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ORIGINAL RESEARCH

Clinical Features and a Prediction Model for Early Prediction of Composite Outcome in *Chlamydia psittaci* Pneumonia: A Multi-Centre Retrospective Study in China

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Introduction: C. psittaci pneumonia has atypical clinical manifestations and is often ignored by clinicians. This study analyzed the clinical characteristics, explored the risk factors for composite outcome and established a prediction model for early prediction of composite outcome among C. psittaci pneumonia patients.

Methods: A multicenter, retrospective, observational cohort study was conducted in ten Chinese tertiary hospitals. Patients diagnosed with C. psittaci pneumonia were included, and their clinical data were collected and analyzed. The composite outcome of C. psittaci pneumonia included death during hospitalization, ICU admission, and mechanical ventilation. Univariate and multivariable logistic regression analyses were conducted to determine the significant variables. A ten-fold cross-validation was performed to internally validate the model. The model performance was evaluated using various methods, including receiver operating characteristics (ROC), C-index, sensitivity, specificity, positive/negative predictive value (PPV/NPV), decision curve analysis (DCA), and clinical impact curve analysis (CICA).

Results: In total, 83 patients comprised training cohorts and 36 patients comprised validation cohorts. CURB-65 was used to establish predictive Model 1. Multivariate logistic regression analysis identified three independent prognostic factors, including serum albumin,

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CURB-65, and white blood cells. These factors were employed to construct model 2. Model 2 had acceptable discrimination (AUC of 0.898 and 0.825 for the training and validation sets, respectively) and robust internal validity. The specificity, sensitivity, NPV, and PPV for predicting composite outcome in the nomogram model were 91.7%, 84.5%, 50.0%, and 98.4% in the training sets, and 100.0%, 64.7%, 14.2%, and 100.0% in the validation sets. DCA and CICA showed that the nomogram model was clinically practical.
Conclusion: This study constructs a refined nomogram model for predicting the composite outcome in C. psittaci pneumonia patients. This nomogram model enables early and accurate C. psittaci pneumonia patients' evaluation, which may improve clinical outcomes.
Keywords: *Chlamydia psittaci* pneumonia, nomogram, prediction model, composite outcome

Background

Chlamydia psittaci (C. psittaci) is a Gram-negative intracellular bacterium, which is mainly transmitted between birds, and occasionally transmitted to humans by infected birds. Recent studies have shown that C. psittaci has the potential to evolve human-to-human transmission via various routes.[1] The severity of C. psittaci infection in humans may vary from mild flu-like symptoms to life-threatening severe pneumonia.[2] One study showed that the proportion of community acquired pneumonia (CAP) cases caused by C. psittaci ranged from 0% to 6.7%.[3]

The clinical symptoms and signs of C. psittaci pneumonia are usually nonspecific and mild, but some patients could progress to respiratory failure, rhabdomyolysis, multiple organ failure, and even death.[4,5] According to previous research, provided that patients receive prompt and adequate antibiotic treatment, the mortality rate associated with C. psittaci infection is less than 1%.[2] Traditional diagnostic tools, including culture, serologic testing, and polymerase chain reactions (PCR), are prone to false negative results, which may lead to the lower detection rate. In fact, C. psittaci pneumonia is often mis- and underdiagnosed in the past. With the progress of molecular biology in recent years, more and more studies have found that metagenomic next-generation sequencing (mNGS) or targeted next-generation sequencing (tNGS) can enhance our ability to diagnose C. psittaci pneumonia.[6,7] While there have been some case reports or case series on the clinical manifestations of C. psittaci pneumonia or risk factors in severe patients, the sample sizes are limited.[8,9] Currently, there is limited information available on predicting the risk of severe C. psittaci pneumonia. It is imperative to identify prognostic factors and incorporate them into a user-friendly prediction system to aid clinicians in making informed decisions and to provide more accurate patient stratification.

A multi-center retrospective study was conducted including 119 C. psittaci pneumonia patients diagnosed using mNGS or tNGS, with the aim of describing clinical characteristics, identifying prognostic factors, and developing an easy-to-use nomogram to predict the composite outcome in C. psittaci pneumonia on admission.

Methods

Study Design and Subjects

In this retrospective, multi-center study, collected clinical data from patients who were diagnosed with C. psittaci pneumonia from June 25, 2019, to June 25, 2022, in ten Chinese major tertiary hospitals. The inclusion criteria were as follows: first, patients met with the diagnostic criteria for community-acquired pneumonia;[10] second, mNGS or tNGS from an airway sample revealed a specific DNA fragment in C. psittaci; third, no other causative organisms present. Children, pregnant or those with missing or incomplete additional data were excluded.

Data Collection

Demographic characteristics and clinical manifestations of all patients were collected via electronic case systems. Clinical data included expose history, symptoms, comorbidities [chronic obstructive pulmonary disease (COPD), diabetes, hypertension, cardiovascular diseases, tumor, kidney diseases, liver diseases, and hematological diseases], laboratory tests [white blood cell (WBC), neutrophil percentage, lymphocyte percentage, C-reaction protein (CRP), procalcitonin, albumin (ALB), lactate dehydrogenase, total bilirubin, blood urea nitrogen, alanine aminotransferase, aspartate aminotransferase, blood sodium, blood potassium, and activated partial thromboplastin time], severity of illness scores (mainly CURB-65), computed tomography, systemic use of glucocorticoids and clinic outcomes. Baseline laboratory tests were performed within 24h after patient admission.

