

Metabolic Dysfunction Outweighs Inflammatory Burden in Association with Hyperuricemia: A Cross-Sectional Study in a Large Health Examination Cohort

Xinxin Fan, Yiqing Shen, Wentao Zhu, Yanhua Zhu, Yunzhi Ling 

Department of Clinical Laboratory, Civil Aviation Shanghai Hospital, Shanghai, People's Republic of China

Correspondence: Yunzhi Ling, Department of Clinical Laboratory, Civil Aviation Shanghai Hospital, No. 398 Hongbaoshi Road, Changning District, Shanghai, 200000, People's Republic of China, Tel +86-18017336065, Email lyz19840126@163.com

Background: Hyperuricemia is a common metabolic abnormality frequently identified during routine health examinations, but the relative contributions of metabolic dysfunction and systemic inflammation remain incompletely understood.

Methods: In this cross-sectional study, data from individuals undergoing routine health examinations were analyzed. Inflammatory burden was assessed using the neutrophil-to-high-density lipoprotein cholesterol ratio (NHR), and metabolic dysfunction was assessed using the triglyceride-glucose (TyG) index. Associations with hyperuricemia were evaluated using multivariable logistic regression, restricted cubic spline analyses, joint effect models, interaction testing, and subgroup analyses by sex and age.

Results: Among 7959 participants included in the NHR analysis, 1398 (17.6%) had hyperuricemia. A metabolic subcohort of 4193 participants with complete triglyceride, fasting glucose, and covariate data was included in TyG-related analyses, among whom 781 (18.6%) had hyperuricemia. Each 1-SD increase in NHR was associated with hyperuricemia after multivariable adjustment (OR 1.16, 95% CI 1.09–1.25), whereas neutrophil percentage alone was not independently associated (OR 0.97, 95% CI 0.91–1.04). The TyG index showed a stronger association with hyperuricemia (OR 1.60, 95% CI 1.46–1.77). In models including both indices, the association between NHR and hyperuricemia was attenuated (OR 1.00, 95% CI 0.91–1.10), whereas TyG remained robust. Joint analyses showed that the high NHR/high TyG group had the highest risk of hyperuricemia (OR 2.61, 95% CI 2.01–3.39). Associations were generally consistent across sex and age strata.

Conclusion: Metabolic dysfunction appears to have a stronger association with hyperuricemia than inflammatory burden in routine health examination populations. The apparent association between inflammatory burden and hyperuricemia may depend largely on underlying metabolic abnormalities. However, the cross-sectional design precludes causal inference.

Keywords: hyperuricemia, triglyceride-glucose index, neutrophil-to-high-density lipoprotein cholesterol ratio, metabolic dysfunction, systemic inflammation, health examination

Introduction

Hyperuricemia (HUA) is a common metabolic abnormality and an established risk factor for gout, chronic kidney disease, cardiovascular disease, and metabolic syndrome.^{1,2} In China, hyperuricemia has become an increasingly relevant public health concern. A comprehensive meta-analysis reported a pooled prevalence of 17.4% in mainland China, with a higher prevalence in men than in women.³ Health examination populations may have even higher prevalence estimates in some regions, reflecting differences in urbanization, age structure, lifestyle, and cardiometabolic risk profiles.⁴ These data support the need to characterize readily measurable risk indicators for HUA in routine health examination settings.

Beyond disturbances in purine metabolism, hyperuricemia is closely linked to both metabolic dysfunction and chronic low-grade inflammation. Insulin resistance, dyslipidemia, and impaired glucose metabolism may influence uric acid production and renal excretion.^{5–8} Meanwhile, inflammation may contribute to endothelial dysfunction and altered renal

handling of urate. Traditional inflammatory markers in this study refer to single hematologic inflammatory measures, such as leukocyte-related indices and neutrophil percentage; however, these markers may be insufficient to capture the broader inflammatory and lipid-related milieu associated with HUA.

Recently, composite indices integrating multiple biological pathways have been proposed as more informative markers of cardiometabolic risk. The neutrophil-to-high-density lipoprotein cholesterol ratio (NHR), which combines an inflammatory component with a protective lipid fraction, reflects systemic inflammation, dyslipidemia, and oxidative stress. Elevated NHR has been associated with cardiovascular and metabolic diseases.^{9,10} HDL also has recognized anti-inflammatory properties.^{11,12} However, the relationship of NHR with HUA and its incremental value beyond metabolic dysfunction remain incompletely defined.

