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Epidemiological and Clinical Predictors of COVID-19

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Background. Rapid identification of COVID-19 cases, which is crucial to outbreak containment efforts, is challenging due to the lack of pathognomonic symptoms and in settings with limited capacity for specialized nucleic acid–based reverse transcription polymerase chain reaction (PCR) testing.

Methods. This retrospective case-control study involves subjects (7–98 years) presenting at the designated national outbreak screening center and tertiary care hospital in Singapore for SARS-CoV-2 testing from 26 January to 16 February 2020. COVID-19 status was confirmed by PCR testing of sputum, nasopharyngeal swabs, or throat swabs. Demographic, clinical, laboratory, and exposure-risk variables ascertainable at presentation were analyzed to develop an algorithm for estimating the risk of COVID-19. Model development used Akaike's information criterion in a stepwise fashion to build logistic regression models, which were then translated into prediction scores. Performance was measured using receiver operating characteristic curves, adjusting for overconfidence using leave-one-out cross-validation.

Results. The study population included 788 subjects, of whom 54 (6.9%) were SARS-CoV-2 positive and 734 (93.1%) were SARS-CoV-2 negative. The median age was 34 years, and 407 (51.7%) were female. Using leave-one-out cross-validation, all the models incorporating clinical tests (models 1, 2, and 3) performed well with areas under the receiver operating characteristic curve (AUCs) of 0.91, 0.88, and 0.88, respectively. In comparison, model 4 had an AUC of 0.65.

Conclusions. Rapidly ascertainable clinical and laboratory data could identify individuals at high risk of COVID-19 and enable prioritization of PCR testing and containment efforts. Basic laboratory test results were crucial to prediction models.

Keywords. COVID-19; SARS-CoV-2; risk factors, prediction model.

On 31 December 2019, a cluster of atypical pneumonia cases was reported in Wuhan City, China [1]. The etiologic agent was subsequently identified as a novel coronavirus [2], severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) [3]. The disease, named coronavirus disease 2019 (COVID-19) [4], can progress to acute respiratory distress in severe cases [5]. The basic reproduction number of SARS-CoV-2 has been estimated to be 2.2 [6], and human-to-human transmission has since occurred to other parts of China and beyond, affecting 87 137 cases in 59 countries worldwide as of 1 March 2020 [6–10].

The clinical spectrum of COVID-19 is broad and the majority of infected individuals experience only a mild or subclinical illness, especially in the early phase of illness [11, 12]. Approximately 16% to 26% of hospitalized patients diagnosed with COVID-19 develop severe acute respiratory distress requiring oxygen supplementation and/or intensive care. Disease severity and mortality are associated with older age and underlying comorbidities such as diabetes, hypertension, and cardiovascular disease.

In the absence of a vaccine or effective prophylaxis, the containment of SARS-CoV-2 is contingent on interrupting transmission through rapid identification and isolation of all infected individuals. Symptomatic contacts must be isolated early, while close contacts of cases who may be incubating infection need to be quarantined and monitored [13]. Currently, case identification relies on specialized nucleic acid–based reverse transcription polymerase chain reaction (PCR) testing, which is not readily available in resource-limited settings [14, 15]. Even in well-resourced settings the broad range of clinical presentation presents a challenge in deciding whom to test and could strain laboratory testing resources if criteria for testing are overly expansive.

To allow for assessment of the probability of milder cases having COVID-19, we conducted risk factor analysis on a case-control cohort of 54 COVID-19 cases and 734 controls to determine the epidemiological and clinical risk factors that correlate with COVID-19, and to determine the accuracy of risk-scoring systems based on readily available clinical information.

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METHODS

Study Design and Setting

This retrospective case-control study was conducted in Singapore at the National Centre for Infectious Diseases (NCID), a 330-bed infectious diseases treatment facility with the onsite National Public Health Laboratory, which develops certified testing protocols for emerging infectious diseases for the country [16]. This work was completed as part of outbreak operational evaluation and did not require institutional research board review. This study followed the Transparent Reporting of a Multivariable Prediction Model for Individual Prognosis or Diagnosis reporting guideline [17].

