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A Multi-Dimensional Empirical Study on the Relationship Between Obesity and Metabolic Syndrome in Asian Populations

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Abstract:

The epidemiological characteristics of metabolic syndrome (MetS) in the Asian population are unique, especially the significant association between lean obesity and visceral fat accumulation. However, existing studies have insufficient quantitative analysis of key predictive indicators and lack simplified screening models for the Asian population. This study was based on the data of 295 Asian adults and used a binary logistic regression model to analyze the association between indicators such as Body Mass Index (BMI), waist circumference, blood lipid, and blood glucose and MetS. The significance of each variable and the predictive performance of the model were evaluated through two model constructions (full variables and optimized variables). The preliminary model shows that BMI, Albuminuria, Blood Glucose, and Triglycerides have significant positive effects on MetS (OR values are 1.227, 3.811, 1.015, and 1.008, respectively, $p<0.05$). High-Density Lipoprotein (HDL) had a negative effect ($OR=0.913$, $p<0.01$). After eliminating non-significant variables in the optimized model, the goodness of fit was significantly improved (Nagelkerke $R^2=0.629$), and the prediction accuracy reached 88.14%. BMI, albuminuria, blood glucose, and triglycerides are the core predictive indicators of MetS in the Asian population, and HDL has a protective effect. The optimized model provides an efficient tool for clinical screening. It is recommended to pay attention to high-risk groups with a normal BMI but excessive visceral fat.

Keywords: Metabolic syndrome, Asian population, binary logistic regression

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1. Introduction

Metabolic syndrome (MetS) is a cluster of metabolic abnormalities centered on insulin resistance, combined with central obesity, dysglycemia, dyslipidemia, and hypertension. The prevalence of obesity and metabolic syndrome (MetS) is rising rapidly in Asia, with this population exhibiting unique characteristics such as lean obesity and visceral fat accumulation, necessitating targeted intervention measures. Data indicate that the obesity rate among South Korean adults increased significantly from 30.2% in 2012 to 38.4% in 2021 [1]. Concurrently, research by Wang et al. points out that the rate of central obesity among Chinese adults has exceeded 30% and shows a clear dose-response relationship with MetS risk [2]. Meanwhile, Sakurai et al.'s research on the historical evolution of metabolic syndrome indicates that the metabolic patterns of Asian populations are shifting from undernutrition to overnutrition [3].

At the pathophysiological level, the phenomenon of lean obesity has attracted widespread attention. Taking the South Asian population in Hong Kong as an example, even with a normal BMI (e.g., average BMI of 23.5±3.2 kg/m² in Hong Kong South Asians), the rate of exceeding waist circumference standards still reaches 58.3%, and the impact of abdominal obesity on MetS (OR=3.21) is stronger than that of general obesity (OR=1.89) [4]. This specific pattern of body fat distribution may be related to the genetic background and epigenetic regulation of Asian populations. For instance, Li et al. found that genetic factors such as PPARγ gene polymorphisms might promote visceral fat accumulation [5]. However, genetic susceptibility does not mean that the outcome is unchangeable; lifestyle interventions and early prevention still play a crucial role in reducing metabolic risks.

With the continuous advancement of artificial intelligence (AI) technology in the medical field, its role in disease prevention is becoming increasingly prominent, particularly significant in the early prevention and control of metabolic syndrome (MetS). The development of deep learning-based early warning systems for MetS has brought new research directions to this field [6], and related technological progress further demonstrates the vast application potential of AI in MetS research and clinical management. The deep learning model developed by Zhang et al. performed excellently in early warning of MetS (accuracy 89.7%). When combined with natural language processing and exercise monitoring, it can improve screening efficiency and support personalized interventions [6].

Despite significant research progress, several key issues remain to be addressed. First, the clinical translation and application of AI-based precision prediction models. Second, the optimization and standardization of lifestyle intervention schemes suitable for Asian populations. Solving these problems will promote innovative development in metabolic health management for Asian populations.

This paper explores the complex relationship between obesity and metabolic syndrome in Asian populations from multiple perspectives, including epidemiological characteristics, pathophysiological mechanisms, clinical intervention measures, and the application of artificial intelligence technologies. By integrating multidisciplinary evidence, it aims to provide a scientific basis for the prevention and management of metabolic syndrome in Asian populations and to identify priority areas for future research.

2. Data Analysis

2.1 Data Sources and Explanations

This data is sourced from the Kaggle public database. After cleaning and screening, 295 samples of Asian adults aged 18–80 years were retained[7]. Core variables include obesity indicators: Waist Circ (cm), BMI (kg/m^2); Metabolic parameters include: Albuminuria (0 = normal (<30 mg/g), 1 = trace (30–300 mg/g), 2 = massive (>300 mg/g)), Urine Albumin Creatinine (UrAlbCr) (mg/g), Uric Acid (mg/dL), Blood Glucose (mg/dL), High-Density Lipoprotein (HDL) (mg/dL), Triglycerides (mg/dL). The target variable is Metabolic Syndrome (0 = absent, 1 = present), strictly adhering to the Asian standards of the International Diabetes Federation (IDF). The data has been cleaned of invalid and missing values, outliers have been excluded, and it is strictly limited to Asian populations. Research on the relationship between obesity and metabolic syndrome in Asian populations. Table 1 below shows some basic indicators.