In parallel, the triglyceride-glucose (TyG) index has been widely used as a surrogate marker of insulin resistance and metabolic dysfunction.¹³ Accumulating evidence supports a positive association between TyG and HUA in Chinese and other populations.^{14–17} A recent prospective cohort study further examined links among exercise, inflammation, metabolic health, and HUA, using multiple inflammatory and metabolic indicators.¹⁸ However, the relative contribution of NHR compared with TyG, and whether the association between NHR and HUA persists after accounting for TyG, remain clinically relevant questions in health examination practice.

Therefore, in a large cohort of individuals undergoing routine health examinations, we aimed to compare the relative associations of inflammatory burden and metabolic dysfunction with HUA. Specifically, we evaluated the association of NHR with HUA in comparison with traditional inflammatory markers, characterized the dose-response relationships of NHR and TyG with HUA, and examined their independent, joint, and subgroup associations to clarify whether inflammatory burden provides information beyond metabolic dysfunction.

Materials and Methods

Study Design and Population

This cross-sectional study was conducted using data from individuals undergoing routine health examinations at a single health examination center. A total of 8433 participants with serum uric acid measurements were initially identified. After excluding participants with missing data on key inflammatory or clinical covariates, 7959 participants were included in analyses involving inflammatory indices, including NHR. Because triglyceride and fasting glucose measurements were included only in selected health examination packages, TyG-related analyses were restricted to participants with complete triglyceride, fasting glucose, and covariate data, resulting in a metabolic subcohort of 4193 participants.

Data Collection and Laboratory Measurements

Demographic information, including age and sex, was collected at the time of examination. Venous blood samples were obtained after overnight fasting and analyzed using standard laboratory procedures at the certified clinical laboratory of the health examination center. Serum uric acid, triglycerides, fasting plasma glucose, HDL-C, total cholesterol, alanine aminotransferase (ALT), aspartate aminotransferase (AST), creatinine, blood urea nitrogen (BUN), white blood cell count, hemoglobin, platelet count, neutrophil percentage, lymphocyte percentage, glycated hemoglobin, and low-density lipoprotein cholesterol were extracted where available.

Data on body mass index, blood pressure, smoking status, alcohol consumption, dietary habits, physical activity, urate-lowering medication, lipid-lowering medication, glucose-lowering medication, gout symptoms, and pain scores were not available in the current dataset and therefore could not be included in the multivariable models.

Definitions of Variables

Hyperuricemia was identified according to the laboratory uric acid flag recorded in the health examination database, which was based on sex-specific serum uric acid reference intervals. NHR was calculated as neutrophil percentage (%) divided by HDL-C concentration (mmol/L). The TyG index was calculated as $\ln [\text{triglycerides (mg/dL)} \times \text{fasting glucose (mg/dL)} / 2]$. Because triglycerides and fasting glucose were recorded in mmol/L, triglycerides were multiplied by 88.57

and fasting glucose by 18.0 before TyG calculation. For joint effect analyses, NHR and TyG were dichotomized according to their median values and classified into four combined categories.

Estimated glomerular filtration rate (eGFR) was calculated from age, sex, and serum creatinine using the 2021 CKD-EPI creatinine equation and was used in sensitivity analysis for renal function staging.

Statistical Analysis

Continuous variables were assessed for distributional characteristics. Normally distributed variables are presented as mean $\pm$ standard deviation and compared using Student's *t*-test. Skewed variables are presented as median and interquartile range and compared using the Mann–Whitney *U*-test. Categorical variables are presented as counts and percentages and compared using the chi-square test.

Multivariable logistic regression models were used to evaluate associations between inflammatory and metabolic indices and HUA. Odds ratios (ORs) and 95% confidence intervals (CIs) were estimated per 1-standard deviation increase in each index. Model 1 was unadjusted; Model 2 was adjusted for age and sex; Model 3 was further adjusted for ALT, AST, creatinine, BUN, white blood cell count, hemoglobin, and platelet count.

Dose-response relationships were assessed using restricted cubic spline regression with internal knots placed at the 35th and 65th percentiles and boundary knots at the 5th and 95th percentiles of the exposure distribution. The odds ratio was normalized to 1 at the median of the exposure. Joint effects of NHR and TyG were evaluated using combined exposure categories. Multiplicative interaction between NHR and TyG was assessed by including a cross-product term in multivariable logistic regression. Subgroup analyses were performed by sex and age group (<60 and $\geq$ 60 years), and interaction terms were used to evaluate heterogeneity across subgroups. Sensitivity analyses included comparison of participants included in and excluded from the TyG analysis and additional adjustment for eGFR category. Stratified restricted cubic spline analyses were also performed by sex and age group as supplementary analyses.

