2%)	0.003
Malignancy	5(1%)	3(0.7%)	2(4.1%)	0.025
Chronic liver diseases	22(4.5%)	20(4.6%)	2(4.1%)	0.877
Chronic renal diseases	7(1.4%)	5(1.1%)	2(4.1%)	0.101
Others	32(6.6%)	27(6.1%)	5(10.2%)	0.279
Exposure to confirmed cases	186(38.2%)	173(39.5%)	13(26.5%)	0.077
Family cluster				
0	392(80.5%)	352(80.4%)	40(81.6%)	0.031
1	67(13.8%)	63(14.4%)	4(8.2%)	
2	12(2.5%)	12(2.7%)	0(0%)	
>=3	16(3.3%)	11(2.5%)	5(10.2%)	
Recent travel or residence to/in epidemic area	309(63.4%)	285(65.1%)	24(49.0%)	
Time from onset of symptom to admission	2(3)	2(3)	3(5)	0.10

Data are expressed as mean \pm standard deviation (SD), median (interquartile range) or number (percent). Comparisons between mild and severe cases were performed by the Mann-Whitney u test or a Chi-square test.

Table.2 Factors associated with severe COVID-19 at admission

Variables	Unadjusted by time to admission			Adjusted by time to admission		
	OR	95%CI	P value	OR	95%CI	P value
Age	1.06	1.03-1.08	<0.001	1.06	1.03-1.09	<0.001
Male	3.68	1.75-7.75	0.001	3.60	1.69-7.63	0.001
Presence of hypertension	2.71	1.32-5.59	0.007	2.73	1.32-5.65	0.007
Prior exposure to confirmed patients	0.39	0.16-0.89	0.026	---	---	---

Statistical analysis was performed using a step-wise multivariable logistic regression model. Either adjusted by time to admission or not, variables entering multivariate analysis were age, sex, occupation, smoking history, any comorbidity, exposure history, family cluster and epidemic area travel or residence history. Only variables remaining in the final step with statistical significance ($P<0.05$) were represented.

Table.3 Definition of host risk factor score

Variables	Scores
Age	
≥50 (years)	1
<50 (years)	0
Sex	
Male	1
Female	0
Hypertension	
Presence	1
Absence	0

Figures

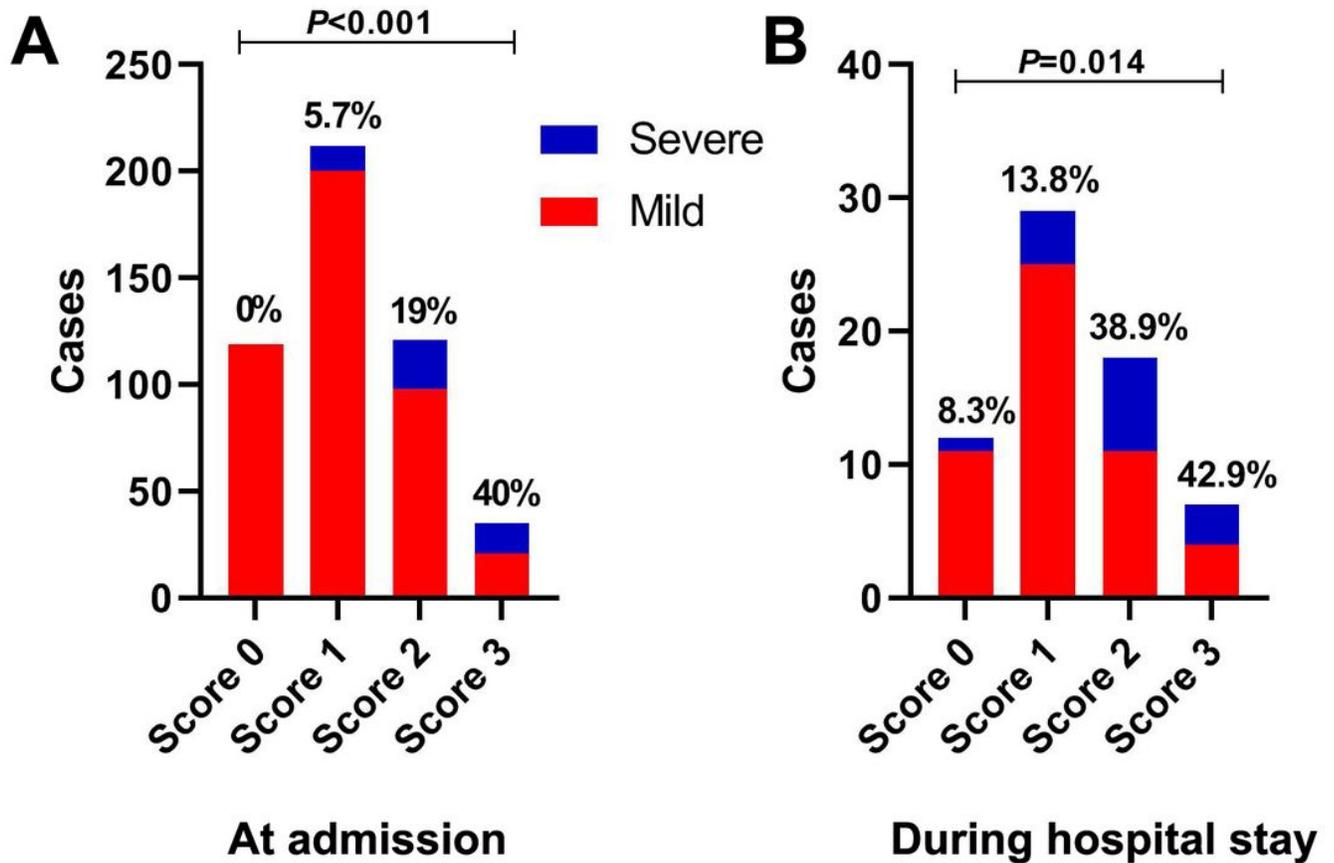


Figure 1

Incidences of severe cases by host risk score. The incidences of severe cases at admission (A) or developing during hospitalization (B) was compared across the different score groups by a linear-by-

linear association test.