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Development and validation of a prediction model for gestational diabetes mellitus risk among women from 8 to 14 weeks of gestation in Western China

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Abstract

Objectives To develop a clinically applicable and promotable prediction model for assessing the risk of gestational diabetes mellitus (GDM) within the context of primary healthcare institutions.

Methods The construction and the internal validation of the prediction model involved a cohort of 6,216 pregnant women observed from January 2019 to June 2019 in a Class A tertiary hospital in western China. External validation was subsequently conducted with 443 pregnant women from October 2020 to June 2021. Core characteristics were identified and the model was established using the least absolute shrinkage and selection operator (LASSO) regression. Internal validation was performed using the Bootstrap method. Model evaluation included discrimination and calibration tests, decision curve analysis (DCA), and the clinical impact curve. Visualization of the model was achieved through a static nomogram and a risk-scoring model.

Results The simplified prediction model possessed seven variables, including age, prepregnancy body mass index (BMI), polycystic ovary syndrome (PCOS), history of GDM, family history of diabetes, fasting plasma glucose (FPG), and urine glucose. This model exhibited a predictive accuracy, as reflected by a C-index of 0.736 (95% CI: 0.720 ~ 0.753) in the training set. The C-indexes were 0.735 and 0.694 in the internal and external testing set. Well-fitted calibration curves, the DCA curve, and the clinical impact curve demonstrated the feasibility of the simplified prediction model. For enhanced clinical application, the static nomogram and the risk-scoring model were employed to visualize the model.

Conclusions This study developed a prediction model for assessing the risk of GDM among women from 8 to 14 weeks of gestation in western China. The model demonstrated moderate discriminatory ability, well-fitted calibration, and convenient visualization, suggesting its suitability for implementation and widespread adoption, particularly within the context of primary healthcare institutions.

Keywords Clinical prediction model, Gestational diabetes mellitus, Nomogram, Screening, Women

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Introduction

Gestational diabetes mellitus (GDM) is defined as diabetes mellitus that manifests during pregnancy in individuals with normal glucose metabolism before conception, exerting a significant and critical impact on both mothers and their offspring [1]. Patients with GDM face elevated risks of obstetric complications, as well as an increased likelihood of developing type 2 diabetes mellitus (T2DM), metabolic disorders, and cardiovascular issues later in life [2]. Offspring born to mothers with GDM are more prone to macrosomia and neonatal hypoglycemia, and polycythemia, with heightened long-term risks of impaired glucose tolerance (IGT), obesity, and metabolic disorders [2, 3]. Attention to early GDM screening and taking scientific and reasonable pregnancy management are essential to mitigate or even prevent related adverse pregnancy outcomes.

As a specific abnormal glucose metabolism (AGM) during pregnancy influenced by a variety of factors such as gene and environment, GDM exhibits a multitude of reported influencing factors [4]. GDM clinical prediction models are designed to utilize parameter-based mathematical models to estimate the risk of suffering from GDM [5, 6]. Presently, the majority of GDM clinical prediction models are from European or North American countries, with the area under receiver operating characteristic curve (ROC) fluctuating between 0.67 and 0.78 [7]. However, recognizing the significance of racial differences in GDM occurrence is crucial [8]. Limited studies exist on Asian populations with substantial sample sizes [7, 9–11]. Previous reports on GDM prediction models tailored for the Chinese population yielded varying area under the curve (AUC) values ranging from 0.69 to 0.77 [9, 12, 13].

Currently, many existing prediction models for GDM are multivariate regression models. These models predominantly focus on discrimination ability (concordance index, C-index), but they lack the feasibility in primary healthcare institutions [14, 15]. Despite some machine-learning prediction models advantages of large samples and diverse indicators, they often rely on limited data sources within electronic medical systems [16]. The accessibility, applicability, and ease of interpretation of model parameters for clinicians are aspects that warrant further exploration [17]. Using LASSO regression to construct a prediction model has advantages in variable screening and controlling the number of variables. It can also avoid the problem of over-fitting, thereby enhancing the model's stability. The latest prediction model for GDM diagnosis utilized LASSO regression. However, it was constrained by a small sample size, and it suffered from a lack of external validation along with a limited set of predictive variables. Thus, the problem of test power deserves consideration [15]. According to the American Diabetes Association (ADA) (2025), early glucose screening should be performed before 15 weeks of gestation for all women who have not been diagnosed [18]. GDM screening is recommended for all pregnant women between 24 and 28 weeks of gestation [19]. A study by Song et al. [20] demonstrated that lifestyle modifications initiated before 15 weeks of gestation can reduce the risk of GDM; however, interventions started after 15 weeks of gestation were found to be ineffective. Previous predictive models are used broad gestational age range, such as 8 to 20 weeks [21]. We aim to develop a method for early and precise prediction of GDM risk, which will allow sufficient time for interventions and potentially reduce the incidence of GDM.

The aim of this study was to establish an early prediction model for GDM that can be widely applied in the primary healthcare system by leveraging a cohort that integrated both clinical and laboratory indicators. We aimed to construct a simplified model by employing LASSO regression, subsequently subject to comprehensive internal and external validation, discrimination, calibration, and clinical utility assessments. The static nomogram and the risk-score model were also planned to enhance comprehension.

Methods

This retrospective cohort study was carried out at the West China Second Hospital of Sichuan University, a Class A tertiary hospital in China with a total annual delivery volume of approximately 15,000. Approval for this study was obtained from the Ethics Committee of the West China Second Hospital of Sichuan University [Approval No.2021 (181)].

Study participants

Model construction and internal validation involved 6,216 pregnant women who established pregnancy archives, underwent regular obstetric examinations, and were subsequently hospitalized for delivery from January 2019 to June 2019. Exclusions were made for individuals under 18 years old, those with twin or multiple pregnancies, not Chinese, non-Han nationality, prepregnancy diabetes, chronic hypertension, severe organ dysfunction, and those not admitted not for delivery purpose. Based on the diagnosis of GDM, participants were categorized into the non-GDM group (5,043 cases) and the GDM group (1,173 cases).

External validation was conducted with 443 pregnant women meeting the inclusion and exclusion criteria. These participants, who established pregnancy archives, underwent regular obstetric examinations, and were hospitalized for delivery, were selected from October 2020

to June 2021. Stratified sampling by month and equidistant sampling within each month were employed for the selection process.