Results

Study Population and TyG Subcohort

A total of 8433 individuals undergoing routine health examinations were initially identified. After excluding participants with missing inflammatory or clinical covariates, 7959 individuals were included in the NHR analysis cohort, among whom 1398 (17.6%) had HUA and 6561 (82.4%) did not. A metabolic subcohort of 4193 participants with complete triglyceride, fasting glucose, and covariate data was included in TyG-related analyses, among whom 781 (18.6%) had HUA. Compared with participants excluded from the TyG analysis, those included were younger but had broadly similar sex distribution; these differences were considered in adjusted and sensitivity analyses ([Supplementary Table S1](#)). The participant selection process is shown in [Figure 1](#).

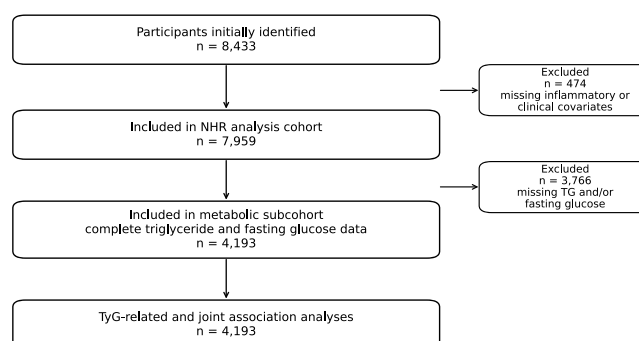


Figure 1 Flowchart of the study population. A total of 8433 participants undergoing routine health examination were initially identified. After excluding 474 participants with missing inflammatory or clinical covariates, 7959 participants were included in the NHR analysis cohort. Among them, 4193 participants with complete triglyceride and fasting glucose data were included in TyG-related and joint association analyses.

Baseline Characteristics According to Hyperuricemia Status

Baseline characteristics stratified by HUA status are presented in Table 1. Participants with HUA were more likely to be male, had higher serum uric acid levels, and showed higher levels of several hematologic, hepatic, renal, and lipid-related indices. NHR was higher in participants with HUA, whereas neutrophil percentage alone did not differ significantly between groups.

Associations of Inflammatory Markers with Hyperuricemia

The associations between inflammatory indices and HUA are summarized in Table 2. In the fully adjusted model, each 1-SD increase in NHR was associated with a higher risk of HUA (OR 1.16, 95% CI 1.09–1.25), whereas neutrophil percentage was not independently associated with HUA (OR 0.97, 95% CI 0.91–1.04). HDL-C showed an inverse association with HUA (OR 0.75, 95% CI 0.69–0.81). Quartile-based associations between NHR and HUA are shown in Figure 2.

Associations of Metabolic Dysfunction and Joint Exposure Patterns

The independent, joint, and interaction associations of NHR and TyG with HUA are summarized in Table 3 and Figure 3. Within the TyG subcohort, each 1-SD increase in TyG was strongly associated with HUA (OR 1.60, 95% CI 1.46–1.77).

Table 1 Baseline Characteristics of Participants According to Hyperuricemia Status

Characteristics	Non-HUA (n = 6561)	HUA (n = 1398)	P value
Age, years	54.56 ± 15.57	52.20 ± 16.37	<0.001
Male, n (%)	3537 (53.9%)	980 (70.1%)	<0.001
Uric acid, μmol/L	311.13 ± 60.70	455.90 ± 58.33	<0.001
White blood cell count, ×10 ⁹ /L	5.81 (4.95–6.88)	6.38 (5.48–7.45)	<0.001
Neutrophil proportion, %	54.48 ± 8.30	54.78 ± 7.75	0.200
Lymphocyte proportion, %	35.46 ± 8.01	35.00 ± 7.39	0.037
Hemoglobin, g/L	143.78 ± 14.65	150.00 ± 13.96	<0.001
Platelet count, ×10 ⁹ /L	235.00 (199.00–274.00)	242.00 (206.00–280.75)	<0.001
Alanine aminotransferase, U/L	18.10 (13.50–25.20)	23.90 (16.73–36.60)	<0.001
Aspartate aminotransferase, U/L	21.00 (18.00–25.00)	23.00 (19.00–29.00)	<0.001
Creatinine, μmol/L	68.00 (58.00–79.00)	78.00 (68.00–88.00)	<0.001
eGFR, mL/min/1.73 m ²	100.31 ± 14.54	95.65 ± 18.79	<0.001
Blood urea nitrogen, mmol/L	5.20 (4.40–6.10)	5.50 (4.70–6.50)	<0.001
HDL cholesterol, mmol/L	1.37 (1.18–1.61)	1.24 (1.08–1.43)	<0.001
Total cholesterol, mmol/L	5.02 (4.35–5.72)	5.25 (4.61–5.96)	<0.001
Triglycerides, mmol/L	1.09 (0.78–1.59)	1.60 (1.13–2.29)	<0.001
Fasting glucose, mmol/L	5.09 (4.82–5.41)	5.17 (4.89–5.49)	<0.001
NHR	39.54 (32.17–47.63)	43.61 (36.41–51.95)	<0.001
TyG index	8.40 ± 0.52	8.76 ± 0.53	<0.001