Study Population

Patients presenting to the NCID for SARS-CoV-2 testing between 26 January and 16 February 2020 were analyzed. Patients were either self-referred, referred from primary care facilities, or were at-risk cases identified by national contact tracing efforts (Supplementary Table 1). Cases were defined as individuals who had a positive SARS-CoV-2 PCR test and controls were defined as individuals for whom all SARS-CoV-2 PCR results were negative (Figure 1 and Supplementary Table 2).

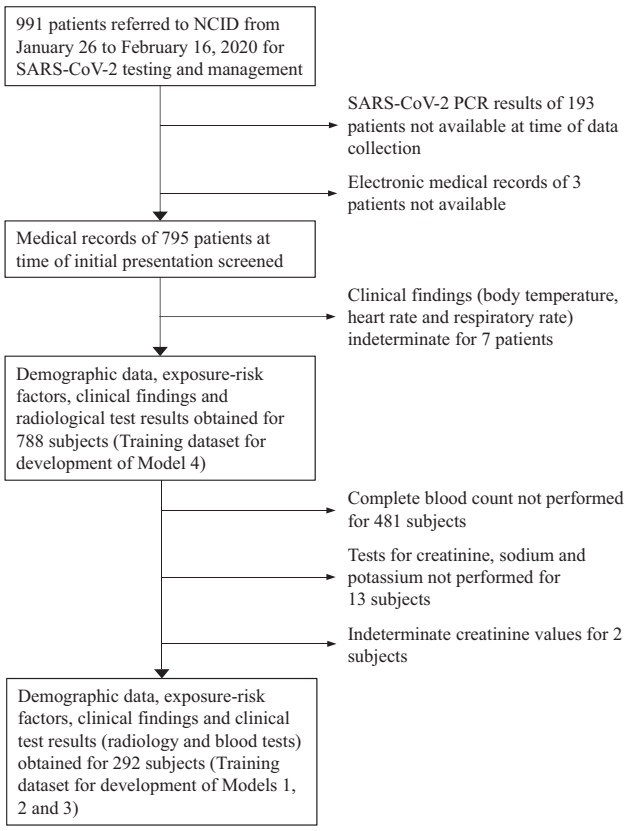

Figure 1. Study subject disposition. Abbreviations: NCID, National Centre for Infectious Diseases, Singapore; PCR, polymerase chain reaction; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

Data Collection

We collected the following data recorded at initial presentation for testing from the electronic medical records: demographic characteristics, medical comorbidities, exposure risk factors (including contact with a known COVID-19 case, contact with travellers from China, recent travel history, and visit to a hospital in China within 14 days prior to symptom onset), symptom days prior to presentation, vital signs at first clinical encounter (respiratory rate, blood pressure, temperature, and pulse rate), respiratory symptoms, gastrointestinal symptoms, physical examination finding of pneumonia, radiologic evidence of pneumonia, and blood investigation results (complete blood count, creatinine, sodium, and potassium).

Investigation for SARS-CoV-2

We collected respiratory specimens in the following order of preference: sputum or endotracheal aspirate, nasopharyngeal swab, and throat swab. For subjects with more than 1 specimen, the first and last specimens were collected at least 24 hours apart. High-risk patients were tested at least twice while low-risk patients were tested at least once according to a predefined algorithm [18]. SARS-CoV-2 tests were performed using one of the methods described in the Supplementary Methods.

Statistical Analyses

Study variables from the 4 abovementioned categories were analyzed for differences between SARS-CoV-2–positive and –negative subjects using Mann-Whitney-Wilcoxon test or Yates' corrected chi-square test. All tests were 2-tailed, and $P < .05$ was considered to be statistically significant.

Development of Risk-Scoring Models

A preliminary filtering of variables was conducted by removing those without sufficient variability (<5 positive readings or scores) or with too many missing values (>80% missing). We also assessed variables for collinearity using variance inflation factor and correlation. We defined a lack of multicollinearity between predictors as a variance inflation factor of less than 2.5 or a correlation coefficient of less than 0.6. When 2 variables were found to be colinear, we selected variables for inclusion based on magnitude of effect and clinical relevance.

Predictors of SARS-CoV-2–positive status were classified into 4 categories: exposure risk factors, demographic variables, clinical findings, and clinical test results. Two datasets were created: one comprising 788 subjects with complete reporting for demographic variables, exposure risk factors, clinical findings, and radiological tests (excluding other clinical tests such as blood tests); the other comprising a subset of 292 subjects with complete reporting for demographic variables, exposure risk factors, clinical findings, and all clinical tests (Figure 1).