Clinical Outcomes

The primary study end point was a composite outcome of C. psittaci pneumonia [died during hospitalization, intensive care unit (ICU) admission, mechanical ventilation].

Selection of Predictor Variables

The clinical features of the patients were retrieved from electronic databases, including demographics, expose history, symptoms, comorbidities, laboratory tests, severity of illness scores (mainly CURB-65), computed tomography, systemic use of glucocorticoids and clinical outcomes. The missing values were interpolated using chain equations for the data set by performing multiple imputations. The variables those missing data >10% will be removed. Univariate logistic regression analysis was performed for each potential risk factor. Factors which turned out to be significant on a level of P<0.2 in univariate logistic regression analysis were included in multivariate logistic regression analysis.

Construction and Validation of a Predictive Nomogram of Composite Outcome

The patients were randomly divided into training and validation cohorts in a ratio of 7:3. Clinical data of the patients on admission in the training cohort were analyzed to develop the prognostic prediction model, which was internally validated using bootstrap resampling. To assess the models' external validity, furthermore, the model was evaluated in a validation cohort. Based on the multivariate logistic regression analysis, a nomogram was developed for the prediction of composite outcome in C. psittaci pneumonia patients. The nomogram was constructed by proportionally converting each regression coefficient in multivariate logistic, and each independent risk factor was assigned a score on the points scale. A higher total point of all independent variables refers to a higher composite outcome rate.

Statistical Analysis

Normally distributed continuous variables are presented as mean ± standard deviation (SD) and compared using Student's *t*-test, while non-normally distributed continuous variables are presented as median (interquartile range) and were compared using the Mann–Whitney *U*-test. The categorical variables were expressed as count and percentage and analysed using the χ^2 test or Fisher's exact test. P<0.05 was considered statistical significance. Univariate logistic regression analysis was performed to determine the possible correlation between composite outcome of C. psittaci pneumonia patients and potential risk factors. Variables with a P value less than 0.2 in the univariate analysis were included in the multivariate logistic regression to adjust for confounding factors. Based on the results of the multivariate logistic regression analysis, we constructed a predictive model for the composite outcome in C. psittaci pneumonia patients, which was further visualized by nomogram. The discriminative ability of the predictive model was assessed using C-index or area under the ROC curve (AUROC), which was internally validated using bootstrap resampling. Calibration was measured by the Hosmer–Lemeshow test and a calibration plot, which was constructed to examine the agreement between the predicted probabilities and the observed frequencies. Decision curve analysis (DCA) was performed to evaluate the clinical usefulness of the nomogram model by quantifying the net benefits under different threshold probabilities. The clinical impact curve analysis (CICA) of the model was further drawn. CICA will display the estimated number of people declared high risk at each risk threshold and visually show the proportion of cases (true positives).

"pROC" package in R software (version 4.2.0) was used for ROC curve; "rms" package for nomogram and calibration curve; "rmda" package for the decision curve and CICA, "care" package for cross validation, and so on. Figures were processed using Adobe Illustrator 2021. A P value of less than 0.05 was considered significant (P<0.05).

Results

Baseline Characteristics of Patients

A total of 119 C. psittaci pneumonia patients were enrolled in this study. The patients were randomly divided into training (n=83) and validation (n=36) cohorts in a ratio of 7:3 (Figure 1). Baseline characteristics are shown in Table 1. The median age was 61 years old (53 to 68), and 68.9% (n=82/119) of them were men. About 40.3% (n=48/119) patients had a history of exposure to parrots or poultry. The most common comorbidities included hypertension (29%, n=35/119),

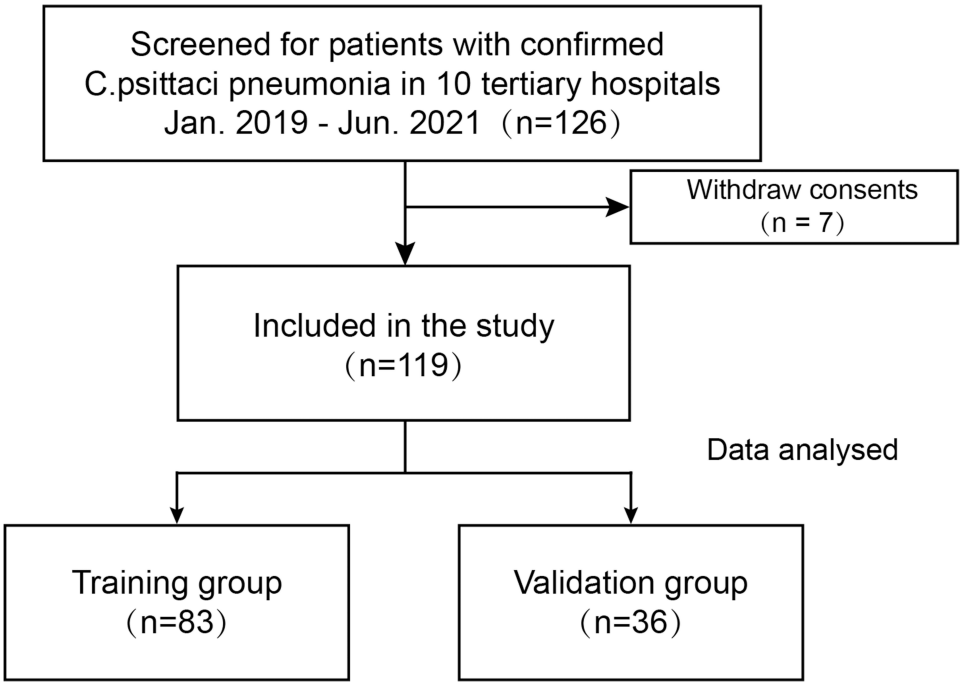

Figure 1 Flow chart of study participants in train and validation groups.