Sample size

The determination of sample size relies on the Event Per Variable (EPV) criterion for a clinical prediction model with binary outcomes, distinguishing between non-GDM and GDM. A crucial consideration is that the effective sample size should be ten times the number of independent variables [22, 23]. Considering the convenience of clinical practice, this study aimed to construct a clinical prediction model that contains 5 to 15 features. Consequently, the cohort should encompass more than 150 GDM patients. Based on prior data indicating a GDM incidence of approximately 17% at the West China Second Hospital of Sichuan University, the total study population should exceed 883 cases. For a model encompassing 7 prediction variables, the number of external verification objects should be more than 412 cases.

Diagnostic criteria

Following the recommendations proposed by ADA, the standard diagnostic approach for GDM is the "one-step" approach, namely, a 75 g oral glucose tolerance test (OGTT) administered at 24 to 28 weeks of gestation. This test necessitates the examinee to adhere to a normal diet for three days and fast for a minimum of 8 h before the examination [1]. Subjects take 300 ml of a liquid containing 75 g anhydrous dextrose within 5 min, followed by the measurement of fasting plasma glucose (FPG), 1-h postprandial glucose (1-h PG), and 2-h postprandial glucose (2-h PG). GDM is diagnosed when any value meets the following criteria: FPG $\geq$ 5.1 mmol/L, 1-h PG $\geq$ 10.0 mmol/L, and 2-h PG $\geq$ 8.5 mmol/L. The measurements were conducted using the hexokinase method by ADVIA 2400 Chemistry System (Siemens, Germany), with a measuring varies from 0.2 to 38.9 mmol/L with reported coefficients of variation (CV) ranging from 0.8% to 3.1%.

Data collection

A retrospective analysis method was employed to collect data on the research subjects, combining domestic and foreign guidelines, previous literature reports, clinical experts' opinions, and availability of pregnancy indicators. A total of 27 candidate variables were selected, including age, prepregnancy weight, height, prepregnancy body mass index (BMI), gravidity, primipara, assisted reproductive technology application (ART), polycystic ovarian syndrome (PCOS), chronic hepatitis B virus (HBV) infection, history of GDM, family history of diabetes and hypertension, and laboratory indicators during 8 to 14 weeks of gestation, such as white blood cell count (WBC), red blood cell count (RBC), hemoglobin (HB), hematocrit (HCT), platelet distribution width (PDW), mean platelet volume (MPV), alanine aminotransferase (ALT), aspartate aminotransferase (AST), creatinine (CREA), cystatin C (Cys-C), uric acid (UA), FPG, ferritin (FER), glucose in urine, ketones in urine (KET).

Statistical analysis

The above variables had less than 15% missing data, and single imputations were conducted using the "mice" R package. Univariate analysis was used to compare baseline characteristics laboratory indexes between the GDM and non-GDM groups. Categorical variables were described as frequencies and percentages (%) and were compared using $\chi 2$ tests. Continuous variables were expressed as mean $\pm$ standard deviation and were compared using student t-tests. The characteristics without definite interaction effect were selected. The least absolute shrinkage and selection operator (LASSO) regression was applied to analyze the training dataset (6,216 cases) and select the candidate predictive features utilizing the "glmnet" R package. Fully considering convenience and clinical significance, the research simplified the clinical prediction model. The simple model was developed using the "rms" R package. Internal validation was performed by the "Bootstrap" method. External validation was performed in a separate dataset (443 cases). Model performance was evaluated in terms of discrimination, calibration, and clinical usefulness, with C-index and its 95% CI, calibration curves, and decision curve analysis (DCA) used as metrics. Visualization of the model was achieved through the static nomogram and the risk-score model.

All statistical analyses were conducted on R Studio, version 4.0.5, and a two-tailed P-value < 0.05 was considered statistically significant.

Results

Participants selection

A total of 7,381 cases were extracted from electronic medical records. Exclusions were applied to 2 cases under 18 years old, 526 cases involving twin or multiple pregnancies, 2 cases of non-Chinese ethnicity, 184 cases of non-Han nationality, 129 cases with prepregnancy diabetes, 106 cases with chronic hypertension, 163 cases experiencing severe organ dysfunction, and 314 cases not intended for delivery purpose. Ultimately, 6,216 patients were included in the final analysis. The participant selection procedure is presented in Fig. 1.