Four prediction models were developed based on these 2 overlapping datasets: model 1 included covariates from all

4 categories; model 2 included demographic variables, clinical findings, and clinical test results; model 3 included demographic variables, clinical findings, and clinical test results (excluding radiology); and model 4 included only demographic variables and clinical findings. Model 4 was built using all 788 subjects (54 cases and 734 controls). Of these 788 subjects, a complete blood count was not performed for 481; testing for creatinine, sodium, and potassium was not performed for 13; and 2 subjects had incomplete creatinine, sodium, and potassium test results. The dataset for models 1, 2, and 3, which included laboratory blood tests, comprised a subset of 292 subjects (49 cases and 243 controls) (Figure 1).

The variables for our final models were selected through stepwise use of Akaike's information criterion to build multivariate logistic regression models, which were then translated into prediction scores.

Evaluation of Risk-Scoring Models

The predictive performance of our final models in determining whether a patient is positive for SARS-CoV-2 was assessed using receiver operating characteristic (ROC) curves and the corresponding area under the ROC (AUC) values with confidence intervals (CIs) for the specificity at a given sensitivity derived using bootstrapping. We performed leave-out-one cross-validation to obtain corrected estimates of sensitivity, specificity, and AUCs of the risk-scoring models. Specifically, each individual was withheld in turn, the model refit to the remaining individuals, and then used to estimate the withheld patient's risk of COVID-19. This provides a good estimate of the out-of-sample performance of each model. An AUC of 1.00 corresponds to perfect discrimination, whereas an AUC of 0.50 corresponds to no discriminating ability.

RESULTS

A total of 991 patients were referred to the NCID for SARS-CoV-2 testing between 26 January and 16 February 2020. We excluded 193 patients whose SARS-CoV-2 results were not yet available, 3 patients whose electronic medical records were not yet available, and 7 patients with unavailable vital sign records. Of the 788 patients included in the analysis, 54 were COVID-19 cases and 734 were controls (Figure 1). The median age was 34 years (range, 7–98 years; interquartile range [IQR], 27–45 years). The majority were female (407, 51.7%) and Singapore citizens (414, 52.5%). Of the 54 cases, the median age was 42 years (range, 16–79 years; IQR, 34–54 years), 29 (53.7%) were male and 48 (88.9%) were ethnic Chinese. Singapore citizens and Chinese nationals comprised 34 (63%) and 13 (24.1%) cases, respectively. In the control group, the median age was 34 years (range, 7–98 years; IQR, 27–43 years), 351 (47.9%) were male, and 553 (75.3%) were ethnic Chinese. Singapore citizens and Chinese nationals comprised 379 (51.7%) and 132 (18.0%) cases, respectively (Table 1).

Positive cases were more likely to be older compared with controls ($P < .001$). Positive cases were not more likely to have any of the comorbidities documented than controls. In terms of exposure risk factors, positive cases were more likely to have contact with a known COVID-19 case (32 out of 54 cases [59.3%]; 126 out of 734 controls [17.2%]) or have recently travelled to Wuhan, China (15 out of 54 cases [27.8%]; 42 out of 734 controls [5.7%]). Positive cases were more likely to have an elevated body temperature ($P = .003$) at clinical presentation. Of clinical test results, positive cases were more likely to have radiological findings suggestive of pneumonia (23 out of 54 cases [42.6%]; 81 out of 734 controls [11.1%]) as well as lower blood counts of white blood cells, platelets, neutrophils, lymphocytes, eosinophils, and basophils (all $P < .001$) (Table 1).

Significant Predictors of a SARS-CoV-2–Positive Test

The final covariate risk estimates of each of the 4 multivariable models are detailed in Table 2. In model 1, exposure risk factors most predictive for COVID-19 were travel to Wuhan Province in China since 1 December 2019, around the time of the first outbreak in Wuhan [6] (model 1: adjusted odds ratio [AOR], 23.05; 95% CI, 3.29–268.08) and contact with a confirmed COVID-19 case in Singapore (model 1: AOR, 6.04; 95% CI, 1.54–27.61).