diabetes (18%, n=21/119), and liver diseases (8%, n=10/119). The most common symptoms included fever (98.3%, n=117/119), cough (79.8%, n=95/119), sputum (58.0%, n=69/119), and dyspnea (42.0%, n=50/119). Interestingly, laboratory findings on admission showed most patients presented with significantly decreased lymphocyte and increased

Table 1 Baseline Characteristics of Patients

Variables [n (%), Median (IQR) or mean ± SD]	Overall (n = 119)	Training Cohort (n = 83)	Validation Cohort (n = 36)	p-value
Age, years	61(53 to 68)	61.0 (55.5 to 68.0)	59.5(48.5 to 68.0)	0.36
Gender				
Male	82(68.9%)	59 (71.08%)	23 (63.89%)	
Female	37(31%)	24 (28.92%)	13 (36.11%)	0.57
Expose history	48 (40.3%)	35 (42.17%)	13 (36.11%)	0.68
Comorbidity				
COPD	7(5.9%)	5 (6.0%)	2 (5.6%)	1
Diabetes	21 (18%)	18 (21.69%)	3 (8.33%)	0.14
Hypertension	35 (29%)	26 (31.33%)	9 (25%)	0.63
Cardiovascular diseases	8 (7%)	6 (7.23%)	2 (5.56%)	1
Tumor	4 (3%)	2 (2.41%)	2 (5.56%)	0.75
Kidney diseases	3 (3%)	3 (3.61%)	0 (0%)	0.6
Liver diseases	10 (8%)	6 (7.23%)	4 (11.11%)	0.73
Hematological diseases	3 (3%)	2 (2.41%)	1 (2.78%)	1
Signs and symptoms				
Fever	117(98.3%)	81 (97.59%)	34 (94.44%)	0.75
Tmax	39.5 (1, 39–40)	39.42 (0.72)	39.41 (0.85)	0.43
Cough	95 (79.8%)	66 (79.52%)	29 (80.56%)	1
Sputum	69 (58.0%)	53 (63.86%)	16 (44.44%)	0.08
Dyspnea	50 (42%)	39 (46.99%)	11 (30.56%)	0.14
Headache	42 (35%)	28 (33.73%)	14 (38.89%)	0.74

(*Continued*)

Table 1 (Continued).

Variables [n (%), Median (IQR) or mean ± SD]	Overall (n = 119)	Training Cohort (n = 83)	Validation Cohort (n = 36)	p-value
Severity of illness scores				
CURB-65	1 (1, 0–1)	0.95 (0.92)	0.89 (0.82)	0.85
WBC (×109/L)	7.2 (4.8, 5.77 to 10.51)	7.3 (6.05 to 10.51)	6.84 (5.07 to 10.63)	0.42
Neutrophil percentage (%)	82.9 (10, 77.95 to 87.8	82.8 (77.75 to 87.8)	83.4 (78.2 to 88.1)	0.96
Lymphocyte percentage (%)	10 (6.5, 6.8 to 13.25)	10.0 (6.55 to 13.15)	10.0(7.0 to 13.7)	0.55
Lym (×109/L)	0.76 (0.48 to 1.04)	0.77 (0.49 to 1.07)	0.76 (0.42 to 1.01)	0.98
Platelet (×109/L)	180.87 ± 75.31	178.13 (120.0–225.0)	187.17 (124.5–231.5)	0.55
CRP (mg/L)	143.19 ± 74.74	145.7 ± 77.86	137.42± 67.67	0.56
PCT (ng/mL)	0.52 (0.2 to 1.89	0.54 (0.21 to 1.89)	0.38 (0.17 to 1.68)	0.55
ALB (g/L)	33 (28.95 to 37)	33.3(28.35 to 37.95)	31.7 (29.35 to 36.6)	0.4
LDH (U/L)	264 (204.5 to 396.5)	265(209.4 to 381)	254.5(200.5 to 429.5)	0.8
TBil (mmol/L)	12.8 (8.47 to 18.75)	13.9(8.6 to 20.68)	11.55(8.28 to 14.13)	0.14
BUN (mmol/L)	6.06 (4.16 to 9.61)	6.06(4.39 to 9.70)	5.96 (3.48 to 9.15)	0.59
ALT(U/L)	54.3 (24.95 to 94)	54.0 (23.35 to 72.9)	66.5(29.45 to 99.2)	0.31
AST(U/L)	55.2 (37.35 to 116.65)	54.0 (37.35 to 87.5)	77.0 (38.5 to 159.25)	0.12
NA(mmol/L)	135(131.0 to 139.6)	135.0(130.5 to 139.05)	133.75(131.05to 140.45)	0.86
K(mmol/L)	3.84(3.41 to 4.09)	3.9(3.49 to 4.10)	3.53(3.23 to 3.99)	0.081
APTT(s)	34.2(30.95 to 36.75)	34.2(31.4 to 36.7)	32.45(30.2 to 36.95)	0.4
Computed tomography images				
Consolidation	113(95.0%)	79 (95.18%)	34 (94.44%)	1.000
Interstitial change	83 (69.7%)	56 (67.47%)	27 (75%)	0.55
Pleural effusion	63 (53%)	44 (53.01%)	19 (52.78%)	1.00
Lesion in multiple lobes	54 (45%)	39 (46.99%)	15 (41.67%)	0.740
Lesion in single lobe	65 (55%)	44 (53.01%)	21 (58.33%)	0.740
Systemic use of glucocorticoids	35(29.4%)	23 (27.7%)	12 (33.3%)	0.536
Composite outcome	14(12%)	12 (14.46%)	2 (5.56%)	0.28