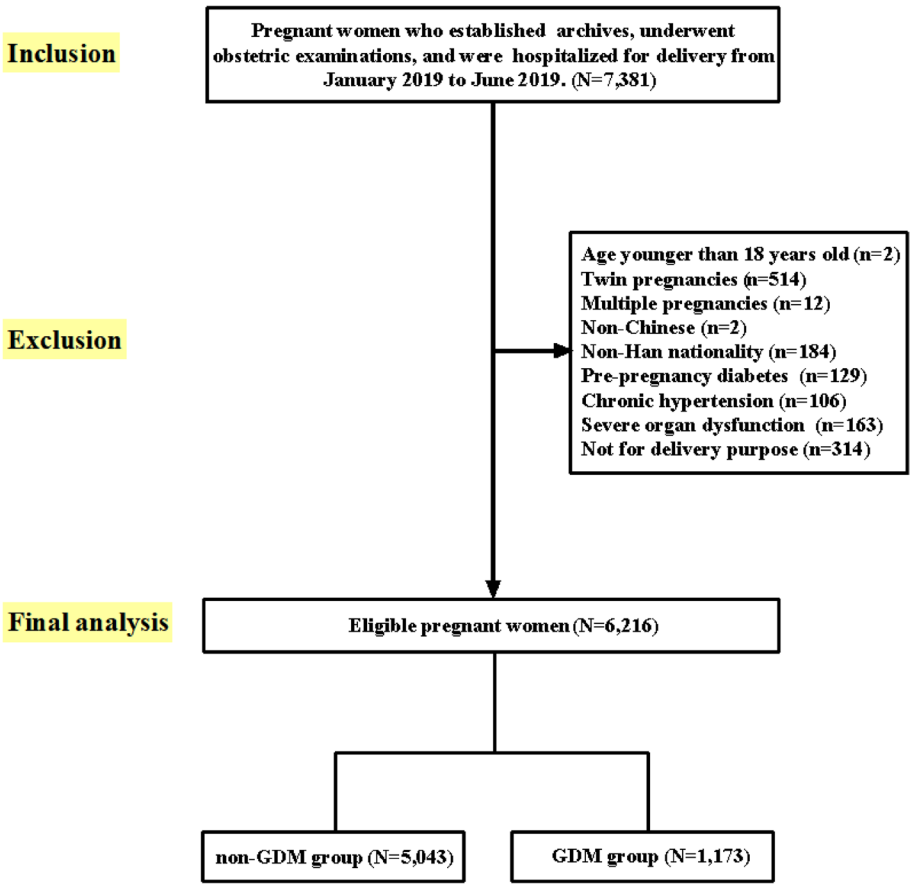


Fig. 1 Participant selection procedure

Candidate predictors selection

Baseline characteristics and laboratory indexes in the first trimester of pregnancy of eligible participants, classified by GDM diagnosis, were demonstrated in Table 1 and Table 2. There were significant statistical differences between the non-GDM and GDM groups, including age ($P<0.001$), prepregnancy weight ($P<0.001$), height ($P<0.001$), prepregnancy BMI ($P<0.001$), gravidity ($P<0.001$), primipara ($P<0.001$), ART application ($P=0.016$), PCOS ($P<0.001$), chronic HBV infection ($P=0.013$), history of GDM ($P<0.001$), family history of diabetes ($P<0.001$), WBC ($P<0.001$), RBC ($P<0.001$), HB ($P<0.001$), HCT ($P<0.001$), ALT ($P<0.001$), AST ($P=0.039$), UA ($P<0.001$), FPG ($P<0.001$), FER ($P=0.009$), and urine glucose ($P<0.001$). Following univariate analysis, 19 variables (11 continuous and 8 categorical variables) were selected as candidate variables from the initial 27 variables for LASSO. Considering the collinearity of weight, height, and prepregnancy BMI, only prepregnancy BMI was included as a candidate variable.

Clinical prediction model development

In this study, LASSO regression was employed to optimize variable selection and improve model stability. By obtaining a set of regression coefficients (β), the method aimed to minimize the sum of the residual sum of squares (RSS) and the penalty term (λ). By adjusting λ, certain β values corresponding to specific variables were reduced to zero, thereby achieving effective variable selection. Additionally, LASSO regression helps mitigate the risk of model overfitting to some extent, enhancing the model's overall stability and generalizability.

We narrowed down the selection of potential predictors to 12 from a pool of 19 features by employing LASSO, including age, prepregnancy BMI, PCOS, history of GDM, family history of diabetes, WBC, RBC, HCT, lg (ALT), UA, FPG, and urine glucose (Fig. 2A and 2B). Subsequently, we subjected these twelve factors to multivariate, logistic analysis, and developed the original model. The AUC of this model was 0.745 (0.729 ~ 0.761). At the point where the Youden index reached its maximum value of 0.366, the total score (S) was −1.515. An S exceeding −1.515 indicated a diagnosis of GDM. Notably,

Table 1 Baseline characteristics of eligible participants

Baseline characteristics	Non-GDM group	GDM group	MD/OR (95%CI)	*P*
No	5,043	1,173		
Age, mean (SD), years	30.95 (3.92)	32.54 (4.22)	1.593 (1.340 ~ 1.846)	< 0.001
Prepregnancy weight, mean (SD), kg	52.77 (7.03)	55.44 (8.05)	2.673 (2.171 ~ 3.174)	< 0.001
Height, mean (SD), cm	160.42 (4.83)	159.60 (4.86)	−0.815 (−1.123 ~ −0.507)	< 0.001
Prepregnancy BMI, mean (SD), kg/m^2	20.50 (2.51)	21.75 (2.94)	1.252 (1.069 ~ 1.435)	< 0.001
Gravidity, n (%)				
= 1	2,035 (40.4)	371 (31.6)	0.684 (0.597 ~ 0.783)	< 0.001
= 2	1,478 (29.3)	342 (29.2)	0.993 (0.863 ~ 1.142)	0.918
= 3	822 (16.3)	212 (18.1)	1.133 (0.959 ~ 1.338)	0.142
≥ 4	708 (14.0)	248 (21.1)	1.642 (1.397 ~ 1.929)	< 0.001
Primipara, n (%)	3,291 (65.3)	697 (59.4)	0.780 (0.684 ~ 0.888)	< 0.001
ART application, n (%)	341 (6.8)	103 (8.8)	1.327 (1.054 ~ 1.671)	0.016
PCOS, n (%)	47 (0.9)	29 (2.5)	2.695 (1.689 ~ 4.300)	< 0.001
Chronic HBV infection, n (%)	234 (4.6)	75 (6.4)	1.404 (1.074 ~ 1.836)	0.013
History of GDM, n (%)	25 (0.5)	49 (4.2)	8.750 (5.382 ~ 14.227)	< 0.001
Family history of diabetes, n (%)	327 (6.5)	183 (15.6)	2.660 (2.192 ~ 3.227)	< 0.001
Family history of hypertension, n (%)	859 (17.1)	225 (19.2)	1.154 (0.980 ~ 1.358)	0.085

GDM gestational diabetes mellitus, *MD* mean deviation, *OR* odds ratio, *CI* confidence interval, *BMI* body mass index, *ART* assisted reproductive technology, *PCOS* polycystic ovary syndrome, *HBV* hepatitis B virus

Table 2 Laboratory indexes of eligible participants from 8 to 14 weeks of gestation