The other 3 models exclude exposure risk factors. Clinically, elevated body temperature (model 1: AOR, 4.81; 95% CI, 1.97–13.12; model 2: AOR, 2.55; 95% CI, 1.32–5.21; model 3: AOR, 2.43; 95% CI, 1.25–5.02; model 4: AOR, 2.27; 95% CI, 1.5–3.44) was the strongest predictor across all 4 models, except for model 2 where gastrointestinal symptoms fared slightly better (model 2: AOR, 2.69; 95% CI, 1.08–6.89). Gastrointestinal symptoms were also selected in model 1 and model 3 (model 1: AOR, 3.73; 95% CI, 1.23–12.45; model 3: AOR, 2.31; 95% CI, .92–5.93). Elevated respiratory rate (model 1: AOR, 1.21; 95% CI, .93–1.5; model 2: AOR, 1.29; 95% CI, 1.07–1.59; model 3: AOR, 1.3; 95% CI, 1.07–1.6) and absence of symptoms such as sore throat (model 1: AOR, .35; 95% CI, .1–1.06; model 3: AOR, .53; 95% CI, .22–1.25; model 4: AOR, .63; 95% CI, .34–1.14) and sputum production (model 1: AOR, .23; 95% CI, .06–.78; model 2: AOR, .29; 95% CI, .1–.72; model 3: AOR, .3; 95% CI, .11–.79) were strong predictors in the models in which they were selected.

In terms of clinical test results, radiologic evidence of pneumonia (model 1: AOR, 6.18; 95% CI, 1.68–25.75) was the overall strongest predictor in model 1 and also contributed significantly to model 2 (model 1: AOR, 2.86; 95% CI, 1.09–7.69). Radiology results were excluded in models 3 and 4. Interestingly, blood parameters were found to contribute significantly to the predictive value of all the models in which they were selected (models 1, 2, and 3). The white blood count subsets most closely correlated with risk were lower neutrophil (model 1: AOR, .32 per 1×10^9/L; 95% CI, .19–.49; model 2: AOR, .39 per 1×10^9/L; 95% CI, .26–.54; model 3: AOR, .38 per 1×10^9/L; 95% CI, .25–.53) and eosinophil (model 1: AOR, .85 per 1×10^9/L; 95%

Table 1. Baseline Characteristics of SARS-CoV-2–Positive and SARS-CoV-2–Negative Subjects