Notes: Data are presented as mean ± standard deviation, median (interquartile range), or n (%), as appropriate. P values were calculated using Student's *t*-test, Mann–Whitney *U*-test, or chi-square test, as appropriate. For variables with incomplete measurements, summary statistics were calculated using available data; TyG-related variables were available in the metabolic subcohort.

Table 2 Associations of Inflammatory Indices with Hyperuricemia

Exposure	Model 1 OR (95% CI)	P value	Model 2 OR (95% CI)	P value	Model 3 OR (95% CI)	P value
Neutrophil proportion (%)	1.04 (0.98–1.10)	0.220	1.03 (0.98–1.10)	0.257	0.97 (0.91–1.04)	0.429
HDL-C (mmol/L)	0.62 (0.58–0.66)	<0.001	0.68 (0.63–0.73)	<0.001	0.75 (0.69–0.81)	<0.001
NHR (%/mmol/L)	1.39 (1.31–1.47)	<0.001	1.28 (1.21–1.36)	<0.001	1.16 (1.09–1.25)	<0.001

Notes: ORs are presented per 1-SD increase. Model 1 was unadjusted. Model 2 was adjusted for age and sex. Model 3 was further adjusted for ALT, AST, creatinine, BUN, white blood cell count, hemoglobin, and platelet count.

When NHR and TyG were included simultaneously, the association between NHR and HUA was attenuated (OR 1.00, 95% CI 0.91–1.10), whereas TyG remained robustly associated (OR 1.61, 95% CI 1.45–1.77). Joint exposure analysis showed that compared with the low NHR/low TyG group, the high NHR/high TyG group had the highest risk of HUA (OR 2.61, 95% CI 2.01–3.39), followed by the low NHR/high TyG group (OR 2.35, 95% CI 1.77–3.12), whereas the high NHR/low TyG group did not show a statistically significant increase in risk (OR 1.14, 95% CI 0.84–1.56). The continuous NHR-by-TyG interaction term was statistically significant ($P=0.010$), although the categorical interaction term was not significant ($P=0.887$).

Subgroup and Sensitivity Analyses

In sex-stratified analyses, both NHR and TyG were associated with HUA in men and women, with stronger associations observed in women. For NHR, the adjusted ORs were 1.11 (95% CI 1.03–1.20) in men and 1.40 (95% CI 1.22–1.60) in women (P for interaction<0.001). For TyG, the adjusted ORs were 1.49 (95% CI 1.34–1.66) in men and 2.04 (95% CI 1.66–2.52) in women (P for interaction<0.001). In age-stratified analyses, TyG remained associated with HUA in both age groups, with adjusted ORs of 1.53 (95% CI 1.37–1.71) in participants younger than 60 years and 1.93 (95% CI 1.58–2.36) in those aged 60 years or older. The sex- and age-stratified logistic regression results are summarized in [Supplementary Table S2](#). Sensitivity analyses using eGFR category instead of creatinine and BUN produced similar findings for NHR and TyG ([Supplementary Table S3](#)). Stratified restricted cubic spline analyses are shown in [Supplementary Figures S1–S4](#). The TyG-HUA association remained consistently positive across sex and age strata, whereas the NHR-HUA pattern was weaker and varied across strata, particularly in men and participants aged ≥ 60 years.