Laboratory indexes	Non-GDM group	GDM group	MD/OR (95%CI)	*P*
No	5,043	1,173		
WBC, mean (SD), 10^9 /L	8.09 ± 0.94	8.44 ± 1.89	0.344 (0.216 ~ 0.472)	< 0.001
RBC, mean (SD), 10^{12} /L	4.15 ± 0.41	4.24 ± 0.41	0.090 (0.063 ~ 0.117)	< 0.001
HB, mean (SD), g/L	124.13 ± 9.98	126.14 ± 10.16	2.010 (1.347 ~ 2.674)	< 0.001
HCT, mean (SD), %	36.70 ± 2.73	37.35 ± 2.60	0.657 (0.478 ~ 0.837)	< 0.001
PDW, mean (SD), fL	14.19 ± 3.18	14.30 ± 3.21	0.107 (−0.111 ~ 0.324)	0.337
MPV, mean (SD), fL	11.25 ± 1.29	11.34 ± 1.70	0.086 (−0.008 ~ 0.179)	0.133
ALT, mean (SD), U/L	22.66 ± 19.68	25.48 ± 23.65	2.821 (1.298 ~ 4.344)	< 0.001
AST, mean (SD), U/L	22.30 ± 11.81	23.29 ± 14.80	0.996 (0.173 ~ 1.820)	0.039
CREA, mean (SD), μmol/L	41.95 ± 9.01	41.81 ± 12.21	−0.136 (−0.779 ~ 0.506)	0.678
Cys-C, mean (SD), mg/L	0.62 ± 0.15	0.63 ± 0.20	0.008 (−0.005 ~ 0.020)	0.227
UA, mean (SD), μmol/L	226.21 ± 48.12	236.85 ± 49.58	10.643 (7.414 ~ 13.872)	< 0.001
FPG, mean (SD), mmol/L	4.42 ± 0.34	4.65 ± 0.47	0.226 (0.196 ~ 0.251)	< 0.001
FER, mean (SD), ng/mL	78.12 ± 62.75	84.00 ± 66.22	5.889 (1.651 ~ 10.128)	0.009
Urine glucose, n (%)				
-	4,895 (97.1)	1,065 (90.8)	0.298 (0.231 ~ 0.385)	< 0.001
± ~ +	72 (1.4)	48 (4.1)	2.946 (2.033 ~ 4.269)	< 0.001
2 + ~ 4 +	76 (1.5)	60 (5.1)	3.523 (2.496 ~ 4.973)	< 0.001
Urine ketone, n (%)				
-	4,098 (81.2)	947 (80.7)	0.966 (0.822 ~ 1.136)	0.677
± ~ +	559 (11.1)	135 (11.5)	1.043 (0.854 ~ 1.274)	0.678
2 + ~ 4 +	386 (7.7)	91 (7.8)	1.015 (0.800 ~ 1.287)	0.904

GDM gestational diabetes mellitus, *MD* mean deviation, *OR*, odds ratio *CI* confidence interval, *WBC* white blood cell count, *RBC* red blood cell count, *HB* hemoglobin, *HCT* hematocrit, *PDW* platelet distribution width, *MPV* mean platelet volume, *ALT* alanine aminotransferase, *AST* aspartate aminotransferase, *CREA* creatinine, *Cys-C* cystatin C, *UA*, uric acid, *FPG* fasting blood glucose, *FER* ferritin

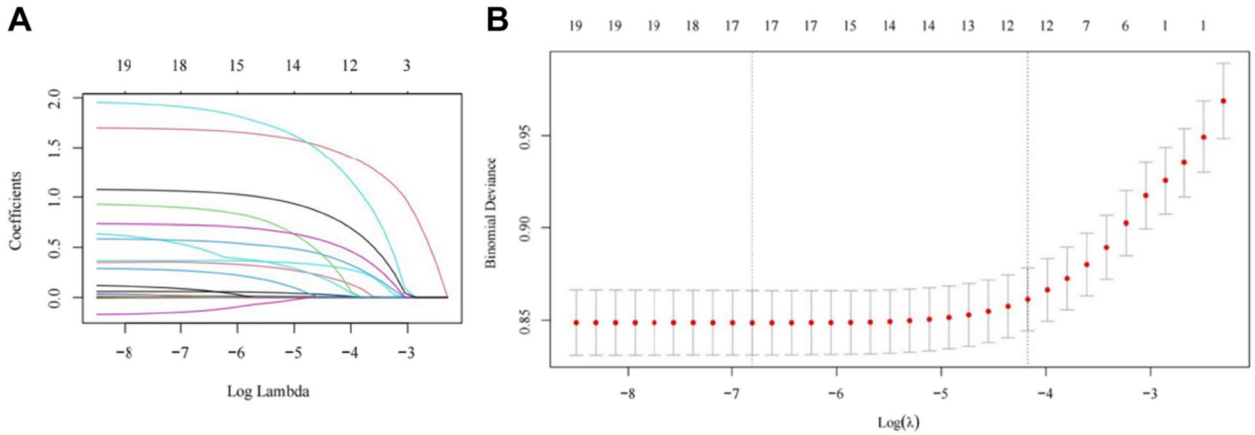


Fig. 2 Candidate predictors selection by LASSO. **A**. Coefficient trendlines of 19 variables for GDM diagnosis. The coefficient profile plot was created against the log (λ) sequence. By obtaining a set of regression coefficients (β), the method aimed to minimize the sum of the RSS and the penalty term (λ). By adjusting λ, certain β values corresponding to specific variables were reduced to zero, thereby achieving effective variable selection. **B** Tuning parameter (λ) selection of deviance in the LASSO regression based on the minimum criteria (left dotted line) and the 1-SE criteria (right dotted line), where 12 nonzero coefficients were selected, including age, prepregnancy BMI, PCOS, history of GDM, family history of diabetes, WBC, RBC, HCT, lg (ALT), UA, FPG, and urine glucose. Notes: LASSO, least absolute shrinkage and selection operator; λ, lambda; RSS, residual sum of squares; SE, standard error.

the specificity and sensitivity were measured at 0.692 and 0.674, respectively.

Clinical prediction model simplification

The original model was refined the original model into a more straightforward version, considering factors such as the weights of predictive variables, clinical expert opinions, model convenience, susceptibility of blood tests (WBC, RBC, HCT) to confounding factors, the necessity for liver and kidney detection for ALT and UA, and the complexity of ALT logarithmic conversion. The simple model included seven variables, including age, prepregnancy BMI, PCOS, history of GDM, family history of diabetes, FPG, and urine glucose. The AUC of the simple model was 0.736 (0.720 ~ 0.753). At the point where the Youden index reached its maximum value of 0.358, the S was −1.293. An S greater than −1.293 indicated the likelihood of GDM, with specificity and sensitivity values of 0.775 and 0.583, respectively. The decision to accept the results of the simple model was influenced by spline curves, demonstrating an approximately linear relationship with dependent variables, the absence of strong influence points, and the absence of multicollinearity problems. (Table 3,Fig. 3).