Abbreviations: IQR, interquartile ranges; SD, standard deviation; COPD, chronic obstructive pulmonary disease; WBC, white blood cell; Neu, neutrophil; Lym, lymphocyte; CRP, C-reaction protein; PCT, procalcitonin; ALB, Albumin; LDH, lactate dehydrogenase; TBil, total bilirubin; BUN, blood urea nitrogen; ALT, alanine aminotransferase; AST, aspartate aminotransferase; NA, Blood sodium; K, Blood potassium; APTT(s), activated partial thromboplastin time.

neutrophil percentage. As for infection biomarkers, CRP was increased in most patients, while procalcitonin (PCT) was normal in most patients. Biochemistry tests showed normal alanine aminotransferase (ALT) and aspartate aminotransferase (AST) levels in most patients. Chest computed tomography (CT) on admission showed that the most common imaging findings on CT included consolidation (95.0%, n=113/119), interstitial change (69.7%, n=83/119), and pleural effusion (53.0%, n=63/119). About 45% (n=54/119) patients presented with lesion in multiple lobes on CT. Systemic glucocorticoids were used in 29.4% (n=35/119) of patients. Eleven (9.3%) patients used mechanical ventilation, 13 (10.9%) patients were admission to the ICU, while 4 (3.4%) patients died during hospitalization. Overall, there was no significant difference in baseline clinical characteristics between training and validation cohorts.

Selection of Predictor Variables

Spearman rank correlation showed no significant correlation was found between the variables (Figure 2A). For C. psittaci pneumonia patients, based on univariate and multivariate logistic regression analysis, three independent prognostic factors were identified in the training cohort. ALB (OR, 0.77; 95% CI, 0.62–0.90; p = 0.005), CURB-65 (OR, 3.68; 95% CI, 1.65–10.46; p = 0.004), and WBC (OR, 1.31; 95% CI, 1.06–1.72; p = 0.026) were confirmed significantly associated with composite outcome in C. psittaci pneumonia patients (Figure 2B).

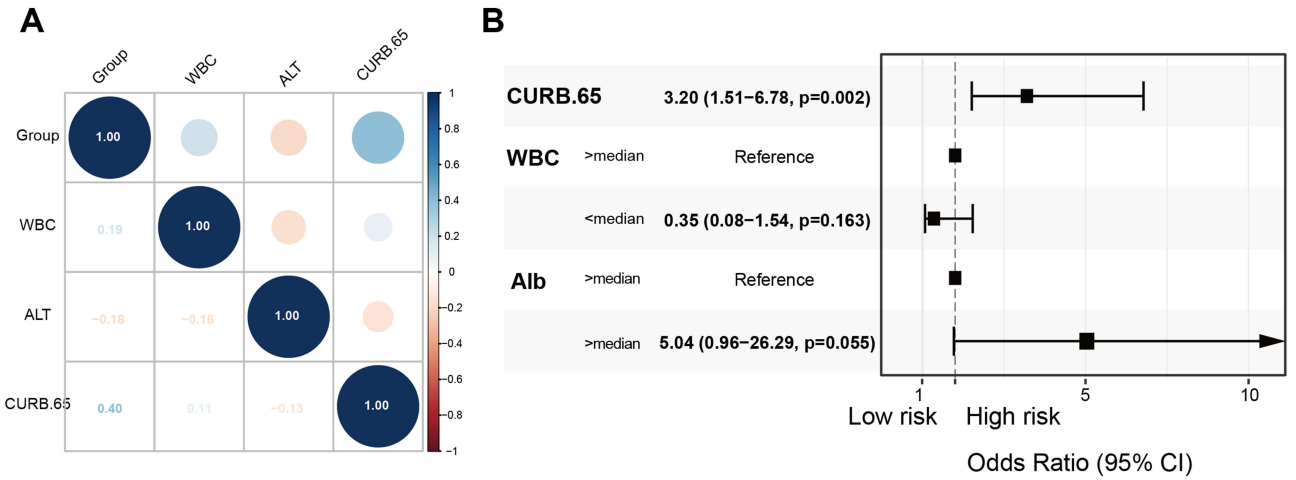

Figure 2 (**A**) spearman rank correlation, red indicates positive association while blue indicates inverse association. (**B**) Risk factors for the composite outcome in multivariate logistic regression analysis in the training cohort.

Construction and Validation of a Predictive Nomogram of Composite Outcome

Based on the multivariate logistic regression analysis, a nomogram was developed for the prediction of composite outcome in C. psittaci pneumonia patients (Figure 3). The C-index of the nomogram model was 0.898 (95% CI 0.825 to 0.971), showing a great discrimination ability, with an optimistic bootstrap-corrected C-index of 0.876 (95% CI 0.825 to 0.971). The ROC curves of the nomogram model for predicting the composite outcome in both the training and validation cohorts were shown in Figure 4A and B. The calibration plot indicated good agreement between the estimated risk by the nomogram model and the actual composite outcome of C. psittaci pneumonia patients in both the training cohort and the validation cohort (Figure 4C–F). The Hosmer–Lemeshow χ^2 of the nomogram model was 0.481 (p=0.786), demonstrating that there was no significant difference from a perfect fit.