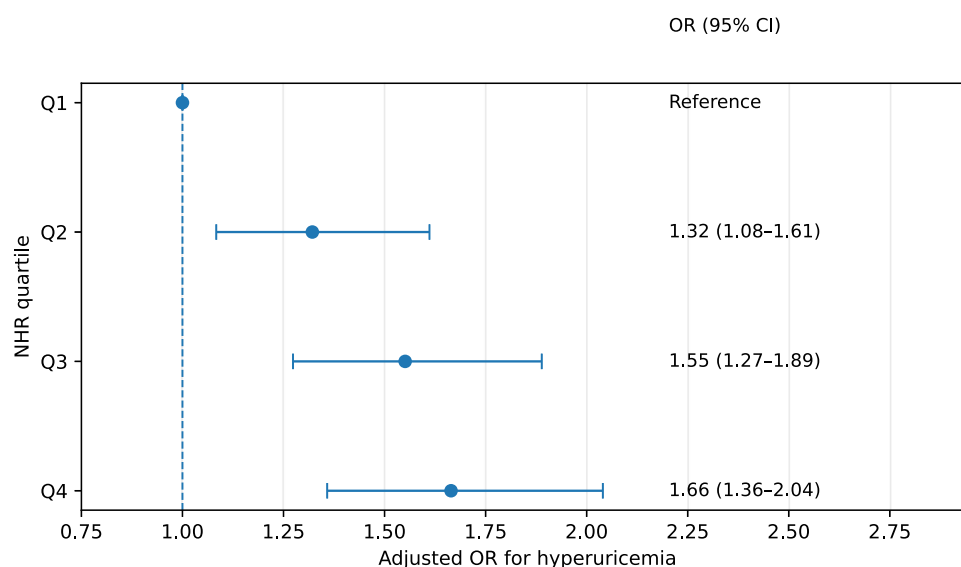


Figure 2 Association between NHR quartiles and hyperuricemia. Adjusted odds ratios (ORs) and 95% confidence intervals (CIs) for hyperuricemia across quartiles of the neutrophil-to-high-density lipoprotein cholesterol ratio (NHR). Analysis was conducted in the NHR analysis cohort ($n = 7959$). Multivariable models were adjusted for age, sex, alanine aminotransferase, aspartate aminotransferase, creatinine, blood urea nitrogen, white blood cell count, hemoglobin, and platelet count.

Table 3 Independent, Joint, and Interaction Associations of NHR and TyG with Hyperuricemia in the Metabolic Subcohort

A. Independent and interaction associations						
Exposure		OR (95% CI)		P value		
NHR, per 1-SD		1.13 (1.03–1.24)		0.009		
NHR adjusted for TyG		1.00 (0.91–1.10)		0.974		
TyG, per 1-SD		1.60 (1.46–1.77)		<0.001		
TyG adjusted for NHR		1.61 (1.45–1.77)		<0.001		
NHR × TyG, continuous interaction		0.90 (0.83–0.97)		0.010		
B. Joint associations						
NHR/TyG group		n	HUA cases	HUA prevalence	OR (95% CI)	P value
Low NHR/Low TyG		1318	108	8.2%	1.00 (reference)	—
High NHR/Low TyG		778	96	12.3%	1.14 (0.84–1.56)	0.391
Low NHR/High TyG		778	171	22.0%	2.35 (1.77–3.12)	<0.001
High NHR/High TyG		1319	406	30.8%	2.61 (2.01–3.39)	<0.001

Notes: Analyses were conducted in participants with complete triglyceride, fasting glucose, NHR, and covariate data (n=4193). Models were adjusted for age, sex, ALT, AST, creatinine, BUN, white blood cell count, hemoglobin, and platelet count. NHR and TyG were dichotomized at their respective median values.

Dose-Response Relationships

Restricted cubic spline analyses demonstrated positive dose-response relationships of NHR and TyG with HUA (Figures 4 and 5). NHR showed a significant overall association with HUA (P-overall = 0.002), without statistically significant evidence of nonlinearity (P-nonlinear = 0.083). The TyG index showed a strong overall association with HUA