Internal and external model validation

For internal validation of the simple model, utilizing the Bootstrap method yielded a calculated AUC of 0.735. The external validation dataset demonstrated an AUC of 0.694, which included 321 non-GDM cases and 122 GDM cases, with an average age and prepregnancy BMI of 31.56 ± 3.59 years and 21.44 ± 2.97 kg/m^2. (Fig. 4A) The Youden index's optimum values corresponded to specificity and sensitivity values of 0.769 and 0.582. Calibration curves for both internal and external validation exhibited strong predictive power, with solid, dotted, and forty-five-degree lines approaching. (Fig. 4B, 4C).

Table 3 Development the original and simple GDM clinical prediction models by LASSO regression

Variables	Original model		Simple model	
	Estimate	*P*	Estimate	*P*
Intercept	−16.880	< 0.001	−13.742	< 0.001
Age, years	0.073	< 0.001	0.063	< 0.001
Prepregnancy BMI, kg/m^2	0.092	< 0.001	0.122	< 0.001
PCOS	0.900	< 0.001	0.965	< 0.001
History of GDM	1.925	< 0.001	1.935	< 0.001
Family history of diabetes	0.698	< 0.001	0.692	< 0.001
WBC, 10^9/L	0.062	0.001	-	-
RBC, 10^{12}/L	0.344	0.003	-	-
HCT, %	0.013	0.468	-	-
lg(ALT), U/L	0.391	0.006	-	-
UA, μmol/L	0.003	< 0.001	-	-
FPG, mmol/L	1.642	< 0.001	1.663	< 0.001
Urine glucose (+)	1.067	< 0.001	1.079	< 0.001

GDM gestational diabetes mellitus, *LASSO* least absolute shrinkage and selection operator, *BMI* body mass index, *PCOS* polycystic ovary syndrome, *WBC* white blood cell count, *RBC* red blood cell count, *HCT* hematocrit, *ALT* alanine aminotransferase, *UA* uric acid, *FPG* fasting blood glucose

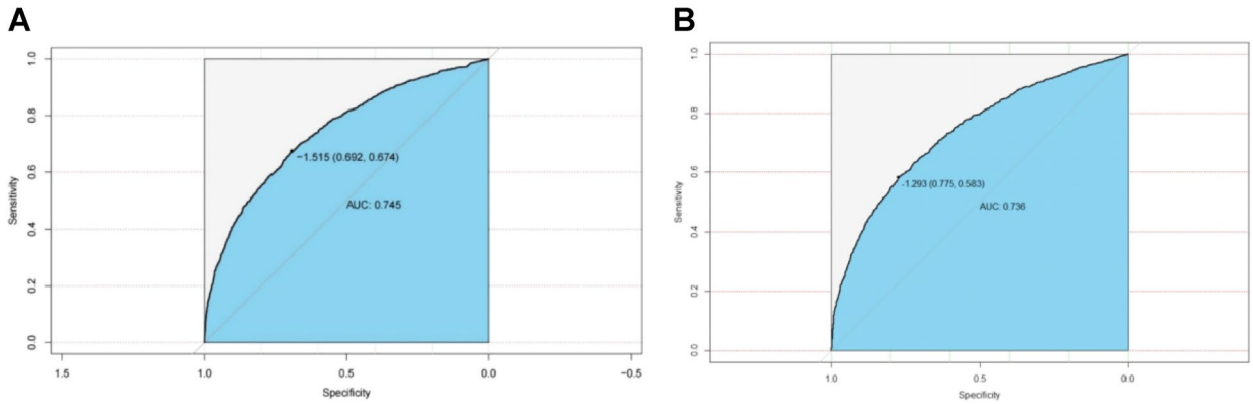


Fig. 3 ROC curves of the original model and the simple model. **A** The AUC value of the original model was 0.745 (0.729 ~ 0.761). At the point where the Youden index reached its maximum value of 0.366, the total score (S) was −1.515. An S exceeding −1.515 indicated a diagnosis of GDM. Notably, the specificity and sensitivity were measured at 0.692 and 0.674, respectively. **B** The AUC value of the simple model was 0.736 (0.720 ~ 0.753). At the point where the Youden index reached its maximum value of 0.358, the S was −1.293. An S greater than −1.293 indicated the likelihood of GDM, with specificity and sensitivity values of 0.775 and 0.583, respectively. Note: Receiver operating characteristic, ROC; area under curve, AUC; GDM, gestational diabetes mellitus.

Prediction model comparison

The DCA curve illustrated similar net profit rates for the original model (red line) and the simple model (blue line) within the threshold range of 0.1 to 0.8. Notably, the application of the simple model incurred only a marginal reduction in the net profit rate. The clinical impact curve showed the number of objects diagnosed with GDM by the simple model and the number of objects with actual GDM at each threshold probability. Combining application convenience and clinical significance, the simple model had more practical application values compared to the original model. (Fig. 5).

Prediction model visualization

The static nomogram drew scaled line segments in proportion, accumulated scores based on the values of individual variables. Subsequently, the cumulative scores were utilized to calculate the incidence risk of the object suffering from GDM. (Fig. 6) The risk-scoring model comprised a table presenting risk scores and a diagram reflecting the correlation between these risk scores and the associated prediction probabilities. (Table 4).

Discussion

In this study, we aimed to establish an early prediction model for GDM that can be easy and early used and popularized. Data from 6,216 eligible women were collected, encompassing a total of 27 clinical features. Based on the earliest gestational weeks when routine blood tests (e.g., WBC, RBC, FPG, ALT, AST) were conducted during prenatal examinations in the pre-survey, we decided