Comparison of Predictive Accuracy for Composite Outcome Between the Nomogram Model and CURB-65

The C-index was calculated to estimate the discrimination ability of CURB-65 [0.784 (95% CI 0.643 to 0.925)]. The C-index of the nomogram model in training was higher than that based on the CURB-65 score (0.898 vs 0.784),

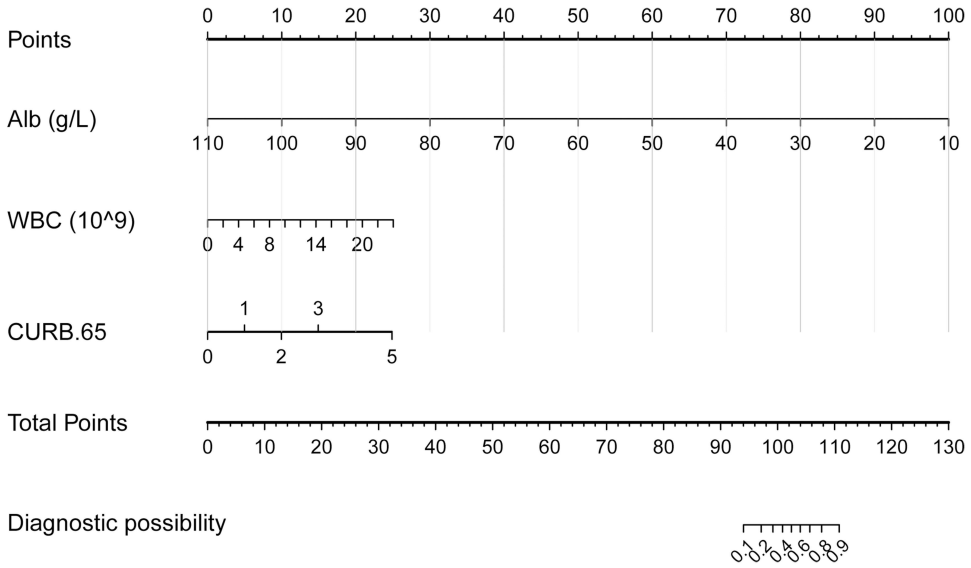

Figure 3 Nomogram for the prediction of composite outcome in C. psittaci pneumonia patients.