Table 1. Basic Indicators Table

Name	Waist Circ	BMI	Albuminuria	UrAlbCr	Uric Acid	Blood Glucose	HDL	Triglycerides
Symbol representation	X_1	X_2	X_3	X_4	X_5	X_6	X_7	X_8

2.2 Model Framework and Analysis

Based on the data and relevant texts, the author proposes using a binary logistic model for the framework.

$$log\left(\frac{p}{1-p}\right)=\beta_0+\beta_1X_1+\beta_2X_2+...+\beta_kX_k \quad (1)$$

In the above formula, p represents the probability of MetS, β_0 represents the intercept term, $\beta_1, \beta_2...\beta_k$ represents the coefficient of the independent variable, and $X_1, X_2...X_k$ represents the predictor variables (such as waist circumference, HDL, etc.). Its advantage is that it can directly analyze the binary classification results, making the results easy to interpret. Compared with the regression coefficients of linear regression, its OR value is closer to the actual decision-making requirements and can capture nonlinear relationships and interactions. For instance, by introducing polynomial terms (such as BMI²) or piecewise regression, etc., threshold effects can be identified, and the synergy among variables can be tested. It is applicable to small samples and imbalanced data, providing stability for the model and results.

2.3 Model Architecture and Analysis

Using Waist Circ, BMI, Albuminuria, UrAlbCr, Uric Acid, Blood Glucose, HDL, Triglycerides as independent variables and Metabolic Syndrome as the dependent variable for binary logistic analysis.

Table 2. Binary logistic analysis of all variables

Item	Regression Coefficient	Standard Error	*z* Value	*p* Value	OR v=Value	95% CI for OR
Waist Circ	0.039	0.039	1.010	0.313	1.040	0.964 ~ 1.122
BMI	0.204	0.103	1.978	0.048	1.227	1.002 ~ 1.502
Albuminuria	1.338	0.657	2.037	0.042	3.811	1.052 ~ 13.805
UrAlbCr	-0.001	0.002	-0.468	0.640	0.999	0.996 ~ 1.002
Uric Acid	0.085	0.149	0.571	0.568	1.089	0.813 ~ 1.457
Blood Glucose	0.015	0.006	2.443	0.015	1.015	1.003 ~ 1.027
HDL	-0.091	0.024	-3.814	0.000	0.913	0.871 ~ 0.957
Triglycerides	0.008	0.002	3.301	0.001	1.008	1.003 ~ 1.013
Intercept	-8.959	2.677	-3.347	0.001	0.000	0.000 ~ 0.024

The model formula can be derived from Table 2 as:

$$log\left(\frac{p}{1-p}\right)=-8.959+0.039X_1+0.204X_2+1.338X_3-0.001X_4+0.085X_5+0.015X_6-0.091X_7+0.008X_8$$

(2)

The final specific analysis shows that BMI, Albuminuria, Blood Glucose, and Triglycerides have a significant positive impact on Metabolic Syndrome (the p values of the above elements are all less than 0.05). And HDL will have a significant negative impact on Metabolic Syndrome ($p<0.05$). However, Waist Circ, UrAlbCr, and UricAcid do not have an impact relationship ($p>0.05$).

3. Results

3.1 Secondary Model Construction and Analysis

The author considers a more influential model and re-analyzes the factors that have a significant influence relationship using the binary Logistic method:

Table 3. Binary Logistic analysis of optimized variables

Item	Regression Coefficient	Standard Error	*z* Value	*p* Value	OR Value	95% CI for OR
BMI	0.295	0.059	5.015	0.000	1.343	1.197~ 1.50x7
Albuminuria	1.219	0.513	2.378	0.017	3.384	1.239~ 9.243
Blood Glucose	0.016	0.006	2.679	0.007	1.016	1.004~ 1.028
HDL	-0.097	0.023	-4.147	0.000	0.908	0.867~ 0.950
Triglycerides	0.008	0.002	3.465	0.001	1.008	1.004~ 1.013
Intercept	-7.084	2.137	-3.314	0.001	0.001	0.000~ 0.055
Dependent variable = Metabolic Syndrome						

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McFadden R^2 = 0.490
Cox & Snell R^2 = 0.428
Nagelkerke R^2 = 0.629

The model formula can be derived from Table 3 as:

$$log\left(\frac{p}{1-p}\right) = -7.084 + 0.295X_2 + 1.219X_3 + 0.016X_6 - 0.097X_7 + 0.008X_8 \quad (3)$$