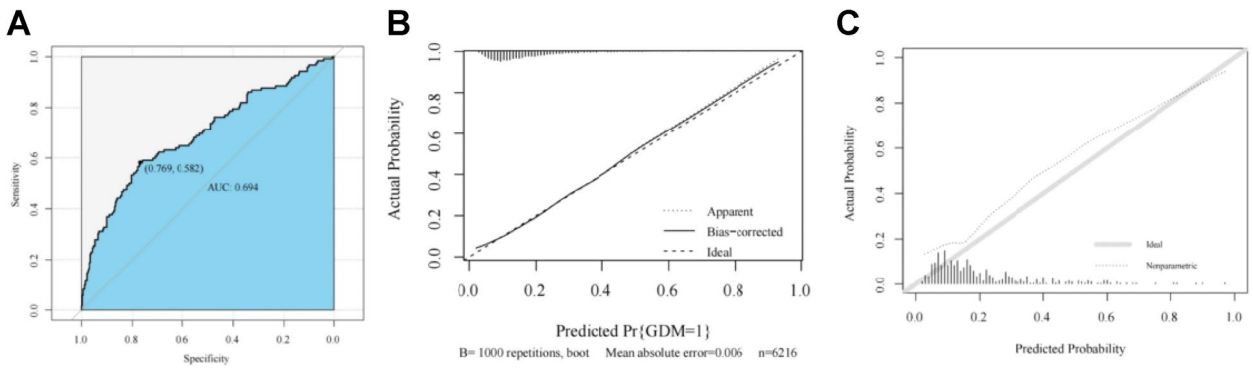


Fig. 4 **A** The ROC curve of the simple model in the external validation dataset. The AUC value of the simple model in the external validation was 0.694. The Youden index's optimum values corresponded to specificity and sensitivity values of 0.769 and 0.582. **B** Calibration curve for internal validation exhibited strong predictive power, with solid, dotted, and forty-five-degree lines approaching. **C** Calibration curve for external validation exhibited strong predictive power, with dotted and forty-five-degree lines approaching. The x-axis represented the predicted GDM risk while the y-axis represents the actual GDM diagnosing ratio. Note: Receiver operating characteristic, ROC; area under curve, AUC; GDM, gestational diabetes mellitus.

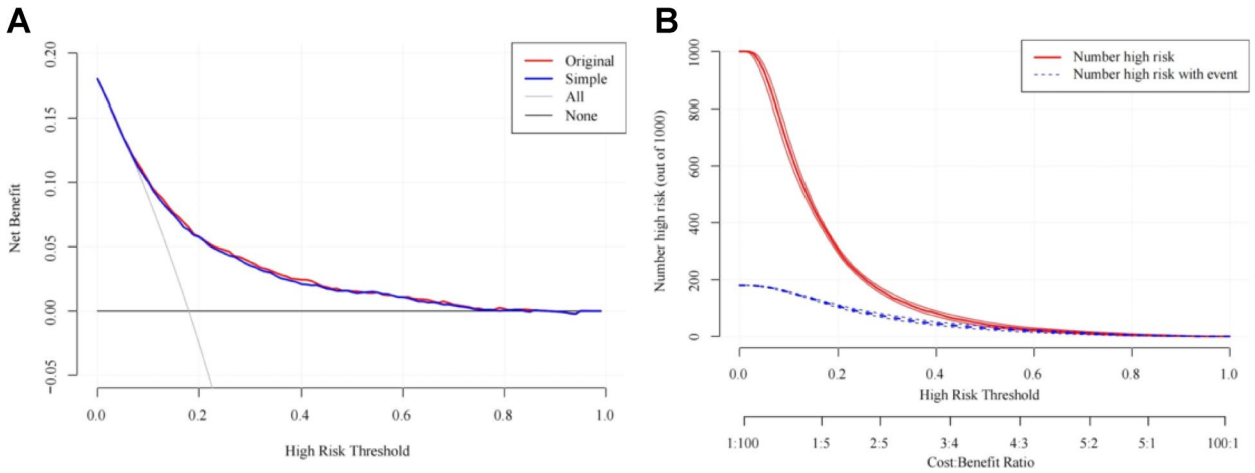


Fig. 5 **A** The DCA decision curve of the original model and the simple model. The transverse solid line represented the probability of risk that none of objects suffered from GDM, the oblique solid line represents the probability of risk that object suffer from GDM, and the y-axis assessed the net benefit. The DCA curve illustrated similar net profit rates for the original model (red line) and the simple model (blue line) within the threshold range of 0.1 to 0.8. Notably, the application of the simple model incurred only a marginal reduction in the net profit rate. **B** The clinical impact curve showed the number of objects diagnosed GDM by the simple model and the number of objects with actual GDM at each threshold probability. Combining application convenience and clinical significance, the simple model had more practical application values compared to the original model. Note: decision curve analysis, DCA; GDM, gestational diabetes mellitus

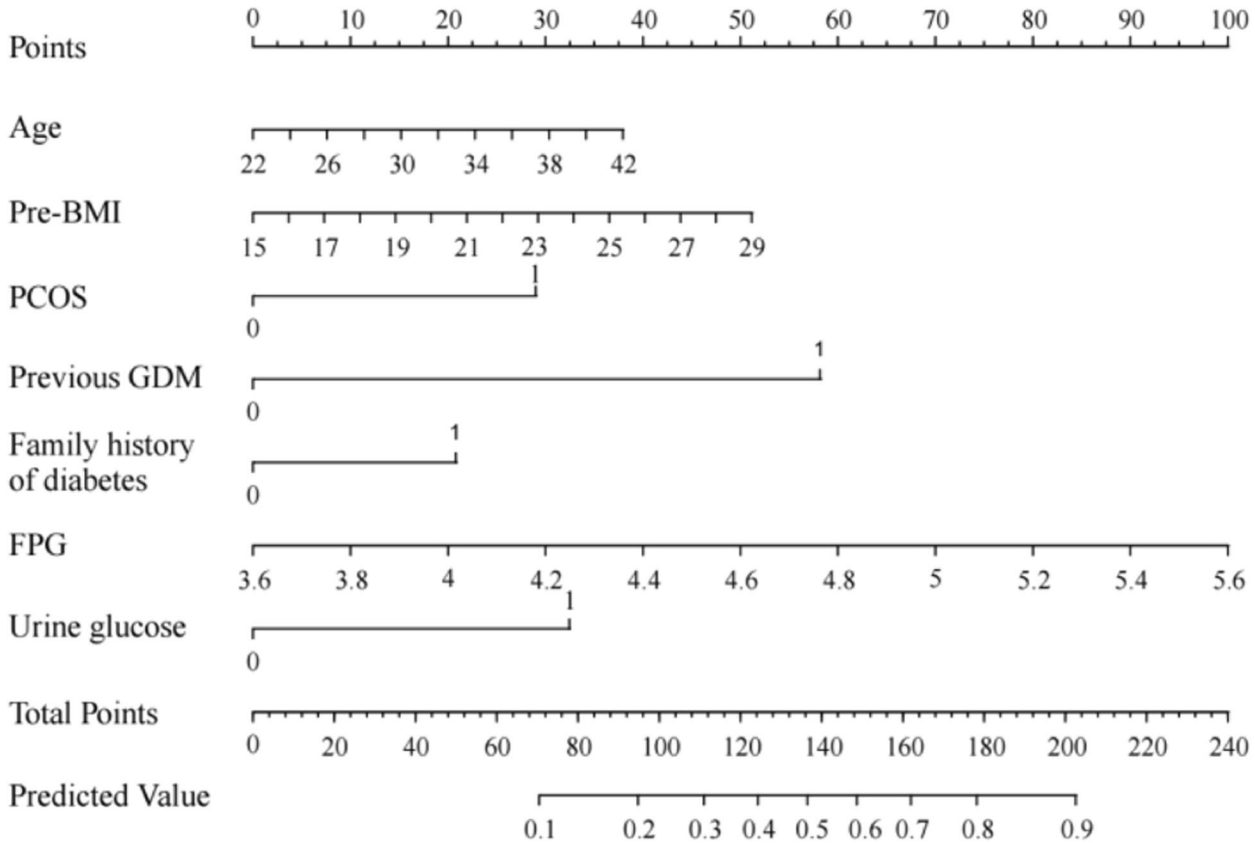
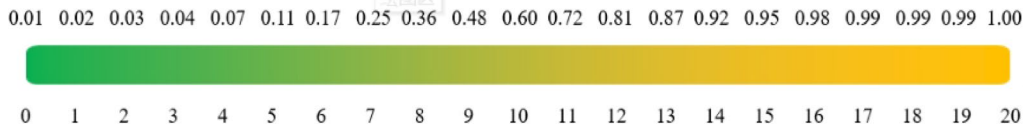