Characteristics	All (N = 788)	Cases (n = 54)	Controls (n = 734)	P[a]
Demographics				
Age, median, years	34	42	34	<.001
Gender				
Male	380 (48.7)	29 (53.7)	351 (47.9)	.488
Female	407 (51.7)	25 (46.3)	382 (52.1)	
Ethnicity				
Chinese	601 (76.3)	48 (88.9)	553 (75.3)	.045
Malay	59 (7.5)	1 (1.9)	58 (7.9)	
Indian	69 (8.8)	5 (9.3)	64 (8.7)	
Others	59 (7.5)	0	59 (8.0)	
Nationality				
Singaporean	414 (52.5)	34 (63.0)	380 (51.8)	.027
Chinese	145 (18.4)	13 (24.1)	132 (18.0)	
Malaysian	79 (10.0)	0	79 (10.8)	
Others	150 (19.1)	7 (13)	143 (19.5)	
Comorbidities				
Any	75 (9.5)	5 (9.3)	70 (9.5)	1.000
Obstructive pulmonary disease	10 (1.3)	0	10 (1.4)	.815
Congestive heart failure	1 (0.1)	0	1 (0.1)	1.000
Connective tissue disease	4 (0.5)	0	4 (0.5)	1.000
Cerebrovascular disease	7 (0.9)	0	7 (1.0)	1.000
Dementia	4 (0.5)	0	4 (0.5)	1.000
Myocardial infarction	9 (1.1)	0	9 (1.2)	.877
Leukemia	1 (0.1)	0	1 (0.1)	1.000
Solid tumor	14 (1.8)	0	14 (1.9)	.624
Chronic kidney disease	8 (1.0)	0	8 (1.1)	.946
Diabetes mellitus	54 (6.9)	5 (9.3)	49 (6.7)	.655
Chronic liver disease	3 (0.4)	0	3 (0.4)	1.000
Exposure risk factors				
Healthcare worker	79 (10.0)	0	79 (10.8)	.021
Contact with				
A known COVID-19 case	158 (20.1)	32 (59.3)	126 (17.2)	<.001
A traveller from China (from 1 December 2019)	174 (22.1)	11 (20.4)	163 (22.2)	.885
A group of travellers from China (from 1 December 2019)	84 (10.7)	7 (13)	77 (10.5)	.734
History of travel (from 1 December 2019) to				
Wuhan, China	57 (7.2)	15 (27.8)	42 (5.7)	<.001
China (including Wuhan)	236 (30.0)	17 (31.5)	219 (29.8)	.920
Other countries (other than China)	216 (27.4)	18 (33.3)	198 (27)	.394
Visited any hospital in China recently (14 days since onset of symptoms)	6 (0.8)	0	6 (0.8)	1.000
Clinical signs and symptoms				
Number of subjects with >5 days of symptoms (n = 758)[b]	252 (33.2)	20 (38.5)	232 (32.9)	.38
Body temperature, median, °C	37.1	37.5	37.1	.003
Heart rate, median, beats per minute	89	87	89	.379
Respiration rate, median, breaths per minute	18	18	18	.159
Systolic blood pressure, median, mmHg	131	131	131	.502
Diastolic blood pressure, median, mmHg	78	78	78	.596
Cough	564 (71.5)	36 (66.7)	528 (71.9)	.502
Sputum production	212 (26.9)	13 (24.1)	199 (27.1)	.744
Shortness of breath	100 (12.7)	7 (13)	93 (12.7)	1.000
Rhinnorhea or nasal congestion	238 (30.2)	12 (22.2)	226 (30.8)	.242
Sore throat	350 (44.4)	18 (33.3)	332 (45.2)	.120
Auscultation finding of pneumonia (eg, crackles)	42 (5.3)	6 (11.1)	36 (4.9)	.100
Respiratory symptoms (other than those listed above)	45 (5.7)	2 (3.7)	43 (5.9)	.723
Gastrointestinal symptoms	258 (32.8)	20 (37)	238 (32.4)	.585
Clinical tests				
CXR/CT suggestive of pneumonia (n = 788)	104 (13.2)	23 (42.6)	81 (11.1)	<.001

Table 1. Continued

Characteristics	All (N = 788)	Cases (n = 54)	Controls (n = 734)	P[a]
Complete blood count (n = 307)[c]				
White blood cells, median, $\times 10^9$/L	7.1	4.7	7.8	<.001
Hemoglobin, median, g/dL	13.5	13.9	13.4	.102
Platelets, median, $\times 10^9$/L	242	205	249	<.001
Neutrophils, median, $\times 10^9$/L	4.4	2.5	4.9	<.001
Lymphocytes, median, $\times 10^9$/L	1.6	1.2	1.7	<.001
Eosinophils, median, $\times 10^9$/L	0.09	0.02	0.10	<.001
Basophils, median, $\times 10^9$/L	0.03	0.02	0.04	<.001
Renal panel (n = 294)[d]				
Creatine, median, μmol/L	63	64	62	.977
Sodium, median, mmol/L	141	141	141	.600
Potassium, median, mmol/L	3.6	3.5	3.6	.156

Data are presented as n (%) unless otherwise indicated.

Abbreviations: COVID-19, coronavirus disease 2019; CT, chest computed tomography scan; CXR, chest X-ray; SARS-CoV-2, severe acute respiratory syndrome coronavirus 2.

[a]The Yates' corrected χ^2 test and Mann-Whitney-Wilcoxon test were used to calculate *P* values for categorical and continuous variables, respectively.

[b]There were a total of 758 subjects who were symptomatic on presentation (52 cases and 706 controls); 30 subjects were asymptomatic on presentation (2 cases and 28 controls).

[c]Complete blood count was performed for 307 subjects (out of 788), of whom 52 were cases (out of 54) and 255 were controls (out of 734).

[d]Renal panel results were obtained for 294 subjects (out of 788), of whom were 51 were cases (out of 54) and 243 were controls (out of 734).

CI, .78–.91); model 2: AOR, .89 per 1×10^9/L; 95% CI, .83–.94; model 3: AOR, .9 per 1×10^9/L; 95% CI, .84–.96) counts.