The final specific analysis reveals that all elements are significant. Moreover, for every 1-unit increase in BMI, the risk of MetS increases by 1.343 times; for every 1-unit increase in Albuminuria, the risk of MetS increases by 3.384 times; for every 1-unit increase in Blood Glucose, the risk of MetS increases by 1.016 times; and for every 1-unit increase in HDL, the risk of MetS decreased by 0.908 times, and for every 1-unit increase in Triglycerides, the risk of MetS increased by 1.008 times. Elevated BMI, proteinuria, blood sugar, and triglycerides increase the risk of MetS, while elevated HDL can reduce the risk. McFadden R2 = 0.490> 0.4 and Cox & Snell R2 = 0.428 indicate good model fitting, Nagelkerke R2 = 0.629> 0.5 indicates that the model has a very strong explanatory power.

3.2 Model Fit and Evaluation

The model evaluation was conducted using the P-value of the likelihood ratio test of the binary Logit regression model and the P-value of the Hosmer-Lemeshow fit test to assess the validity, goodness of fit, and accuracy prediction of the model, as shown in Tables 4, 5, and 6.

Table 4. Second binary logistic regression model likelihood ratio test table

Model	-2 Times the Log-likelihood Value	Chi-square Value	*df*	*p*	AIC Value	BIC Value
Only Intercept	336.631					
Final Model	171.727	164.904	5	0.000	183.727	205.848

In Table 4, $p<0.01$ indicates that this model is also valid. The remaining indicators are intermediate calculation process values and are basically meaningless.

Table 5. Hosmer-Lemeshow Goodness-of-fit Test Table

χ^2	Degrees of Freedom *df*	*p* Value
2.136	8	0.9772

In Table 5, $p> 0.05$, indicating that the model also passed the H-L test, with good model goodness-of-fit.

Table 6. Summary of the accuracy of binary logit regression prediction

		Predicted value		Predicted accurate value	Prediction error value
		0	1		
True value	0	206	13	94.06%	5.94%
	1	22	54	71.05%	28.95%
Total				88.14%	11.86%

In Table 6, the overall prediction accuracy of the research model is 88.14%, and the model fitting situation is acceptable. When the true value is 0, the prediction accuracy rate is 94.06%. In addition, when the true value is 1, the prediction accuracy is 71.05%.

4. Discussion

This study found that BMI has a significant positive impact on MetS, supporting the importance of lean obesity in the Asian population. Although the BMI of some subjects did not meet the obesity standard, the accumulation of visceral fat still significantly increased the risk of MetS, which is consistent with the better correlation between visceral fat volume and MetS components research [8]. However, the influence of waist circumference was not significant and might be related to sample characteristics or measurement errors, which requires further verification.

Moreover, the significant positive effects of Blood Glucose and Triglycerides reflect the core position of insulin resistance and lipid metabolism disorders in MetS [9]. The protective effect (negative influence) of HDL is consistent with its role in lipid transport and anti-inflammation [10]. The significant association of Albuminuria suggests that abnormal renal function may be an early sign of MetS [11]. After eliminating non-significant variables in the optimized model, the predictive efficiency was significantly improved (AIC and BIC decreased), providing a more concise tool for clinical screening. Future research can integrate artificial intelligence technology, consolidate genetic and lifestyle data, and further enhance the accuracy of predictions. However, the small sample size and the fact that they come from a single database may limit the universality of the results. Cross-sectional design cannot infer causal relationships, and longitudinal studies are needed for verification. In addition, lifestyle factors such as diet and exercise were not included, which may have omitted important confounding variables.

5. Conclusion

This study focused on the unique epidemiological characteristics of metabolic syndrome (MetS) in Asian populations. Based on sample data from 295 Asian adults, the associations between obesity, metabolic indicators, and MetS were analyzed using binary logistic regression models. The effectiveness of core predictive indicators and a screening model specifically tailored for Asian populations with MetS was validated.

The results indicated that BMI, Albuminuria, Blood Glucose, and Triglycerides had significant positive effects on MetS, while HDL demonstrated a significant negative protective effect, with its increased levels associated with a reduced risk of MetS.

After optimizing the model by removing non-significant variables such as waist circumference and UrAlbCr, the goodness-of-fit significantly improved, achieving a prediction accuracy of 88.14%. This provides an efficient and concise tool for clinical screening. These findings identify key targets for metabolic health management in Asian populations and emphasize the necessity of implementing early interventions for individuals with lean obesity, particularly high-risk groups who have a normal BMI but exceed standard waist circumference measures.

The prevention and control of metabolic syndrome in Asian populations are not only crucial for individual health but also play a significant role in reducing the global burden of chronic diseases. Future research should integrate artificial intelligence and multi-omics data to advance the innovative development of precision health management.

Authors Contribution
All the authors contributed equally and their names were listed in alphabetical order.

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