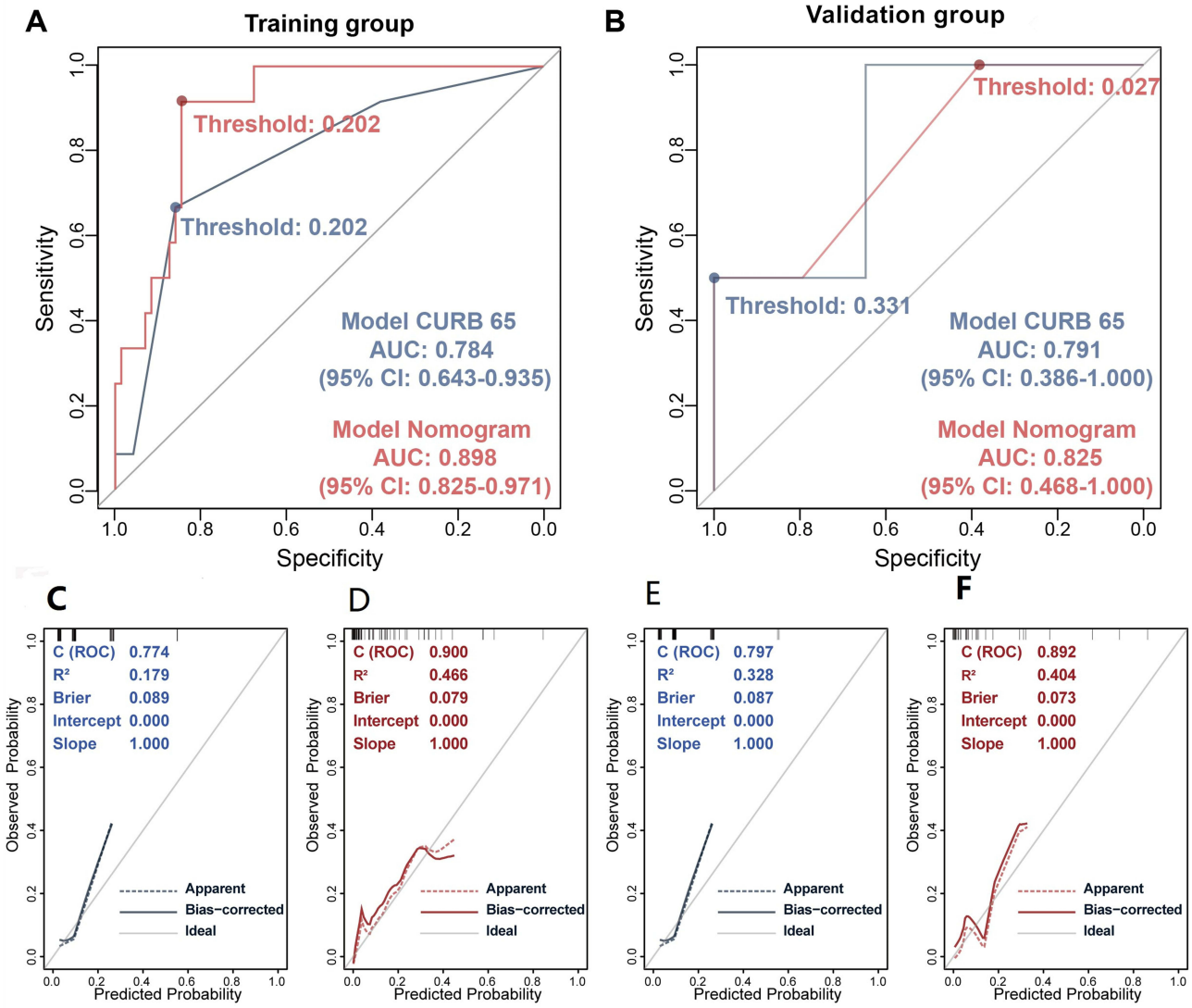

Figure 4 (**A**) ROC of the nomogram and CURB-65 for composite outcome in patients with C. psittaci pneumonia in the training group. **(B)** ROC of the nomogram and CURB-65 for composite outcome in patients with C. psittaci pneumonia in the validation group. **(C)** Calibration curve of CURB-65 for composite outcome in patients with C. psittaci pneumonia in the training group. **(D)** Calibration curve of the nomogram for the composite outcome in patients with C. psittaci pneumonia in the training group. **(E)** Calibration curve of CURB-65 for composite outcome in patients with C. psittaci pneumonia in the validation group. **(F)** Calibration curve of the nomogram for the composite outcome in patients with C. psittaci pneumonia in the validation group.

indicating the nomogram model had a higher predictive accuracy than CURB-65 score. Furthermore, the AUCs of the nomogram model were higher than CURB-65 score, shown in Figure 4A and B (AUC: 0.784 VS 0.898). The sensitivity, specificity, positive predictive value, and negative predictive value of the nomogram, and CURB-65 in identifying composite outcome in C. psittaci pneumonia patients were 91.7%, 84.5%, 50.0%, and 98.4% in the training cohort, and 100.0%, 64.7%, 14.2%, and 100.0% in the validation cohort, and 66.7%, 85.9%, 43.3%, and 93.8% in the training cohort, and 50.0%, 100.0%, 14.2%, and 97.1% in the validation cohort, respectively, shown in Figure 5A–D.

The DCA can depict the overall net benefit of using predictive models compared with the treat-none-patients and treat-all scheme, which was plotted to assess the clinical usefulness in real practice. Figure 4A and B showed that the net benefit of the nomogram model was over the CURB-65 score. DCA and CICA demonstrated that within a wide and practical threshold probability range, the nomogram model has good overall net income (Figure 6A–F).

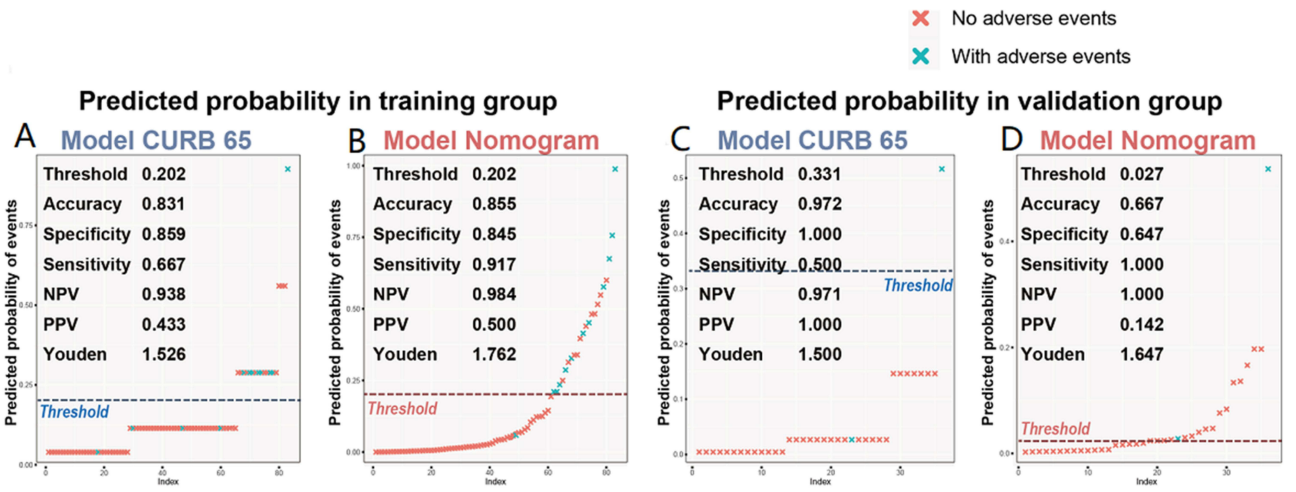

Figure 5 In the training set, the specificity, sensitivity, NPV, and PPV for predicting composite outcome in CURB-65 (**A**) and nomogram model (**B**), In the internal validation set, the specificity, sensitivity, NPV, and PPV for predicting composite outcome in CURB-65 (**C**) and nomogram model (**D**).