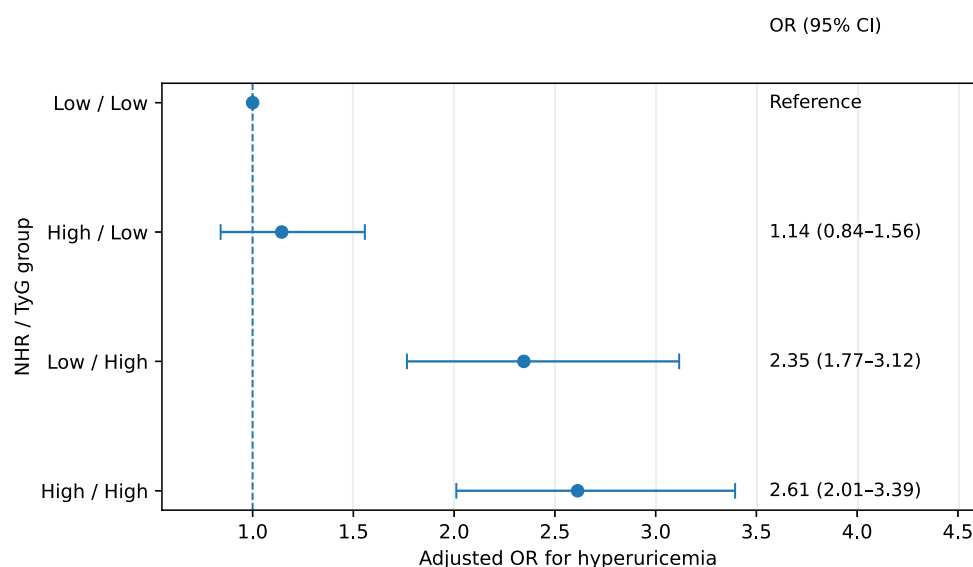


Figure 3 Joint association of NHR and TyG index with hyperuricemia. Adjusted odds ratios (ORs) and 95% confidence intervals (CIs) for hyperuricemia according to combined categories of NHR and triglyceride-glucose (TyG) index. Analysis was conducted in the metabolic subcohort with complete triglyceride and fasting glucose data (n = 4193). The low NHR/low TyG group served as the reference. Models were adjusted for age, sex, liver and renal function markers, and hematological parameters.

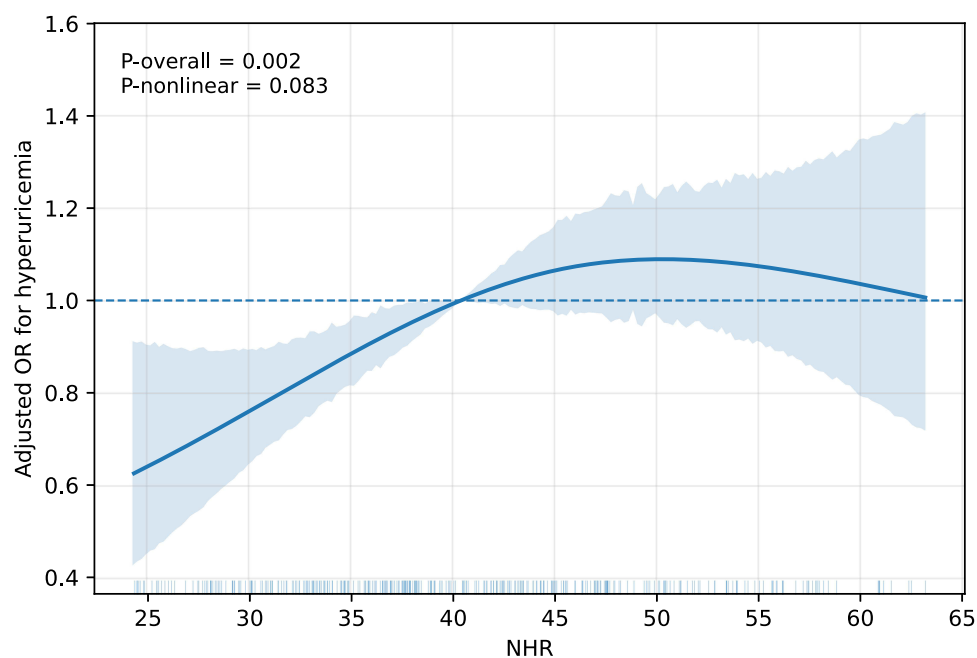


Figure 4 Restricted cubic spline analysis of the association between NHR and hyperuricemia. Restricted cubic splines with internal knots placed at the 35th and 65th percentiles and boundary knots at the 5th and 95th percentiles of NHR were fitted in a multivariable logistic regression model. Analysis was conducted in the NHR analysis cohort ($n = 7959$). The solid line represents the adjusted odds ratio (OR) of hyperuricemia across the continuous range of NHR, and the shaded area indicates the 95% confidence interval. The OR was normalized to 1 at the median NHR. The model was adjusted for age, sex, alanine aminotransferase, aspartate aminotransferase, creatinine, blood urea nitrogen, white blood cell count, hemoglobin, and platelet count.