Fig. 6 Visualization of the simple model by static nomogram to estimate the probability of developing GDM. A nomogram utilized the selected variables in the simple model to predict the likelihood of GDM. Identify the predictor points on the point scale that corresponds to each variable of interest and sum them. The total points projected to the bottom scale indicate the probability of developing GDM. Note: GDM, gestational diabetes mellitus; BMI, body mass index; PCOS, polycystic ovary syndrome; FPG, fasting plasma glucose

Table 4 The risk scoring model for the predicting risk of GDM

Variables	Classification	Score
Age, years	＜20	0
	20~29	1
	30~39	3
	≥40	4
Prepregnancy BMI, kg/m^2	＜18.5	0
	18.5~23.0	1
	≥23.0	2
PCOS	No	0
	Yes	2
History of GDM	No	0
	Yes	4
Family history of diabetes	No	0
	Yes	1
FPG from 8 to 14 weeks of gestation, mmol/L	＜4.0	0
	4.0~4.5	2
	4.6~5.0	3
	≥5.1	5
Urine glucose（+）	No	0
	Yes	2



The risk-scoring model comprised a table presenting risk scores and a diagram reflecting the correlation between these risk scores and the associated prediction probabilities

Note: *BMI* body mass index, *PCOS* polycystic ovary syndrome, *FPG* fasting plasma glucose. lower horizontal axis, risk score; upper horizontal axis, predicting risk of GDM

to include indicators in the first trimester at 8–14 weeks of gestation. Since the predictive variables in the model should be normally or approximately normally distributed, we applied a logarithmic transformation to the skewed variables to make them approximately normally distributed. Following univariate analysis, nineteen primary prediction variables were identified and screened. LASSO regression further narrowed down the selection to twelve prediction variables, containing age, prepregnancy BMI, PCOS, history of GDM, family history of diabetes, WBC, RBC, HCT, lg(ALT), UA, FPG, and urine glucose. Considered the susceptibility of blood tests (WBC, RBC, HCT) to confounding factors, the necessity for liver and kidney detection for ALT and UA, and the complexity of ALT logarithmic conversion, we simplified the model to seven variables, including seven variables, including age, prepregnancy BMI, PCOS, history of GDM, family history of diabetes, FPG, and urine glucose. This model demonstrated moderate discriminatory ability.

Variable selection plays a crucial role in the construction of predictive models for GDM because many factors may contribute to or indicate the onset of GDM to some extent. The choice of predictive variables directly affects the model's accuracy, clinical applicability, and generalizability. It is widely accepted that age is a significant factor in the occurrence of both GDM and T2DM. Defects in insulin secretion and insulin sensitivity are vital physiologic processes. A high prepregnancy BMI or elevated FPG levels are associated with impaired insulin sensitivity, potentially leading to GDM [13]. Insulin resistance is one of the common accompanying symptoms of PCOS. A personal or family history of hyperglycemia may suggest genetic predispositions or environmental influences

linked to diabetes. During pregnancy, there is an increase in glucose leakage, while the reabsorption capacity may not increase correspondingly, causing incomplete glucose reabsorption and its subsequent appearance in urine, resulting in positive urine glucose tests. Although positive urine glucose is not a definitive screening or diagnostic criterion for GDM, our research has identified it as a valuable predictor.

Previous studies have included a wide range of predictors. In comparison with the model proposed by Guo F et al. [13], our study added PCOS, history of GDM, and urine glucose as essential features, resulting in a significant increase in AUC (0.69 to 0.736). Additionally, the internal and external validation AUCs for our model were 0.735 and 0.694, respectively. Another nomogram by Zhang H et al. achieved a powerful discrimination with an AUC of 0.754 among 924 pregnant women in Beijing [24]. For practicality and clinical significance, our study constructed a simplified model with seven prediction variables, including age, prepregnancy BMI, PCOS, history of GDM, family history of diabetes, FPG, and urine glucose. The model demonstrated moderate discriminative ability for GDM prediction in the first trimester of pregnancy, with an AUC ranking at an upper-middle level among current studies. The study also employed visualization methods, including a static nomogram and a risk-score model.