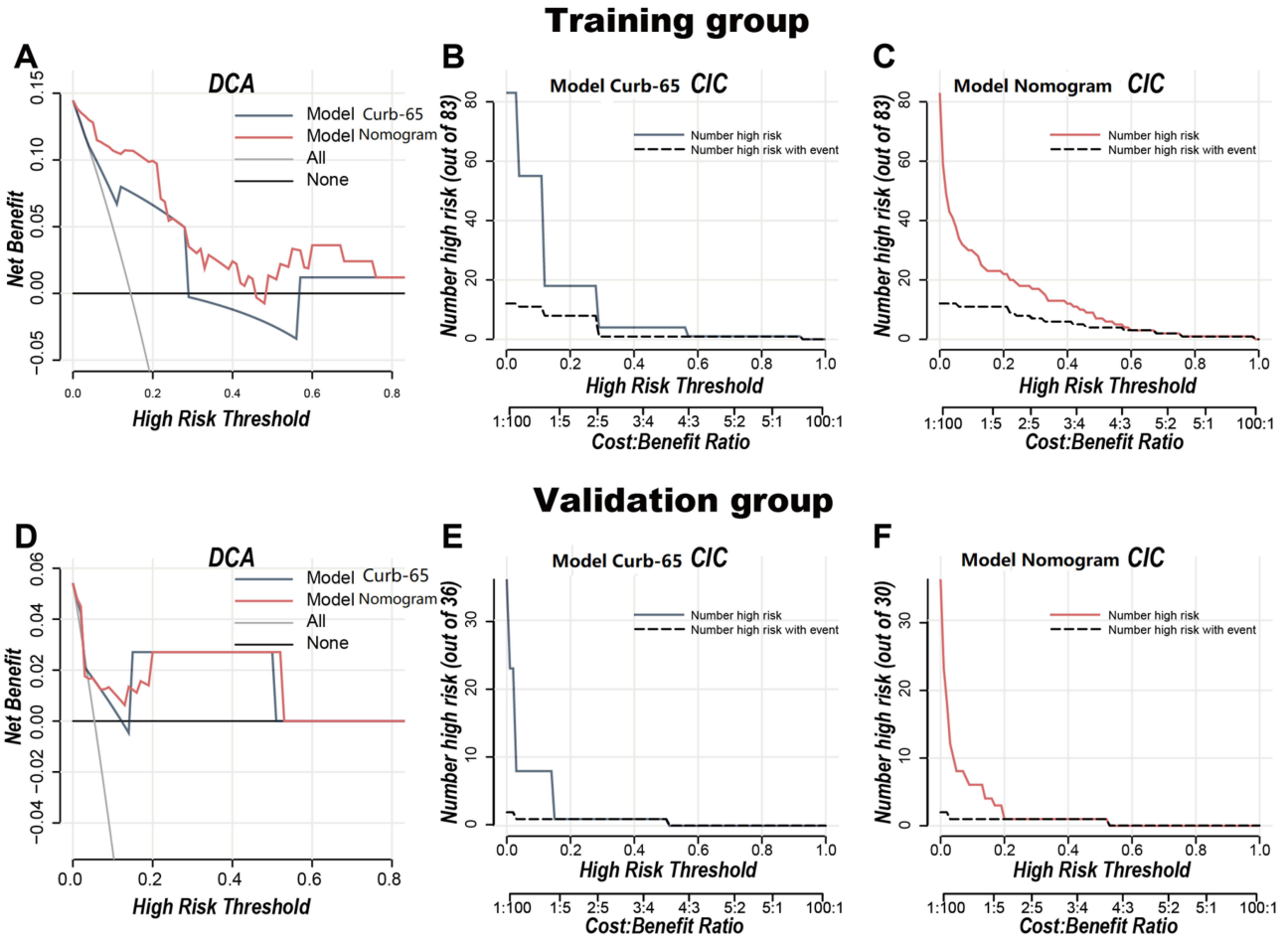

Figure 6 DCA and CICA. (**A–C)** training set; (**D–F)** validation set. Decision curve analysis for the nomogram and CURB-65 in the training cohort (**A**) and validation cohort(**D**).The clinical impact curve plots the number of high-risk cases of patients with C. psittaci pneumonia and the number of high-risk cases of patients with C. psittaci pneumonia under each high-risk threshold (**B–F**).

Discussion

In the present study, we described the epidemiological and clinical characteristics of 119 C. psittaci pneumonia patients and constructed a predictive model to better predict prognosis in patients with C. psittaci pneumonia. To our knowledge, this is the first study to build a nomogram model to predict the prognosis of patients with C. psittaci pneumonia to date. The model shows good performance in both the training and the validation cohorts, which enables early and accurate estimation in C. psittaci pneumonia patients.

This study showed that the average age of the onset population was 61 years old and male-dominated (68.9%), which were consistent with previous studies.[9,11] Su SS et al conducted a study of 27 patients with severe psittacosis pneumonia and found that about 85% of the patients had been in contact with birds,[8] while only 15.5% of patients had an exposure history in another study.[9] In this study, only about 40.3% of the patients could be traced back to a clear exposure history. This discrepancy may be due to the difficulty of following all patient exposure histories in retrospective studies. The symptoms of C. psittaci pneumonia are not typical, mainly manifested as fever, cough, sputum, dyspnea, and headache, and some patients manifested as high fever, which are similar to pneumonia caused by other pathogens. Regarding laboratory tests, in our study, the average white blood cell count was normal, but most patients had significantly decreased lymphocytes and increased percentage of neutrophils, which were consistent with previous study, which revealed that 93% of critically ill patients had hypolymphocytemia.[5] In addition, CRP levels were found to be significantly higher than normal value, while PCT was normal. Based on CT results, the imaging changes were mainly different degrees of exudation, manifested as consolidation, interstitial changes, pleural effusion, and 54 (45%) patients presented with lesion in multiple lobes on CT. All 119 cases included in the study were diagnosed by mNGS or tNGS.