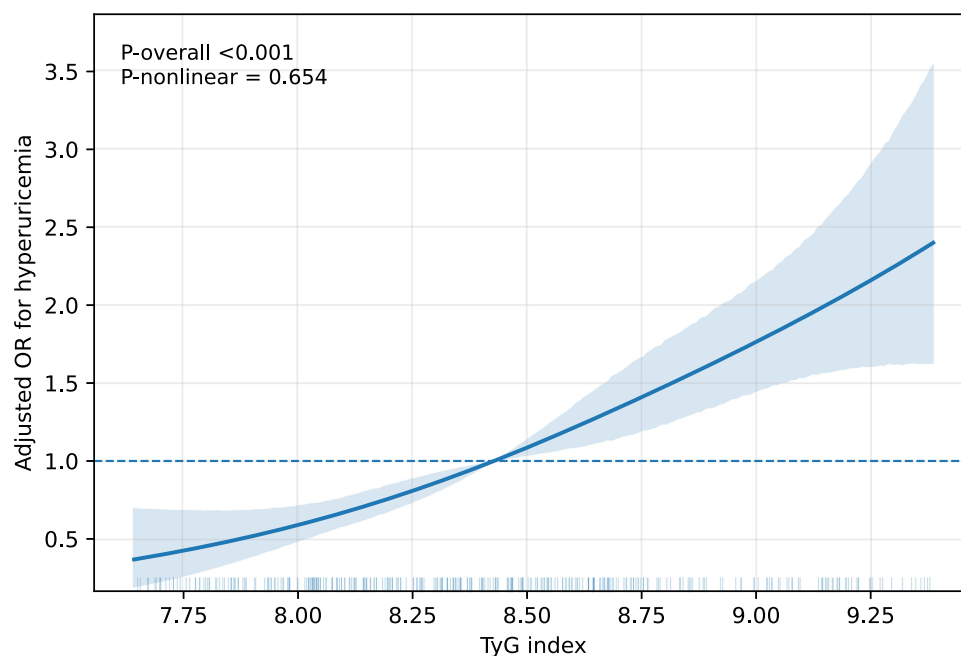


Figure 5 Restricted cubic spline analysis of the association between TyG index and hyperuricemia. Restricted cubic splines with internal knots placed at the 35th and 65th percentiles and boundary knots at the 5th and 95th percentiles of the TyG index were fitted in a multivariable logistic regression model. Analysis was conducted in the metabolic subcohort with complete triglyceride and fasting glucose data ($n = 4193$). The solid line represents the adjusted odds ratio (OR) of hyperuricemia across the continuous range of TyG, and the shaded area indicates the 95% confidence interval. The OR was normalized to 1 at the median TyG. The model was adjusted for age, sex, alanine aminotransferase, aspartate aminotransferase, creatinine, blood urea nitrogen, white blood cell count, hemoglobin, and platelet count.

(P -overall < 0.001), also without evidence of significant nonlinearity (P -nonlinear = 0.654). These findings support a more consistent dose-response association for TyG than for NHR.

Discussion

The principal finding of this study is that metabolic dysfunction appears to be more strongly associated with HUA than inflammatory burden in a large health examination population. Although NHR was positively associated with HUA, this association was substantially attenuated after accounting for TyG, whereas TyG remained robustly associated. Joint exposure analysis further showed that elevated NHR without elevated TyG did not confer a statistically significant increase in HUA risk. These findings support a metabolic-dominant risk profile for HUA in routine health examination settings.

Our findings are broadly consistent with previous studies reporting positive associations between TyG and HUA in Chinese and other populations.^{14–17} A recent prospective cohort study by He et al examined exercise effects on the link between inflammation, metabolic health, and HUA and included a larger sample size, a cohort design, BMI, lifestyle variables, eGFR, and several inflammatory indices.¹⁸ The present study differs in its focus on a head-to-head comparison between NHR and TyG in a routine health examination cohort and on the attenuation of NHR after adjustment for TyG. Therefore, our study does not aim to replace prior cohort evidence but adds a clinically simple comparison of routinely available inflammatory-lipid and metabolic indices.