Model Performance of the Prediction Models

Models 1, 2, 3, and 4 differentiated between patients who did and did not have COVID-19 with optimism bias-corrected performance AUCs of 0.91 (95% CI, .86–.96), 0.88 (95% CI, .83–.93), 0.88 (95% CI, .83–.93), and 0.65 (95% CI, .57–.73), respectively (Figure 2). All models incorporating clinical test results had comparable AUCs (≥0.88). Additionally, comparing model 2 with model 3, the exclusion of chest radiology did not result in an appreciable decrease in AUC.

DISCUSSION

Although the epidemiological and clinical characteristics of patients with COVID-19 are well described [19, 20], it is challenging for healthcare workers in the primary care or

Table 2. Final Covariates in the 4 Multivariate Models for COVID-19 Infection

	Model 1		Model 2		Model 3		Model 4	
Variable	AOR (95% CI)	*P*	AOR (95% CI)	*P*	AOR (95% CI)	*P*	AOR (95% CI)	*P*
Age	…		…				1.03 (1.02–1.05)	<.001
Male sex	5.98 (1.23–36.05)	.038	3.67 (1.03–14.12)	.051	3.51 (.97–13.89)	.063	…	
Contact with a COVID-19 case	6.04 (1.54–27.61)	.013	…		…		…	
Travel to Wuhan since 1 December 2019	23.05 (3.29–268.08)	.004	…		…		…	
Travel to China (including Wuhan) since 1 December 2019	0.02 (0–.19)	.002	…		…		…	
Temperature	4.81 (1.97–13.12)	.001	2.55 (1.32–5.21)	.007	2.43 (1.25–5.02)	.011	2.27 (1.5–3.44)	<.001
Heart rate	0.95 (.91–1)	.044	0.95 (.92–.99)	.01	0.96 (.92–.99)	.029	0.97 (.95–.99)	.01
Respiration rate	1.21 (.93–1.5)	.079	1.29 (1.07–1.59)	.005	1.3 (1.07–1.6)	.004	…	
Systolic blood pressure	…		…		…		0.97 (.95–.99)	.016
Diastolic blood pressure	1.04 (.99–1.1)	.103	1.04 (1–1.09)	.061	1.05 (1–1.1)	.044	1.03 (1–1.06)	.102
Sore throat	0.35 (.1–1.06)	.073	…		0.53 (.22–1.25)	.149	0.63 (.34–1.14)	.132
Sputum production	0.23 (.06–.78)	.024	0.29 (.1–.72)	.011	0.3 (.11–.79)	.019	…	
Shortness of breath	…		…		2.76 (.67–10.7)	.145	…	
Gastrointestinal symptoms	3.73 (1.23–12.45)	.024	2.69 (1.08–6.89)	.035	2.31 (.92–5.93)	.076	…	
CXR/CT suggestive of pneumonia	6.18 (1.68–25.75)	.008	2.86 (1.09–7.69)	.033	…		…	
Lymphocytes (per 1×10^9/L)	…		…		0.56 (.25–1.12)	.117	…	
Neutrophils (per 1×10^9/L)	0.32 (.19–.49)	<.001	0.39 (.26–.54)	<.001	0.38 (.25–.53)	<.001	…	
Eosinophils (per 1×10^9/L)	0.85 (.78–.91)	<.001	0.89 (.83–.94)	<.001	0.9 (.84–.96)	.002	…	
Creatinine (per μmol/L)	0.96 (.9–1)	.111	0.96 (.91–1)	.062	0.96 (.92–1)	.079	…	
Sodium (per mmol/L)	1.17 (.96–1.43)	.133	…		…		…	

Abbreviations: AOR, adjusted odds ratio; CI, confidence interval; COVID-19, coronavirus disease 2019; CT, chest computed tomography scan; CXR, chest X-ray.