Racial differences play a crucial role in the incidence of GDM [8], so that the population involved in constructing the prediction model is preferably from the same region where the model will be used. Most current prediction models are derived from European or North American countries, with limited large-scale studies in east Asia [9, 25]. For example, Ruiter et al. [7] conducted a multicenter prospective study comparing 12 prediction models, revealing AUC fluctuations between 0.67 and 0.78. Common predictors included race, age, BMI, history of GDM, and family history of diabetes [7]. Benhalima et al. [26] highlighted that many foreign prediction models were validated in high-risk GDM groups determined by selective screening or a two-step approach. According to the WHO (2013) criteria, the AUC after internal validation of the their prediction model was 0.68 [26]. Several studies developed prediction models specifically tailored to Chinese women. For example, Zheng T et al.[21] proposed a straightforward prediction formula incorporating age, prepregnancy BMI, FPG, and triglycerides (TG), achieving an AUC of 0.766. However, this study lacked adequate assessments of model performance, such as calibration, clinical utility, and external validation.

Furthermore, uncertainties persist regarding the generalizability of the model across diverse populations due to disparities in population characteristics and diagnostic criteria. In contrast to our "one-step" approach resulting in an 18.9% GDM incidence, Zheng T et al. employed a "two-step" approach yielding a significantly lower incidence of 12.8% [21]. Additionally, a logistic prediction model was constructed among women in Shanghai by Guo F et al., including age, prepregnancy BMI, FPG during the first trimester of gestation, and family history of diabetes as prediction variables. However, this model exhibited a C-index below 0.7 and lacked laboratory index selection [13]. Gao S et al. developed two risk scores, one based on variables available at the first visit (AUC = 0.710) and other incorporating additional collectible variables during pregnancy (AUC = 0.712) [9]. Among Asian populations, short stature was identified as a significant risk factor for GDM [27]. Nevertheless, considering height and prepregnancy BMI as predictors having multicollinearity, the model stability may be impacted [9].

The choice of model construction methods plays a crucial role in determining the predictive performance and clinical applicability. As for machine-learning prediction models, original data primarily comes from the electronic medical records, lacking an exploration of clinical risk factors [17]. Some parameters in these models may be inconvenient for clinicians to obtain, promote, and interpret, posing challenges to practical application. Currently, the random forest model does not include laboratory indicators, such as FPG, and urine glucose, that are readily available in the first trimester [28]. The reported incidence of GDM in the XGBoost model was 7.6% [29], much lower than that of the HAPO study using IADPSG criteria [30]. LASSO regression offers advantages in variable selection and limiting the number of predictors, effectively preventing overfitting and improving model stability. Previous studies on GDM prediction models utilized LASSO regression, examining GDM metabolic characteristics in a cohort of among 358 subjects [31], and exploring diabetes risk after delivery in a cohort of 257 subjects [32]. The recent GDM diagnosis prediction model employed LASSO regression but was limited to 824 subjects in central China, lacking external validation and crucial patient information such as gravidity, parity, previous medical history, and family history [15].

The time required for data acquisition and the availability of predictors crucially influence the initial time and feasibility of model application. According to the ADA (2025), early glucose screening is recommended before 15 weeks of gestation for all women who have not been previously diagnosed with diabetes [18]. Previous studies also pointed that interventions started after 15 weeks of gestation were found to be ineffective for GDM [20]. However, some predictive models are suitable for broad gestational age range (8 to 20 weeks of gestation) [21] and

include predictors collected at the time of GDM screening [9]. We selected indicators that can be accessed at 8–14 weeks of gestation to predict GDM, to ensure sufficient time for intervention and ultimately reducing its incidence.

One of the key strengths of this study is that we selected simple indexes obtainable in early pregnancy in primary healthcare settings. Additionally, this prediction model keeps a balance between the number of variables and discriminatory ability, with moderate predictive value and fully validated. There are several limitations that should be acknowledged. Metrics such as the net reclassification index (NRI), integrated discrimination improvement (IDI), and the t-SNE algorithm need to be included as evaluation indicators in the prediction model. Second, this study didn't explore a multi-classification model aligned with pre-care measures. Achieving an AUC greater than 0.8 for GDM-related prediction models may be challenging due to the multifactorial nature of GDM, which is influenced by genetic, intrinsic, and environmental factors. These complexities underscore the need for continued research to refine and improve predictive accuracy.

Conclusions

This study developed a prediction model for assessing the risk of GDM among women from 8 to 14 weeks of gestation in western China. The model demonstrated moderate discriminatory ability, well-fitted calibration, and convenient visualization, suggesting its suitability for implementation and widespread adoption, particularly within the context of primary healthcare institutions.

Abbreviations

GDM	Gestational diabetes mellitus
LASSO	Least absolute shrinkage and selection operator
DCA	Decision curve analysis
BMI	body mass index
PCOS	Polycystic ovary syndrome
FPG	Fasting plasma glucose
T2DM	Type 2 diabetes mellitus
IGT	Impaired glucose tolerance
AGM	Abnormal glucose metabolism
ROC	Receiver operating characteristic curve
AUC	Area under the curve
C-index	Concordance index
ADA	American Diabetes Association
EPV	Event per variable
OGTT	Oral glucose tolerance test
CV	Coefficient of variation
ART	Assisted reproductive technology application
HBV	Hepatitis B virus
WBC	White blood cell count
RBC	Red blood cell count
HB	Hemoglobin
HCT	Hematocrit
PDW	Platelet distribution width
MPV	Mean platelet volume
ALT	Alanine aminotransferase
AST	Aspartate aminotransferase
CREA	Creatinine
Cys-C	Cystatin C
UA	Uric acid
FER	Ferritin
KET	Ketones in urine
RSS	Residual sum of squares
TG	Triglyceride
NRI	Net reclassification index
IDI	Integrated discrimination improvement

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Authors' contributions

JNZ, QC, CHM, JFX, YQL, DJC, and XDW designed research; JNZ, QC, CHM, YM, GQH, and XXD collected and analyzed the data; JNZ drafted the manuscript; TTX, FZ and XDW revised the manuscript. All authors had responsibility for final content. All authors read and approved the final manuscript.

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Data availability

The data that support the findings of this study are available from the corresponding author upon reasonable request.

Declarations

Ethics approval and informed consent to participate

The study was in accordance with the Declaration of Helsinki and was approved by the Ethics Committee of the West China Second Hospital of Sichuan University [Approval No.2021(181)]. Due to the retrospective nature of the study, the need for informed consent was waived by the Ethics Committee of the West China Second Hospital of Sichuan University in accordance with the national legislation.

Consent for publication

Not applicable.

Competing interests

The authors declare no competing interests.

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