CURB-65 is widely used in community-acquired pneumonia (CAP) prognostic scoring systems due to the easy application (confusion, urea, respiratory rate, blood pressure, age ≥65 years). With the increase in its score, the mortality rate of CAP patients also increased. So, clinicians often use CURB-65 to help guide inpatient versus outpatient treatment decisions.[12,13] In this study, we found that CURB-65 (OR, 3.6793; 95% CI, 1.65–10.46) was an independent risk predictor and significantly associated with composite outcome in C. psittaci pneumonia patients. Previous studies have demonstrated that decreased ALB level on admission to the hospital is a poor prognostic factor of CAP. Ito et al conducted a study of 1834 patients with CAP and found that low ALB level was a risk factor for mortality patients with CAP.[14] Zhao L et conducted a study a prospective, multi-center study including 366 CAP patients, showed that ALB was an independent prognostic variable for 30-day survival in patients with CAP, and ALB ≤30 g/L was associated with a significantly higher mortality risk.[15] Another study showed serum albumin was independently associated with 28-day mortality and had an additive role when combined with Pneumonia Severity Index (PSI) for predicting ICU admission, vasopressor use, or the need for mechanical ventilation.[16] In this study, multivariate logistic regression analysis confirmed that low ALB (OR, 0.769; 95% CI, 0.619–0.902) was independently associated with the risk for composite outcome of CAP caused by C. psittaci, which were consistent with previous studies. Interestingly, the findings showed that elevated serum WBC was an independent risk factor for composite outcome in C. psittaci pneumonia patients (OR, 1.314; 95% CI, 1.06–1.73). This can be explained by the hypothesis that high WBC levels are correlated with the severity of inflammation.

We established and validated a nomogram model to predict composite outcome in C. psittaci pneumonia based on three variables, including ALB, CURB-65, and WBC. The selected variables are easily accessible, which makes the nomogram model easy to use. Each level of three clinical variables (ie, CURB-65, serum ALB level, and WBC) was assigned a score on the points scale, and the total score was obtained by adding the scores of three variables. By calculating the total points, doctors can make early prognosis prediction of patients with C. psittaci pneumonia. More importantly, this model exhibited good model discrimination performance, with C index of 0.898 (95% CI 0.825 to 0.971) in predicting composite outcome in C. psittaci pneumonia patients in the training cohorts. The ROC curve also demonstrated that the nomogram model provided good prediction accuracy and exhibited an excellent AUROC of 0.898. Furthermore, the calibration plot was well fitted. In addition, the study compared its performance with the CURB-65 scoring system. By visual inspection of AUROC, the nomogram model showed better performance than CURB-65 score individual. The DCA showed that the net benefit of the nomogram model was better than that of CURB-65 score. The outstanding advantage of the predictive model was its simplicity and accuracy, with only three parameters in the model. More importantly, all these parameters are easily obtained

on hospital admission. This user-friendly predictive model could provide a simple and accurate way to predict in-hospital composite outcome in patients with C. psittaci pneumonia, which could provide important guidance for physicians' decision-making, with the hope of improving patient outcomes.

There were several limitations. First, clinical data from patients in the cohort were retrospectively collected, which may have some inherent biases. Second, due to the relative small sample size (n=119), validity of the nomogram model may have been affected. And thus, further large-scale prospective studies are needed to verify the prognostic model. Finally, the database that we collected did not cover information on smoke history, time from illness onset to first hospital admission, sequence number of C. psittaci, and combined detection of other microorganisms, which might affect composite outcome in patients with C. psittaci pneumonia.

Conclusion

The study provides a refined nomogram model for predicting the composite outcome in patients with CAP caused by C. psittaci. This nomogram model shows excellent performance, enables early and accurate estimation in C. psittaci pneumonia patients, and guides early management strategies for patients with C. psittaci pneumonia.

Abbreviations

C. psittaci, Chlamydia psittaci; ROC, receiver operating characteristics; AUROC, area under the ROC curve; PPV, positive predictive value; NPV, negative predictive value; DCA, decision curve analysis; CICA, clinical impact curve analysis; ALB, Albumin; WBC, white blood cell; CAP, community acquired pneumonia; PCR, polymerase chain reactions; mNGS, metagenomic next-generation sequencing; tNGS, targeted next-generation sequencing; COPD, chronic obstructive pulmonary disease; SD, standard deviation; CRP, C-reaction protein; PCT, procalcitonin; ALT, alanine aminotransferase; AST, aspartate aminotransferase; CT, computed tomography; ICU, Intensive care unit.

Data Sharing Statement

The datasets generated and analysed during the current study are not publicly available due privacy and ethical restrictions but are available from the corresponding author on reasonable request.

Ethical Approval and Consent to Participate

The study was approved by the institutional ethics review board at Shenzhen People's (approval number 2024-102-01). Verbal informed consent was obtained for all the investigations, and written informed consent was obtained from each participant in the study prior to enrollment. All methods were carried out in accordance with relevant guidelines and regulations or Declaration of Helsinki.

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Author Contributions

All authors made a significant contribution to the work reported, whether that is in the conception, study design, execution, acquisition of data, analysis and interpretation, or in all these areas; took part in drafting, revising or critically reviewing the article; gave final approval of the version to be published; have agreed on the journal to which the article has been submitted; and agree to be accountable for all aspects of the work. Xue Yang, Man Wu, and Tangzhiming Li contributed equally to this work and shared the first authorship. Zhiguo Zhou and Ming Lu are co-correspondence authors for this study.

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Disclosure

The authors declare that they have no conflicts of interest in this work.

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