The stronger association between TyG and HUA is biologically plausible. TyG is a surrogate marker of insulin resistance, which may promote renal tubular urate reabsorption and reduce urate excretion. Hypertriglyceridemia and impaired glucose metabolism may also reflect energy and purine metabolic disturbances that increase uric acid production. These mechanisms^{19,20} provide a plausible explanation for the sustained association between TyG and HUA across adjusted, joint, subgroup, and sensitivity analyses.

The attenuation of NHR after adjustment for TyG suggests that the NHR-HUA association may be partly dependent on underlying metabolic dysfunction. Insulin resistance and dyslipidemia may act upstream of both HUA and low-grade inflammatory changes. NHR incorporates neutrophil percentage and HDL-C, and therefore may reflect downstream inflammatory and lipid-related alterations secondary to metabolic dysfunction rather than an independent pathway. Recent studies also support associations of systemic inflammation-related indices and lipid ratios with HUA.^{21–23} However, because the study is cross-sectional, this interpretation should be viewed as hypothesis-generating rather than causal.

The subgroup analyses indicated stronger associations of both NHR and TyG with HUA in women. This finding is consistent with known sex differences in uric acid metabolism and HUA prevalence. Estrogen-related urate clearance, menopausal changes, body composition, and cardiometabolic risk patterns may modify associations between metabolic indices and HUA. These findings suggest that sex-specific risk interpretation may be useful in health examination practice, although further validation is required.

From a clinical perspective, the distinction between metabolic-dominant and inflammation-related risk profiles may help guide preventive strategies. Individuals with elevated TyG, particularly those with concurrent NHR elevation, may represent a priority group for lifestyle and metabolic risk management. In contrast, isolated NHR elevation without metabolic dysfunction may have limited value for identifying HUA risk. These findings support the use of routinely available laboratory indicators for early risk stratification in health examination settings.

It is also important to distinguish HUA from symptomatic gout. Serum uric acid level does not necessarily correlate with pain severity or gout flare activity, which are more directly related to monosodium urate crystal deposition and inflammatory activation, including NLRP3 inflammasome-mediated IL-1 β pathways. Because gout symptoms, pain scores, crystal deposition, and inflammatory cytokines were unavailable in this dataset, the present findings should be interpreted as risk stratification for HUA rather than prediction of symptomatic gout or pain burden.

Limitations

Several limitations should be considered. First, the cross-sectional design precludes causal inference, and longitudinal studies are needed to clarify temporal relationships. Second, although extensive adjustment was performed, residual

confounding cannot be excluded. Information on body mass index, blood pressure, smoking status, alcohol consumption, diet, physical activity, medication use, gout history, pain symptoms, and inflammatory cytokines was unavailable. Third, TyG-related analyses were restricted to a subcohort with complete triglyceride and fasting glucose data. Although we compared included and excluded participants and performed adjusted analyses, selection bias cannot be fully excluded. Fourth, this was a single-center health examination study, and external validation in other populations is needed.

Future Perspectives

Future studies should validate these findings in prospective cohorts with repeated uric acid measurements, detailed lifestyle and medication data, BMI, blood pressure, and measured eGFR. Comparisons among TyG, NHR, NHHR, SII, SIRI, and obesity-related TyG indices may further clarify the relative roles of metabolic dysfunction and systemic inflammation. Risk prediction models incorporating routine laboratory indicators may be developed for health examination settings, and intervention studies are needed to determine whether improving insulin resistance and dyslipidemia can reduce incident HUA, gout, or kidney-related outcomes.

Conclusion

In conclusion, both inflammatory burden and metabolic dysfunction were associated with HUA in this health examination cohort, but metabolic dysfunction showed a stronger and more consistent association. The relationship between NHR and HUA appeared to be largely influenced by metabolic status, whereas TyG remained robustly associated across analyses. These findings support the potential value of routine metabolic and inflammatory indices, particularly TyG, in identifying individuals at increased risk of HUA in general health examination settings. Causal inference requires prospective validation.

Data Sharing Statement

The data used in this study are not publicly available because they were derived from routine health examination records and may contain potentially identifiable information, but they are available from the corresponding author on reasonable request and subject to institutional approval.

Ethics Statement

This retrospective study was conducted in accordance with the Declaration of Helsinki. The study protocol was reviewed and approved by the Ethics Committee of Civil Aviation Shanghai Hospital (Approval No. 2026-03). The requirement for informed consent was waived by the ethics committee because the study used anonymized data collected during routine health examination programs.

Disclosure

The authors report no conflicts of interest in this work.

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