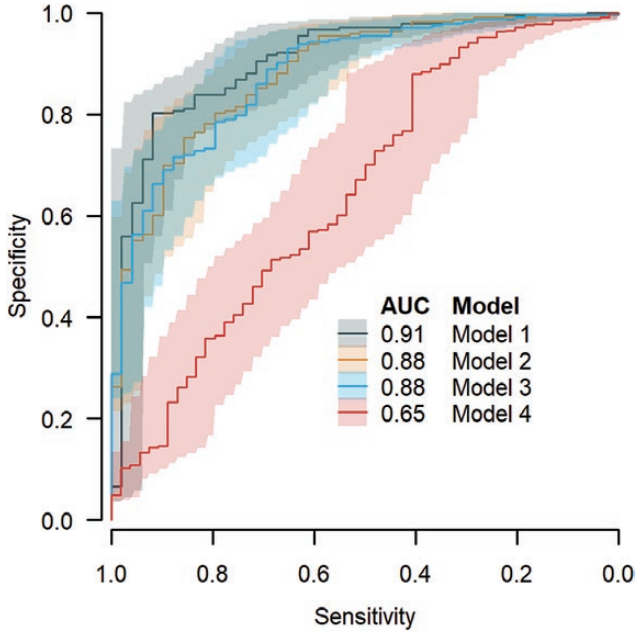

Figure 2. Performance of models 1, 2, 3, and 4 measured using receiver operating characteristic curves, adjusting for overconfidence using leave-one-out cross-validation. Abbreviation: AUC, area under the receiver operating characteristic curve.

emergency room setting to determine individuals who are more likely to have COVID-19 for isolation and testing. Model 1, incorporating all easily ascertainable data at presentation for SARS-CoV-2 testing, performed exceptionally well with an AUC of 0.91. Additionally, the performance of model 2 suggests that, even in the absence of exposure risk factors, clinical findings and tests can identify subjects at high risk of COVID-19. Furthermore, exclusion of radiologic evidence of pneumonia (model 3) did not significantly impact model performance. However, when basic blood test results such as complete blood count were excluded (model 4), predictive accuracy was reduced substantially.

The contact risk factors and clinical findings associated with a positive SARS-CoV-2 test are consistent with the known epidemiology and clinical features of COVID-19. Clinical findings strongly associated with a positive SARS-CoV-2 in our sample were higher temperature, higher respiratory rate, gastrointestinal symptoms, and decreased sputum production. Our results corroborate with a recent analysis [11] incorporating 1099 cases throughout China that found fever (87.9%) and nonproductive cough (67.7%) to be the dominant symptoms. Diarrhea (3.7%), although also reported, was less common. In another study involving 138 SARS-CoV-2–positive inpatients from a hospital in Wuhan, a large proportion of patients presented with fever (98.6%) and dry cough (59.4%). Diarrhea (10.1%) was also reported [12].

Our findings suggest a strong association of reduced white blood cell count with diagnosis of COVID-19. In the above study of 1099 cases, leukopenia was observed in 33.7% of patients on admission and was more prominent in severe cases [11].

The rapid global dissemination of COVID-19, which has significant morbidity with no proven treatment or vaccine, presents a major concern for resource-limited settings with minimal or no access to PCR testing. For well-resourced settings, COVID-19 presents a challenge for healthcare resources to cope with the large numbers of at-risk individuals in need of precautionary (often inpatient) isolation and rapid testing. A risk-scoring system would help prioritize high-risk individuals in primary care and emergency room settings for clinical care, isolation precautions, and contact-tracing efforts.

Most risk-scoring systems for infectious pathogens include exposure risk variables, which are sensitive to the local epidemiologic context and phase of the global outbreak. Our current pilot analysis suggests that it is feasible to derive risk-scoring systems for COVID-19 diagnosis, which are reliant mainly on clinical findings and simple test results and hence robust to changes in transmission risk factors.

The current proposed model is based on a limited dataset and additional validation in larger datasets and across different contexts would increase confidence in its performance and implementation. A trade-off between sensitivity and specificity will also need to be considered—a higher sensitivity will result in larger numbers of individuals needing to be isolated and tested, while a higher specificity will exclude some COVID-19 cases.

Conclusions

Prediction models that include rapidly ascertainable clinical findings and clinical tests, especially basic blood tests, have sufficient predictive value to identify individuals with a higher probability for COVID-19 and should be considered to stratify at-risk populations for laboratory testing (where available), isolation, and contact-tracing measures.

Supplementary Data

Supplementary materials are available at *Clinical Infectious Diseases* online. Consisting of data provided by the authors to benefit the reader, the posted materials are not copyedited and are the sole responsibility of the authors, so questions or comments should be addressed to the corresponding author.

Notes

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